



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:15 am GMT

PDB ID : 1QGH
Title : THE X-RAY STRUCTURE OF THE UNUSUAL DODECAMERIC FER-
RITIN FROM LISTERIA INNOCUA, REVEALS A NOVEL INTERSUB-
UNIT IRON BINDING SITE.
Authors : Ilari, A.; Stefanini, S.; Chiancone, E.; Tsernoglou, D.
Deposited on : 1999-04-27
Resolution : 2.35 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

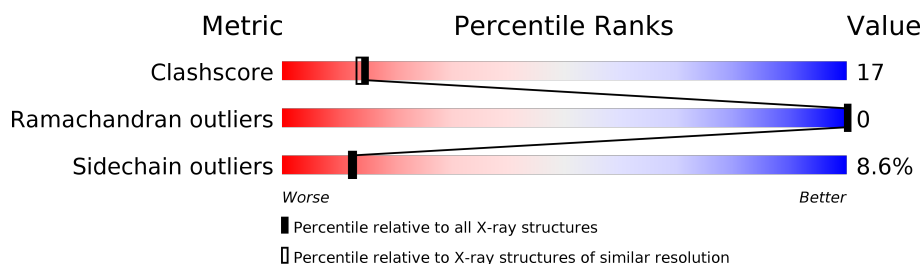
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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))
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)

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 ≥ 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	156	
1	B	156	
1	C	156	
1	D	156	
1	E	156	
1	F	156	
1	G	156	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	H	156	<div><div></div><div>67%25%<div><div></div><div></div><div></div></div></div></div>
1	I	156	<div><div></div><div>63%27%5%<div><div></div><div></div><div></div></div></div></div>
1	J	156	<div><div></div><div>68%25%<div><div></div><div></div><div></div></div></div></div>
1	K	156	<div><div></div><div>65%24%8%<div><div></div><div></div><div></div></div></div></div>
1	L	156	<div><div></div><div>67%25%<div><div></div><div></div><div></div></div></div></div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15155 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 NON-HEME IRON-CONTAINING FERRITIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	150	Total	C	N	O	S	32	0	0
			1222	784	196	235	7			
1	B	150	Total	C	N	O	S	57	0	0
			1222	784	196	235	7			
1	C	150	Total	C	N	O	S	44	0	0
			1222	784	196	235	7			
1	D	150	Total	C	N	O	S	47	0	0
			1222	784	196	235	7			
1	E	150	Total	C	N	O	S	46	0	0
			1222	784	196	235	7			
1	F	150	Total	C	N	O	S	42	0	0
			1222	784	196	235	7			
1	G	150	Total	C	N	O	S	41	0	0
			1222	784	196	235	7			
1	H	150	Total	C	N	O	S	34	0	0
			1222	784	196	235	7			
1	I	150	Total	C	N	O	S	45	0	0
			1222	784	196	235	7			
1	J	150	Total	C	N	O	S	44	0	0
			1222	784	196	235	7			
1	K	150	Total	C	N	O	S	43	0	0
			1222	784	196	235	7			
1	L	150	Total	C	N	O	S	50	0	0
			1222	784	196	235	7			

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Fe	0	0
			1	1		
2	J	1	Total	Fe	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total 1	Fe 1	0	0
2	K	1	Total 1	Fe 1	0	0
2	E	1	Total 1	Fe 1	0	0
2	H	1	Total 1	Fe 1	0	0
2	B	1	Total 1	Fe 1	0	0
2	I	1	Total 1	Fe 1	0	0
2	C	1	Total 1	Fe 1	0	0
2	A	1	Total 1	Fe 1	0	0
2	L	1	Total 1	Fe 1	0	0
2	F	1	Total 1	Fe 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total 38	O 38	0	0
3	B	22	Total 22	O 22	0	0
3	C	36	Total 36	O 36	0	0
3	D	28	Total 28	O 28	0	0
3	E	50	Total 50	O 50	0	0
3	F	42	Total 42	O 42	0	0
3	G	54	Total 54	O 54	0	0
3	H	44	Total 44	O 44	0	0
3	I	33	Total 33	O 33	0	0

Continued on next page...

Continued from previous page...

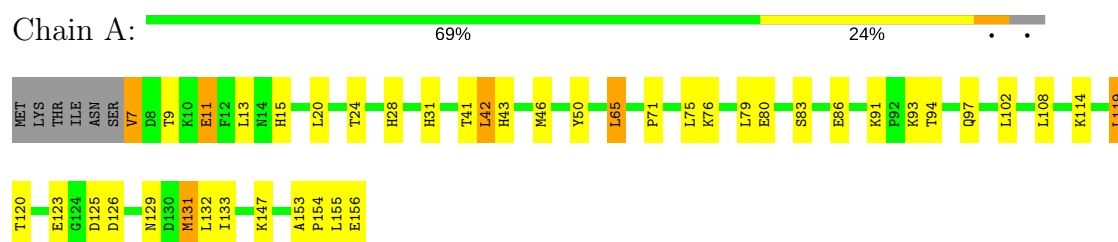
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	46	Total	O	0	0
			46	46		
3	K	41	Total	O	0	0
			41	41		
3	L	45	Total	O	0	0
			45	45		

3 Residue-property plots [i](#)

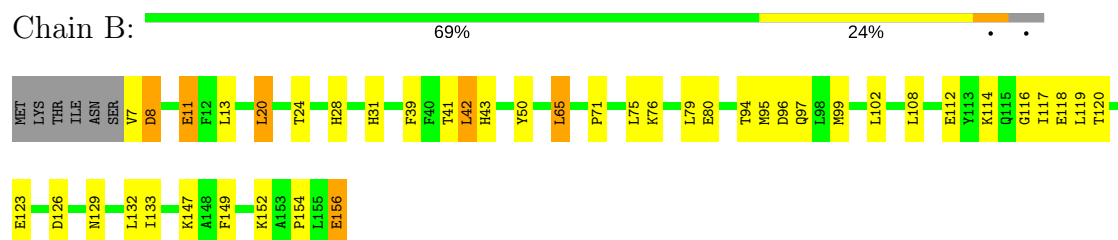
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

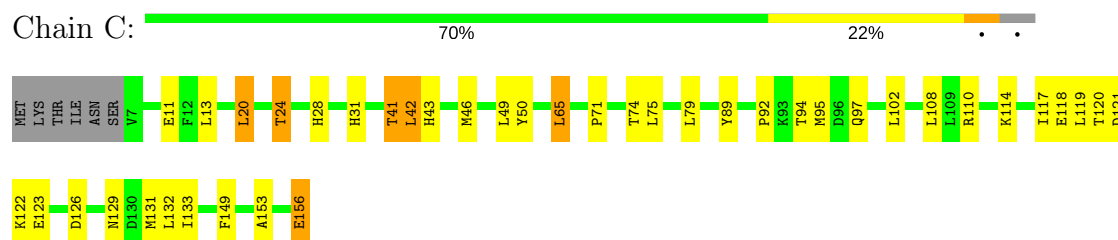
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN



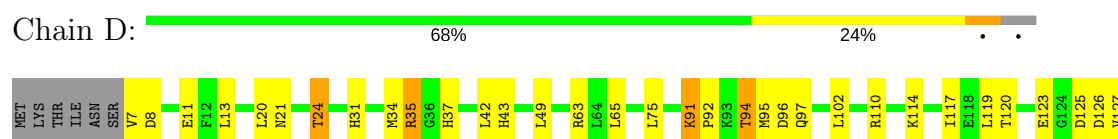
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN

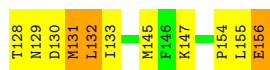


• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN



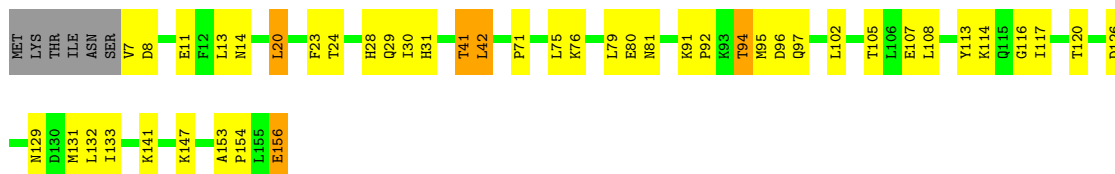
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN





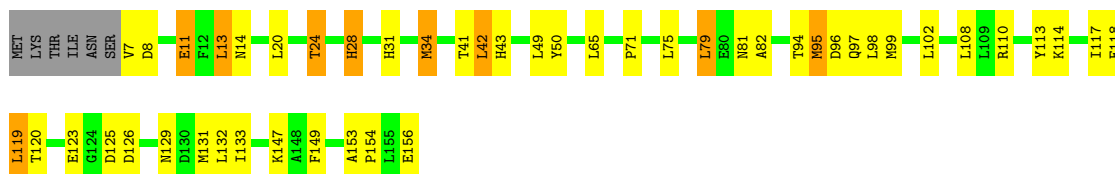
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN

Chain E: 67% 26%



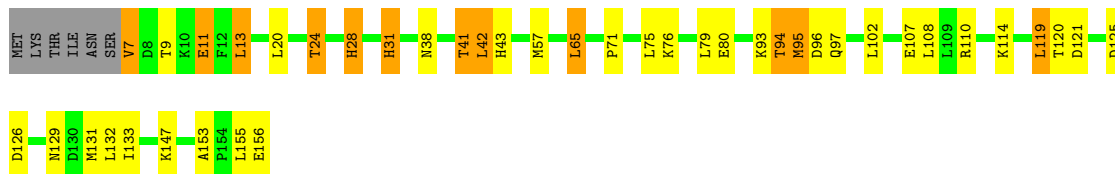
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN

Chain F: 65% 25% 6%



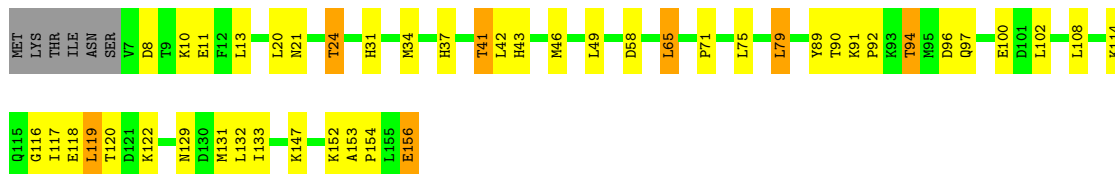
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN

Chain G: 69% 19% 8%



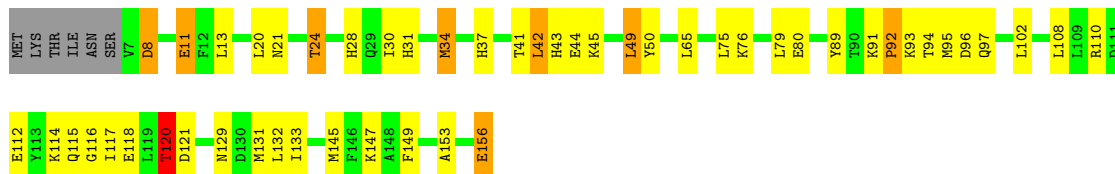
• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN

Chain H: 67% 25%

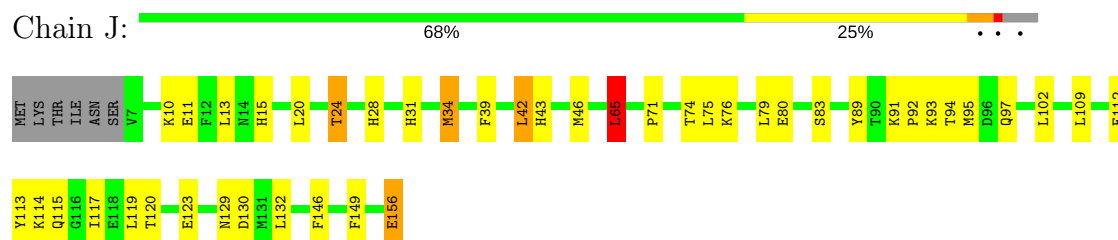


• Molecule 1: NON-HEME IRON-CONTAINING FERRITIN

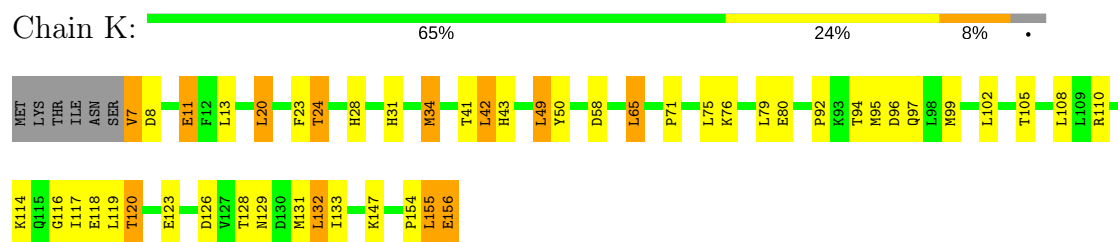
Chain I: 63% 27% 5%



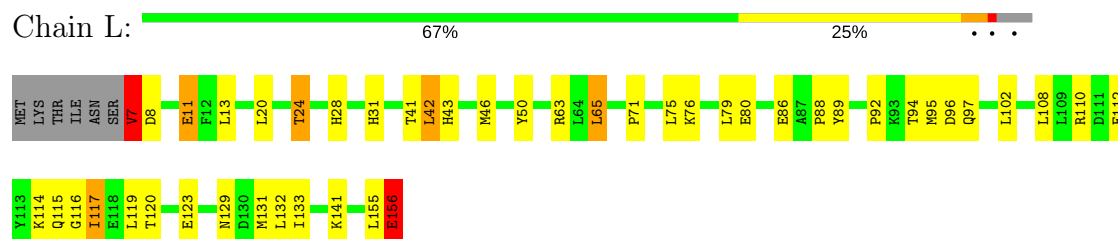
- Molecule 1: NON-HEME IRON-CONTAINING FERRITIN



- Molecule 1: NON-HEME IRON-CONTAINING FERRITIN



- Molecule 1: NON-HEME IRON-CONTAINING FERRITIN



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.54Å 137.50Å 173.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.35	Depositor
% Data completeness (in resolution range)	91.0 (10.00-2.35)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.219 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	15155	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FE

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	0.71	0/1249	1.15	5/1684 (0.3%)
1	B	0.72	0/1249	1.19	1/1684 (0.1%)
1	C	0.70	0/1249	1.14	6/1684 (0.4%)
1	D	0.72	0/1249	1.24	9/1684 (0.5%)
1	E	0.70	0/1249	1.17	7/1684 (0.4%)
1	F	0.68	0/1249	1.20	7/1684 (0.4%)
1	G	0.70	0/1249	1.13	5/1684 (0.3%)
1	H	0.71	0/1249	1.17	6/1684 (0.4%)
1	I	0.71	0/1249	1.21	8/1684 (0.5%)
1	J	0.72	1/1249 (0.1%)	1.20	5/1684 (0.3%)
1	K	0.72	0/1249	1.19	9/1684 (0.5%)
1	L	0.73	1/1249 (0.1%)	1.24	8/1684 (0.5%)
All	All	0.71	2/14988 (0.0%)	1.19	76/20208 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	156	GLU	CD-OE1	6.00	1.32	1.25
1	J	156	GLU	C-O	5.67	1.34	1.23

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	156	GLU	CA-C-O	9.79	140.65	120.10
1	L	156	GLU	OE1-CD-OE2	-9.23	112.23	123.30
1	L	7	VAL	O-C-N	-8.84	108.56	122.70
1	D	110	ARG	NE-CZ-NH1	7.78	124.19	120.30
1	I	110	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	I	131	MET	CA-CB-CG	7.03	125.25	113.30
1	C	110	ARG	NE-CZ-NH1	6.74	123.67	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	110	ARG	NE-CZ-NH2	-6.59	117.00	120.30
1	F	79	LEU	CB-CG-CD2	-6.55	99.86	111.00
1	E	31	HIS	N-CA-CB	-6.44	99.00	110.60
1	J	91	LYS	CD-CE-NZ	6.41	126.45	111.70
1	A	125	ASP	CB-CG-OD2	-6.19	112.73	118.30
1	H	34	MET	CG-SD-CE	6.18	110.09	100.20
1	G	131	MET	CB-CA-C	-6.18	98.05	110.40
1	E	30	ILE	CA-C-O	6.17	133.05	120.10
1	K	131	MET	CA-CB-CG	6.12	123.71	113.30
1	F	34	MET	CG-SD-CE	6.11	109.97	100.20
1	D	156	GLU	CB-CA-C	6.10	122.59	110.40
1	H	58	ASP	CB-CG-OD2	6.09	123.78	118.30
1	J	109	LEU	CB-CG-CD2	-6.02	100.77	111.00
1	F	95	MET	CG-SD-CE	6.01	109.82	100.20
1	G	95	MET	CG-SD-CE	5.97	109.75	100.20
1	J	34	MET	CG-SD-CE	5.92	109.67	100.20
1	E	95	MET	CG-SD-CE	5.92	109.67	100.20
1	L	63	ARG	NE-CZ-NH2	5.91	123.25	120.30
1	D	34	MET	CG-SD-CE	5.85	109.55	100.20
1	D	131	MET	CG-SD-CE	5.83	109.53	100.20
1	A	91	LYS	N-CA-C	-5.79	95.36	111.00
1	K	34	MET	CG-SD-CE	5.78	109.44	100.20
1	D	65	LEU	CA-CB-CG	5.77	128.57	115.30
1	A	65	LEU	CA-CB-CG	5.75	128.53	115.30
1	D	35	ARG	NE-CZ-NH2	5.74	123.17	120.30
1	C	131	MET	CB-CA-C	-5.73	98.94	110.40
1	A	65	LEU	CB-CG-CD2	-5.72	101.27	111.00
1	I	34	MET	CG-SD-CE	5.71	109.34	100.20
1	C	65	LEU	CB-CG-CD2	-5.70	101.30	111.00
1	E	20	LEU	CB-CG-CD1	5.66	120.62	111.00
1	C	46	MET	CG-SD-CE	5.65	109.23	100.20
1	K	110	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	K	110	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	L	65	LEU	CB-CG-CD2	-5.52	101.61	111.00
1	E	7	VAL	CB-CA-C	-5.51	100.93	111.40
1	I	49	LEU	CB-CG-CD2	-5.49	101.67	111.00
1	F	65	LEU	CB-CG-CD2	-5.48	101.69	111.00
1	H	46	MET	CG-SD-CE	5.45	108.92	100.20
1	B	65	LEU	N-CA-CB	-5.43	99.53	110.40
1	L	131	MET	CA-CB-CG	5.40	122.49	113.30
1	I	120	THR	N-CA-CB	-5.37	100.10	110.30
1	H	79	LEU	CB-CG-CD2	-5.34	101.92	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	31	HIS	N-CA-CB	-5.34	100.99	110.60
1	G	65	LEU	N-CA-CB	-5.32	99.76	110.40
1	F	110	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	L	7	VAL	N-CA-C	-5.29	96.72	111.00
1	A	131	MET	CB-CA-C	-5.28	99.85	110.40
1	G	110	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	K	131	MET	CB-CA-C	-5.27	99.86	110.40
1	H	131	MET	CG-SD-CE	5.26	108.62	100.20
1	I	65	LEU	N-CA-CB	-5.24	99.93	110.40
1	I	131	MET	CB-CA-C	-5.23	99.95	110.40
1	I	92	PRO	N-CA-C	-5.15	98.71	112.10
1	F	13	LEU	CB-CG-CD1	5.15	119.75	111.00
1	H	131	MET	CA-CB-CG	5.13	122.03	113.30
1	E	131	MET	CA-CB-CG	5.12	122.00	113.30
1	C	131	MET	CG-SD-CE	5.11	108.38	100.20
1	K	119	LEU	CB-CG-CD2	5.11	119.69	111.00
1	K	155	LEU	CA-CB-CG	-5.11	103.54	115.30
1	D	110	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	L	117	ILE	CG1-CB-CG2	-5.09	100.20	111.40
1	J	65	LEU	CB-CG-CD2	-5.09	102.35	111.00
1	E	131	MET	CB-CA-C	-5.07	100.26	110.40
1	D	65	LEU	CB-CG-CD2	-5.03	102.45	111.00
1	F	131	MET	CB-CA-C	-5.03	100.34	110.40
1	K	58	ASP	CB-CG-OD2	5.03	122.83	118.30
1	C	20	LEU	CB-CG-CD1	5.01	119.52	111.00
1	J	130	ASP	CB-CG-OD1	5.01	122.81	118.30
1	K	49	LEU	CB-CG-CD2	-5.00	102.49	111.00

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	1222	0	1186	32	0
1	B	1222	0	1186	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1222	0	1186	33	0
1	D	1222	0	1186	42	0
1	E	1222	0	1186	38	0
1	F	1222	0	1186	53	0
1	G	1222	0	1186	46	0
1	H	1222	0	1186	33	0
1	I	1222	0	1186	46	0
1	J	1222	0	1186	33	0
1	K	1222	0	1186	63	0
1	L	1222	0	1186	38	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	38	0	0	3	0
3	B	22	0	0	0	0
3	C	36	0	0	3	0
3	D	28	0	0	6	0
3	E	50	0	0	7	0
3	F	42	0	0	6	0
3	G	54	0	0	8	0
3	H	44	0	0	3	0
3	I	33	0	0	3	0
3	J	46	0	0	7	0
3	K	41	0	0	10	0
3	L	45	0	0	4	0
All	All	15155	0	14232	477	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 17.

All (477) 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:G:94:THR:HG22	1:G:97:GLN:H	1.11	1.12
1:F:94:THR:HB	1:F:97:GLN:HG3	1.20	1.12
1:F:94:THR:HG22	1:F:96:ASP:N	1.69	1.08
1:F:7:VAL:HG12	1:F:8:ASP:H	1.22	1.04
1:I:94:THR:HB	1:I:97:GLN:HG3	1.40	1.03
1:K:94:THR:HB	1:K:97:GLN:HG3	1.41	1.03
1:D:94:THR:HB	1:D:97:GLN:HG3	1.37	1.03
1:D:147:LYS:HZ2	1:D:156:GLU:HG2	1.29	0.97
1:K:114:LYS:HA	3:K:164:HOH:O	1.64	0.96
1:E:91:LYS:HG2	1:E:92:PRO:HD2	1.46	0.95
1:F:11:GLU:HG2	3:F:172:HOH:O	1.67	0.93
1:D:147:LYS:NZ	1:D:156:GLU:HG2	1.83	0.91
1:K:117:ILE:HD13	1:K:133:ILE:HG12	1.52	0.91
1:F:120:THR:HG22	1:F:129:ASN:HB2	1.51	0.90
1:F:34:MET:HG2	3:F:178:HOH:O	1.71	0.90
1:G:120:THR:HG22	1:G:129:ASN:HB2	1.53	0.90
1:F:94:THR:HG22	1:F:96:ASP:H	1.29	0.88
1:H:100:GLU:HG2	3:H:160:HOH:O	1.71	0.88
1:B:156:GLU:HA	1:B:156:GLU:OE1	1.75	0.86
1:G:94:THR:HG23	3:G:193:HOH:O	1.74	0.86
1:G:120:THR:HG21	1:G:129:ASN:CA	2.05	0.86
1:F:94:THR:CG2	1:F:96:ASP:H	1.89	0.85
1:H:94:THR:HB	1:H:97:GLN:HG3	1.59	0.85
1:G:94:THR:HG22	1:G:97:GLN:N	1.93	0.84
1:K:94:THR:HG22	1:K:96:ASP:N	1.93	0.84
1:F:113:TYR:O	1:F:117:ILE:HG13	1.77	0.83
1:F:82:ALA:HA	3:F:179:HOH:O	1.78	0.83
1:E:91:LYS:CG	1:E:92:PRO:HD2	2.08	0.82
1:F:120:THR:HG21	1:F:129:ASN:N	1.96	0.81
1:I:120:THR:CG2	1:I:129:ASN:HB2	2.11	0.80
1:G:120:THR:CG2	1:G:129:ASN:HB2	2.11	0.80
1:I:120:THR:HG21	1:I:129:ASN:HA	1.62	0.80
1:H:94:THR:HG22	1:H:97:GLN:H	1.47	0.79
1:I:153:ALA:O	1:I:156:GLU:HB2	1.83	0.78
1:E:94:THR:HB	1:E:97:GLN:HG3	1.63	0.78
1:F:94:THR:HB	1:F:97:GLN:CG	2.07	0.78
1:B:94:THR:HG22	1:B:96:ASP:H	1.49	0.77
1:A:7:VAL:HG12	1:A:11:GLU:CB	2.14	0.77
1:H:116:GLY:O	1:H:120:THR:HG22	1.85	0.77
1:L:155:LEU:O	1:L:156:GLU:HB2	1.84	0.77
1:A:7:VAL:HG12	1:A:11:GLU:HB2	1.66	0.76
1:K:120:THR:HG21	1:K:129:ASN:HA	1.67	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:24:THR:HG23	3:L:199:HOH:O	1.85	0.75
1:G:41:THR:HG21	3:G:180:HOH:O	1.85	0.75
1:L:120:THR:HG21	1:L:129:ASN:HA	1.69	0.75
1:E:94:THR:HG22	1:E:97:GLN:H	1.53	0.74
1:C:120:THR:CG2	1:C:129:ASN:HD22	1.99	0.74
1:K:94:THR:HG22	1:K:96:ASP:H	1.51	0.74
1:G:120:THR:HG21	1:G:129:ASN:N	2.03	0.74
1:K:94:THR:CG2	1:K:96:ASP:H	2.02	0.73
1:I:120:THR:HG21	1:I:129:ASN:CA	2.16	0.73
1:K:120:THR:HG21	1:K:129:ASN:CA	2.18	0.72
1:E:29:GLN:NE2	3:E:207:HOH:O	2.13	0.72
1:K:116:GLY:O	1:K:120:THR:HB	1.89	0.72
1:F:7:VAL:HG12	1:F:8:ASP:N	2.01	0.71
1:E:117:ILE:HD13	1:E:133:ILE:HG12	1.70	0.71
1:C:120:THR:HG21	1:C:129:ASN:HA	1.73	0.71
1:A:119:LEU:HD23	1:A:120:THR:HG23	1.71	0.71
1:F:94:THR:HG21	1:F:96:ASP:HB2	1.72	0.70
1:D:31:HIS:CE1	1:D:43:HIS:CE1	2.80	0.70
1:L:117:ILE:O	1:L:120:THR:HG22	1.91	0.70
1:L:120:THR:CG2	1:L:129:ASN:HD22	2.04	0.70
1:E:141:LYS:HD3	3:E:203:HOH:O	1.92	0.69
1:F:114:LYS:O	1:F:118:GLU:HG3	1.92	0.69
1:K:94:THR:CG2	1:K:96:ASP:HB2	2.22	0.69
1:A:7:VAL:CG1	1:A:11:GLU:HB3	2.23	0.69
1:B:117:ILE:O	1:B:120:THR:HG22	1.93	0.69
1:J:94:THR:HG22	1:J:95:MET:N	2.08	0.68
1:B:114:LYS:HE3	1:B:118:GLU:OE2	1.93	0.68
1:D:129:ASN:O	1:D:133:ILE:HG13	1.92	0.68
1:K:42:LEU:HD23	1:K:95:MET:SD	2.33	0.68
1:F:120:THR:CG2	1:F:129:ASN:HB2	2.21	0.68
1:I:89:TYR:OH	1:I:92:PRO:HA	1.93	0.68
1:D:94:THR:CB	1:D:97:GLN:HG3	2.19	0.68
1:G:120:THR:HG21	1:G:129:ASN:HA	1.76	0.68
3:J:188:HOH:O	1:L:28:HIS:HD2	1.77	0.68
1:D:120:THR:HG21	1:D:129:ASN:HA	1.75	0.68
1:G:76:LYS:HG3	3:G:169:HOH:O	1.94	0.68
1:F:120:THR:HG21	1:F:129:ASN:CA	2.25	0.67
1:G:153:ALA:HB3	1:G:156:GLU:HB2	1.75	0.67
1:J:24:THR:HG23	3:J:202:HOH:O	1.95	0.67
1:J:28:HIS:HD2	3:L:188:HOH:O	1.77	0.67
1:E:28:HIS:HD2	3:G:189:HOH:O	1.78	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:THR:HB	1:D:97:GLN:CG	2.18	0.67
1:D:155:LEU:HB2	3:D:159:HOH:O	1.94	0.66
3:J:158:HOH:O	1:L:88:PRO:HD3	1.95	0.66
1:L:120:THR:HG23	1:L:129:ASN:HB2	1.76	0.66
1:D:119:LEU:HD11	1:D:123:GLU:OE2	1.95	0.66
1:I:120:THR:HG23	1:I:129:ASN:HB2	1.76	0.66
3:A:176:HOH:O	1:C:28:HIS:HD2	1.79	0.66
1:F:94:THR:HG22	1:F:97:GLN:H	1.61	0.65
1:I:31:HIS:CE1	1:I:43:HIS:CE1	2.84	0.65
1:C:120:THR:HG23	1:C:129:ASN:HD22	1.61	0.65
1:I:94:THR:HG22	1:I:96:ASP:H	1.61	0.65
1:B:119:LEU:O	1:B:123:GLU:HG3	1.95	0.65
1:B:94:THR:HB	1:B:97:GLN:HG3	1.77	0.65
1:F:34:MET:N	3:F:178:HOH:O	2.30	0.65
1:K:94:THR:HG22	1:K:97:GLN:H	1.62	0.64
1:L:119:LEU:HD11	1:L:123:GLU:OE2	1.97	0.64
1:F:81:ASN:HB3	3:F:159:HOH:O	1.97	0.64
1:J:119:LEU:O	1:J:123:GLU:HG3	1.97	0.64
1:L:75:LEU:HD12	1:L:75:LEU:N	2.12	0.64
1:E:94:THR:HG23	3:E:196:HOH:O	1.97	0.64
1:K:117:ILE:HD12	3:K:164:HOH:O	1.97	0.64
1:E:91:LYS:HG2	1:E:92:PRO:CD	2.23	0.63
1:A:7:VAL:HG11	1:A:11:GLU:HB3	1.81	0.63
1:D:95:MET:N	3:D:167:HOH:O	2.25	0.63
1:C:117:ILE:O	1:C:121:ASP:HB2	1.99	0.63
1:B:94:THR:HG22	1:B:95:MET:N	2.12	0.63
1:B:94:THR:HG22	1:B:96:ASP:N	2.13	0.63
1:J:120:THR:HG21	1:J:129:ASN:HA	1.80	0.63
1:E:41:THR:HG21	3:E:161:HOH:O	1.99	0.62
1:L:94:THR:HG22	1:L:96:ASP:H	1.63	0.62
1:K:31:HIS:CE1	1:K:43:HIS:CE1	2.87	0.62
1:A:7:VAL:CG1	1:A:11:GLU:CB	2.77	0.62
1:H:120:THR:HG23	1:H:129:ASN:HD22	1.65	0.62
1:F:119:LEU:O	1:F:119:LEU:HD12	1.99	0.62
1:I:145:MET:HE3	3:I:161:HOH:O	1.98	0.62
1:I:120:THR:CG2	1:I:129:ASN:CB	2.77	0.62
1:F:94:THR:CG2	1:F:96:ASP:HB2	2.30	0.62
1:H:94:THR:HG22	1:H:96:ASP:N	2.14	0.61
1:I:120:THR:HG22	1:I:129:ASN:HD22	1.64	0.61
1:G:24:THR:HG23	3:G:166:HOH:O	1.99	0.61
1:L:94:THR:HB	1:L:97:GLN:HG3	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:HIS:HD2	3:C:161:HOH:O	1.83	0.61
1:I:75:LEU:HD12	1:I:75:LEU:H	1.65	0.61
1:L:42:LEU:HD23	1:L:95:MET:SD	2.40	0.61
1:A:129:ASN:O	1:A:133:ILE:HG13	2.01	0.61
1:H:31:HIS:CE1	1:H:43:HIS:CE1	2.89	0.61
1:K:155:LEU:O	1:K:156:GLU:HB3	1.99	0.61
1:K:34:MET:HB2	1:K:95:MET:CE	2.30	0.61
1:F:153:ALA:O	1:F:156:GLU:HB2	2.00	0.61
1:G:94:THR:HB	1:G:97:GLN:HG3	1.81	0.61
1:I:45:LYS:NZ	3:I:161:HOH:O	2.29	0.61
1:C:153:ALA:O	1:C:156:GLU:HB2	2.01	0.61
1:B:152:LYS:HB3	1:B:156:GLU:OE1	2.01	0.61
1:B:65:LEU:HD13	1:B:71:PRO:HD3	1.83	0.60
1:F:24:THR:HG23	3:F:186:HOH:O	2.00	0.60
1:G:7:VAL:CG1	1:G:11:GLU:HB3	2.31	0.60
1:D:126:ASP:HB3	1:F:133:ILE:HD13	1.84	0.60
1:K:94:THR:HG21	1:K:96:ASP:HB2	1.82	0.60
1:K:120:THR:CG2	1:K:129:ASN:HB2	2.31	0.60
1:K:24:THR:HG23	3:K:190:HOH:O	2.00	0.60
1:J:94:THR:HB	1:J:97:GLN:HG3	1.84	0.59
1:E:75:LEU:N	1:E:75:LEU:HD12	2.17	0.59
1:H:129:ASN:O	1:H:133:ILE:HG13	2.01	0.59
1:I:75:LEU:HD12	1:I:75:LEU:N	2.15	0.59
1:G:7:VAL:HG12	1:G:11:GLU:CB	2.32	0.59
1:H:119:LEU:C	1:H:119:LEU:HD23	2.22	0.59
1:L:31:HIS:CE1	1:L:43:HIS:CE1	2.91	0.59
1:I:120:THR:CG2	1:I:129:ASN:HD22	2.16	0.59
1:D:8:ASP:HA	1:D:123:GLU:OE2	2.03	0.58
1:G:94:THR:CG2	1:G:97:GLN:HG3	2.32	0.58
1:I:44:GLU:HG2	3:I:187:HOH:O	2.03	0.58
1:I:120:THR:HG22	1:I:121:ASP:N	2.18	0.58
1:A:94:THR:HG22	1:A:97:GLN:H	1.68	0.57
1:C:117:ILE:HD13	1:C:133:ILE:HG12	1.86	0.57
3:E:171:HOH:O	1:G:28:HIS:HD2	1.87	0.57
1:K:117:ILE:CD1	1:K:133:ILE:HG12	2.28	0.57
1:B:116:GLY:O	1:B:120:THR:HG22	2.03	0.57
1:F:31:HIS:CE1	1:F:43:HIS:CE1	2.93	0.57
1:D:147:LYS:HZ2	1:D:156:GLU:CG	2.10	0.57
1:G:120:THR:CG2	1:G:129:ASN:CB	2.82	0.57
1:A:9:THR:HA	1:A:119:LEU:HD21	1.86	0.57
1:I:42:LEU:HD23	1:I:95:MET:SD	2.45	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:120:THR:HG23	1:J:129:ASN:HB2	1.86	0.57
1:A:31:HIS:CE1	1:A:43:HIS:CE1	2.92	0.57
1:D:7:VAL:HG12	1:D:8:ASP:H	1.68	0.57
1:C:24:THR:HG23	3:C:193:HOH:O	2.04	0.56
1:C:117:ILE:O	1:C:120:THR:HG22	2.06	0.56
1:D:133:ILE:HD13	1:K:126:ASP:HB3	1.87	0.56
1:H:118:GLU:O	1:H:122:LYS:HG3	2.05	0.56
1:K:34:MET:HB2	1:K:95:MET:HE2	1.87	0.56
1:F:119:LEU:C	1:F:119:LEU:HD12	2.26	0.56
1:H:153:ALA:HB3	1:H:156:GLU:HB2	1.87	0.56
1:B:7:VAL:HG12	1:B:8:ASP:N	2.20	0.55
1:E:81:ASN:HB3	3:E:173:HOH:O	2.06	0.55
1:E:120:THR:HG21	1:E:129:ASN:HA	1.88	0.55
1:I:120:THR:HG21	1:I:129:ASN:CB	2.37	0.55
1:B:31:HIS:CE1	1:B:43:HIS:CE1	2.95	0.54
1:G:31:HIS:CE1	1:G:43:HIS:CE1	2.95	0.54
1:I:116:GLY:O	1:I:120:THR:HB	2.06	0.54
1:D:8:ASP:C	1:D:119:LEU:HD21	2.28	0.54
1:F:7:VAL:HG12	1:F:11:GLU:HB2	1.90	0.54
1:F:94:THR:CG2	1:F:95:MET:N	2.70	0.54
1:A:75:LEU:N	1:A:75:LEU:HD12	2.23	0.54
1:I:94:THR:HG22	1:I:96:ASP:N	2.23	0.54
1:F:94:THR:HG22	1:F:96:ASP:CA	2.38	0.54
1:I:28:HIS:HD2	3:K:189:HOH:O	1.90	0.54
1:B:94:THR:CG2	1:B:95:MET:N	2.70	0.54
1:F:94:THR:O	1:F:98:LEU:HG	2.07	0.53
1:L:7:VAL:HG12	1:L:11:GLU:CB	2.38	0.53
1:B:108:LEU:HD23	1:B:108:LEU:C	2.29	0.53
1:G:120:THR:CG2	1:G:129:ASN:CA	2.85	0.53
1:G:93:LYS:HD2	3:G:207:HOH:O	2.09	0.53
1:K:95:MET:O	1:K:99:MET:HG2	2.08	0.53
1:K:75:LEU:HD12	1:K:75:LEU:N	2.23	0.53
1:K:7:VAL:HG11	1:K:11:GLU:HB3	1.89	0.53
1:C:94:THR:HB	1:C:97:GLN:HG3	1.90	0.53
1:L:129:ASN:O	1:L:133:ILE:HG13	2.09	0.53
1:C:94:THR:HG22	1:C:95:MET:N	2.25	0.52
1:F:94:THR:CG2	1:F:97:GLN:H	2.22	0.52
1:G:7:VAL:HG12	1:G:11:GLU:HB3	1.90	0.52
1:L:75:LEU:HD12	1:L:75:LEU:H	1.74	0.52
1:C:94:THR:HG22	1:C:95:MET:H	1.75	0.52
1:I:89:TYR:CE2	1:I:93:LYS:HD3	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:31:HIS:CE1	1:J:43:HIS:CE1	2.98	0.52
1:L:155:LEU:O	1:L:156:GLU:CB	2.57	0.52
1:H:119:LEU:HD23	1:H:120:THR:N	2.25	0.52
1:J:117:ILE:O	1:J:120:THR:HG22	2.09	0.52
1:J:42:LEU:HD23	1:J:95:MET:SD	2.49	0.52
1:E:153:ALA:HB3	1:E:156:GLU:HB2	1.90	0.52
1:B:75:LEU:N	1:B:75:LEU:HD12	2.25	0.52
1:F:75:LEU:N	1:F:75:LEU:HD12	2.25	0.52
1:A:75:LEU:HD12	1:A:75:LEU:H	1.75	0.52
1:I:108:LEU:C	1:I:108:LEU:HD23	2.29	0.52
1:G:76:LYS:O	1:G:80:GLU:HG3	2.10	0.52
1:C:31:HIS:CE1	1:C:43:HIS:CE1	2.97	0.51
1:J:112:GLU:HA	1:J:115:GLN:HG2	1.92	0.51
1:H:94:THR:HB	1:H:97:GLN:CG	2.36	0.51
1:C:108:LEU:C	1:C:108:LEU:HD23	2.31	0.51
1:L:141:LYS:HD3	3:L:193:HOH:O	2.09	0.51
1:B:117:ILE:HD13	1:B:133:ILE:HG12	1.93	0.51
1:E:120:THR:HG23	1:E:129:ASN:HD22	1.76	0.51
1:D:63:ARG:NH2	1:D:127:VAL:HB	2.26	0.51
1:E:75:LEU:H	1:E:75:LEU:HD12	1.75	0.51
1:H:117:ILE:O	1:H:120:THR:HG22	2.10	0.51
1:D:155:LEU:C	1:D:156:GLU:HG3	2.32	0.50
1:H:120:THR:HG21	1:H:129:ASN:HA	1.92	0.50
1:H:147:LYS:HD2	1:H:154:PRO:O	2.11	0.50
1:L:94:THR:HG22	1:L:95:MET:N	2.26	0.50
1:L:75:LEU:CD1	1:L:75:LEU:H	2.25	0.50
1:A:108:LEU:C	1:A:108:LEU:HD23	2.31	0.50
1:C:28:HIS:CD2	1:C:50:TYR:CE2	2.99	0.50
1:K:7:VAL:HG11	1:K:11:GLU:CB	2.42	0.50
1:D:147:LYS:HD2	1:D:154:PRO:O	2.10	0.50
1:I:89:TYR:CZ	1:I:92:PRO:HA	2.47	0.50
1:D:145:MET:HE1	3:D:165:HOH:O	2.11	0.50
1:J:146:PHE:O	1:J:149:PHE:HB3	2.12	0.50
1:D:147:LYS:HZ1	1:D:156:GLU:HG2	1.73	0.50
1:B:116:GLY:O	1:B:120:THR:CG2	2.60	0.49
1:F:120:THR:CG2	1:F:125:ASP:O	2.59	0.49
1:F:99:MET:HG3	1:F:149:PHE:CE2	2.46	0.49
1:L:108:LEU:HD23	1:L:108:LEU:C	2.32	0.49
1:J:24:THR:HG21	3:J:165:HOH:O	2.11	0.49
1:K:108:LEU:C	1:K:108:LEU:HD23	2.33	0.49
1:H:41:THR:HG22	3:H:180:HOH:O	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:117:ILE:HB	3:K:164:HOH:O	2.12	0.49
1:G:94:THR:HG23	1:G:96:ASP:H	1.78	0.49
1:E:147:LYS:HD2	1:E:154:PRO:O	2.13	0.49
1:G:94:THR:CB	1:G:97:GLN:HG3	2.43	0.49
1:J:114:LYS:HD2	1:J:114:LYS:O	2.13	0.49
1:J:120:THR:CG2	1:J:129:ASN:HD22	2.25	0.49
1:B:7:VAL:HG12	1:B:8:ASP:H	1.78	0.48
1:G:42:LEU:HD23	1:G:95:MET:SD	2.53	0.48
1:J:10:LYS:HG3	3:J:179:HOH:O	2.13	0.48
1:C:119:LEU:O	1:C:123:GLU:HG3	2.14	0.48
1:C:94:THR:HB	1:C:97:GLN:H	1.78	0.48
1:F:94:THR:HG22	1:F:97:GLN:N	2.28	0.48
1:I:94:THR:HB	1:I:97:GLN:CG	2.28	0.48
1:D:114:LYS:HD2	1:D:114:LYS:O	2.13	0.48
1:G:120:THR:HG23	1:G:125:ASP:O	2.13	0.48
1:F:7:VAL:CG1	1:F:11:GLU:HB2	2.44	0.48
1:C:75:LEU:N	1:C:75:LEU:HD12	2.29	0.48
1:F:94:THR:H	1:F:97:GLN:HB2	1.78	0.48
1:C:41:THR:HG21	3:C:189:HOH:O	2.13	0.48
1:D:75:LEU:N	1:D:75:LEU:HD12	2.29	0.48
1:G:147:LYS:NZ	1:G:156:GLU:O	2.45	0.48
1:B:42:LEU:HD21	1:B:149:PHE:CZ	2.49	0.48
1:F:126:ASP:OD2	1:K:114:LYS:NZ	2.42	0.48
1:F:7:VAL:CG1	1:F:8:ASP:H	2.05	0.48
1:E:113:TYR:O	1:E:117:ILE:HG13	2.14	0.48
1:K:114:LYS:O	1:K:118:GLU:HG3	2.14	0.48
1:L:76:LYS:O	1:L:80:GLU:HG3	2.14	0.48
1:D:145:MET:CE	3:D:165:HOH:O	2.61	0.47
1:G:57:MET:HE1	3:G:189:HOH:O	2.14	0.47
1:H:114:LYS:O	1:H:114:LYS:HD2	2.14	0.47
1:I:91:LYS:HA	1:I:92:PRO:HD3	1.61	0.47
1:C:94:THR:OG1	1:C:97:GLN:HG3	2.14	0.47
1:E:94:THR:HG22	1:E:96:ASP:N	2.28	0.47
1:K:126:ASP:O	1:K:129:ASN:HB3	2.14	0.47
1:C:114:LYS:HD2	1:C:114:LYS:O	2.15	0.47
1:B:99:MET:HG3	1:B:149:PHE:CE2	2.49	0.47
1:K:117:ILE:CG1	3:K:164:HOH:O	2.62	0.47
1:L:65:LEU:HD13	1:L:71:PRO:HD3	1.95	0.47
1:D:147:LYS:HZ2	1:D:156:GLU:HA	1.79	0.47
1:E:116:GLY:O	1:E:120:THR:HG22	2.14	0.47
1:G:7:VAL:HG11	1:G:11:GLU:HB3	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:94:THR:CG2	1:H:96:ASP:H	2.27	0.47
1:B:7:VAL:HG11	1:B:11:GLU:HG2	1.97	0.47
1:C:89:TYR:OH	1:C:92:PRO:HA	2.15	0.47
1:H:65:LEU:HD13	1:H:71:PRO:HD3	1.97	0.47
1:L:120:THR:HG22	1:L:129:ASN:HD22	1.77	0.47
1:A:86:GLU:CD	1:C:74:THR:HB	2.35	0.47
1:E:126:ASP:OD2	1:I:114:LYS:NZ	2.42	0.47
1:G:79:LEU:HD23	1:G:79:LEU:HA	1.59	0.47
1:I:79:LEU:HA	1:I:79:LEU:HD23	1.54	0.47
1:L:8:ASP:H	1:L:11:GLU:HB2	1.80	0.47
1:B:79:LEU:HD23	1:B:79:LEU:HA	1.55	0.47
1:L:116:GLY:O	1:L:120:THR:HB	2.14	0.47
1:L:75:LEU:N	1:L:75:LEU:CD1	2.77	0.47
1:H:94:THR:HG22	1:H:97:GLN:N	2.23	0.46
1:I:75:LEU:H	1:I:75:LEU:CD1	2.27	0.46
1:C:94:THR:CB	1:C:97:GLN:HG3	2.45	0.46
1:G:126:ASP:OD2	1:L:114:LYS:NZ	2.42	0.46
1:K:94:THR:HG22	1:K:96:ASP:CA	2.44	0.46
1:L:28:HIS:CD2	1:L:50:TYR:CE2	3.03	0.46
1:I:28:HIS:CD2	1:I:50:TYR:CE2	3.04	0.46
1:G:94:THR:HG22	1:G:97:GLN:HG3	1.97	0.46
1:J:76:LYS:O	1:J:80:GLU:HG3	2.16	0.46
1:E:120:THR:CG2	1:E:129:ASN:HD22	2.29	0.46
1:C:126:ASP:HB3	1:H:133:ILE:HD13	1.96	0.46
1:A:147:LYS:HD2	1:A:154:PRO:O	2.16	0.46
1:C:79:LEU:HA	1:C:79:LEU:HD23	1.67	0.46
1:G:119:LEU:HG	1:G:120:THR:N	2.31	0.46
1:H:37:HIS:CD2	3:K:178:HOH:O	2.69	0.46
1:H:75:LEU:N	1:H:75:LEU:HD12	2.31	0.46
1:L:119:LEU:HD12	1:L:119:LEU:C	2.35	0.46
1:K:94:THR:HG22	1:K:96:ASP:HB2	1.97	0.45
1:F:114:LYS:HD2	1:F:114:LYS:O	2.14	0.45
1:G:75:LEU:HD12	1:G:75:LEU:N	2.31	0.45
1:F:108:LEU:HD23	1:F:108:LEU:C	2.37	0.45
1:J:75:LEU:HD12	1:J:75:LEU:N	2.32	0.45
1:A:28:HIS:CD2	1:A:50:TYR:CE1	3.05	0.45
1:K:79:LEU:HA	1:K:79:LEU:HD23	1.65	0.45
1:L:79:LEU:HA	1:L:79:LEU:HD23	1.68	0.45
1:E:42:LEU:HD12	1:E:42:LEU:HA	1.73	0.45
1:F:129:ASN:O	1:F:133:ILE:HG13	2.17	0.45
1:J:79:LEU:HD23	1:J:79:LEU:HA	1.70	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:129:ASN:O	1:G:133:ILE:HG13	2.17	0.45
1:K:24:THR:CG2	3:K:190:HOH:O	2.61	0.45
1:K:76:LYS:O	1:K:80:GLU:HG3	2.17	0.45
1:E:94:THR:HG22	1:E:97:GLN:N	2.27	0.45
1:H:108:LEU:HD23	1:H:108:LEU:C	2.37	0.45
1:I:117:ILE:HD13	1:I:133:ILE:HG12	1.98	0.45
1:K:117:ILE:HD11	1:K:133:ILE:HA	1.98	0.45
1:L:7:VAL:HG12	1:L:11:GLU:HB3	1.98	0.45
1:A:114:LYS:O	1:A:114:LYS:HD2	2.16	0.45
1:A:94:THR:HB	1:A:97:GLN:HG3	1.98	0.45
1:B:28:HIS:CD2	1:B:50:TYR:CE2	3.04	0.45
1:H:10:LYS:HG3	3:H:168:HOH:O	2.17	0.45
1:H:75:LEU:HD12	1:H:75:LEU:H	1.82	0.45
1:D:114:LYS:NZ	1:K:126:ASP:OD2	2.45	0.45
1:A:153:ALA:HB3	1:A:156:GLU:CB	2.47	0.44
1:F:42:LEU:HD21	1:F:149:PHE:CZ	2.52	0.44
1:K:94:THR:HG22	1:K:97:GLN:N	2.31	0.44
1:K:94:THR:H	1:K:97:GLN:CD	2.20	0.44
1:B:39:PHE:O	1:B:43:HIS:HB2	2.17	0.44
1:I:147:LYS:NZ	1:I:156:GLU:HB3	2.32	0.44
1:K:8:ASP:HA	1:K:123:GLU:OE2	2.17	0.44
1:G:107:GLU:OE2	3:G:202:HOH:O	2.21	0.44
1:I:76:LYS:O	1:I:80:GLU:HG3	2.18	0.44
1:B:117:ILE:CD1	1:B:133:ILE:HG12	2.46	0.44
1:D:126:ASP:HB3	1:F:133:ILE:CD1	2.45	0.44
1:F:95:MET:O	1:F:99:MET:HG2	2.17	0.44
1:B:114:LYS:O	1:B:114:LYS:HD2	2.17	0.44
1:E:108:LEU:HD23	1:E:108:LEU:C	2.38	0.44
1:I:42:LEU:HD12	1:I:42:LEU:HA	1.81	0.44
1:B:76:LYS:O	1:B:80:GLU:HG3	2.17	0.44
1:C:28:HIS:NE2	1:C:50:TYR:CE2	2.86	0.44
1:H:94:THR:CG2	1:H:96:ASP:N	2.80	0.44
1:L:42:LEU:O	1:L:46:MET:HG2	2.18	0.44
1:A:79:LEU:HA	1:A:79:LEU:HD23	1.61	0.44
1:J:28:HIS:CD2	3:L:188:HOH:O	2.62	0.44
1:A:126:ASP:OD2	1:E:114:LYS:NZ	2.48	0.44
1:D:117:ILE:O	1:D:120:THR:HG22	2.18	0.44
1:C:42:LEU:HD21	1:C:149:PHE:CZ	2.53	0.43
1:D:21:ASN:O	1:D:24:THR:HG22	2.18	0.43
1:K:75:LEU:H	1:K:75:LEU:HD12	1.83	0.43
1:L:89:TYR:OH	1:L:92:PRO:HA	2.17	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:96:ASP:OD1	1:I:37:HIS:CE1	2.71	0.43
1:G:108:LEU:HD23	1:G:108:LEU:C	2.39	0.43
1:K:7:VAL:CG1	1:K:11:GLU:CB	2.96	0.43
1:A:65:LEU:HD13	1:A:71:PRO:HD3	2.01	0.43
1:G:153:ALA:O	1:G:156:GLU:HB3	2.18	0.43
1:H:79:LEU:HD23	1:H:79:LEU:HA	1.57	0.43
1:C:65:LEU:HD13	1:C:71:PRO:HD3	2.00	0.43
1:D:126:ASP:O	3:D:173:HOH:O	2.21	0.43
1:I:42:LEU:HD21	1:I:149:PHE:CZ	2.53	0.43
1:K:23:PHE:CD1	1:K:105:THR:HG21	2.53	0.43
1:A:153:ALA:HB3	1:A:156:GLU:HB2	2.00	0.43
1:J:94:THR:CG2	1:J:95:MET:N	2.77	0.43
1:G:38:ASN:HB3	1:G:42:LEU:HD22	2.00	0.43
1:I:30:ILE:HG22	1:I:34:MET:HE3	2.01	0.43
1:J:74:THR:HB	1:L:86:GLU:CD	2.39	0.43
1:B:147:LYS:HD2	1:B:154:PRO:O	2.19	0.43
1:K:120:THR:CG2	1:K:129:ASN:CB	2.97	0.43
1:L:112:GLU:HA	1:L:115:GLN:HG2	2.01	0.43
1:D:120:THR:HG21	1:D:129:ASN:CA	2.47	0.43
1:D:120:THR:OG1	1:D:125:ASP:HB3	2.19	0.43
1:F:7:VAL:CG1	1:F:8:ASP:N	2.72	0.43
1:H:90:THR:OG1	1:H:91:LYS:N	2.52	0.43
1:K:147:LYS:HD2	1:K:154:PRO:O	2.19	0.43
1:B:20:LEU:HD12	1:B:20:LEU:HA	1.91	0.43
1:C:118:GLU:O	1:C:122:LYS:HG3	2.19	0.43
1:A:42:LEU:HD12	1:A:42:LEU:HA	1.86	0.42
1:I:112:GLU:HA	1:I:115:GLN:HG2	2.01	0.42
1:K:94:THR:O	1:K:97:GLN:N	2.52	0.42
1:D:91:LYS:HA	1:D:92:PRO:HD3	1.80	0.42
1:K:65:LEU:HD13	1:K:71:PRO:CD	2.50	0.42
1:J:114:LYS:NZ	3:J:178:HOH:O	2.52	0.42
1:K:75:LEU:H	1:K:75:LEU:CD1	2.33	0.42
1:G:94:THR:HB	1:G:97:GLN:OE1	2.19	0.42
1:G:9:THR:HG22	1:G:13:LEU:HD22	2.01	0.42
1:K:7:VAL:CG1	1:K:11:GLU:HB2	2.50	0.42
1:A:155:LEU:HB2	3:A:178:HOH:O	2.19	0.42
1:A:15:HIS:HE1	1:A:83:SER:OG	2.03	0.42
1:A:75:LEU:CD1	1:A:75:LEU:H	2.32	0.42
1:F:28:HIS:CD2	1:F:50:TYR:CE1	3.08	0.42
1:J:42:LEU:O	1:J:46:MET:HG2	2.20	0.42
1:K:114:LYS:HD2	1:K:114:LYS:O	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:20:LEU:HA	1:K:20:LEU:HD12	1.94	0.42
1:E:79:LEU:HD23	1:E:79:LEU:HA	1.59	0.42
1:J:34:MET:HG3	1:J:39:PHE:CD1	2.55	0.42
1:D:120:THR:HG23	1:D:129:ASN:HB2	2.02	0.42
1:F:14:ASN:OD1	1:F:71:PRO:HA	2.19	0.42
1:J:65:LEU:HD13	1:J:71:PRO:CD	2.49	0.42
1:D:37:HIS:CE1	1:G:96:ASP:OD1	2.72	0.41
1:I:75:LEU:N	1:I:75:LEU:CD1	2.83	0.41
1:B:108:LEU:O	1:B:112:GLU:HG3	2.20	0.41
1:E:76:LYS:O	1:E:80:GLU:HG3	2.20	0.41
1:K:28:HIS:CD2	1:K:50:TYR:CE2	3.08	0.41
1:K:65:LEU:HD13	1:K:71:PRO:HD3	2.02	0.41
1:B:129:ASN:O	1:B:133:ILE:HG13	2.20	0.41
1:C:120:THR:HG23	1:C:129:ASN:HB2	2.02	0.41
1:D:75:LEU:HD12	1:D:75:LEU:H	1.85	0.41
1:E:23:PHE:CD1	1:E:105:THR:HG21	2.56	0.41
1:E:114:LYS:O	1:E:114:LYS:HD2	2.21	0.41
1:J:65:LEU:HD13	1:J:71:PRO:HD3	2.02	0.41
1:B:65:LEU:HD13	1:B:71:PRO:CD	2.48	0.41
1:C:42:LEU:HD12	1:C:42:LEU:HA	1.96	0.41
1:J:94:THR:HG22	1:J:95:MET:H	1.85	0.41
1:K:7:VAL:HG12	1:K:11:GLU:HB2	2.01	0.41
1:L:65:LEU:HD13	1:L:71:PRO:CD	2.50	0.41
1:A:42:LEU:O	1:A:46:MET:HG2	2.21	0.41
1:D:128:THR:HG22	1:D:132:LEU:HD22	2.02	0.41
1:K:128:THR:HG22	1:K:132:LEU:HD22	2.02	0.41
1:E:129:ASN:O	1:E:133:ILE:HG13	2.20	0.41
1:G:65:LEU:HD13	1:G:71:PRO:HD3	2.02	0.41
1:J:89:TYR:OH	1:J:92:PRO:HA	2.20	0.41
1:A:119:LEU:O	1:A:123:GLU:HG3	2.20	0.41
1:E:75:LEU:H	1:E:75:LEU:CD1	2.32	0.41
1:E:75:LEU:N	1:E:75:LEU:CD1	2.84	0.41
1:E:94:THR:H	1:E:97:GLN:CD	2.24	0.41
1:K:94:THR:O	1:K:97:GLN:HB2	2.20	0.41
1:A:154:PRO:HD3	3:A:185:HOH:O	2.20	0.41
1:A:76:LYS:O	1:A:80:GLU:HG3	2.21	0.41
1:D:154:PRO:C	1:D:156:GLU:H	2.23	0.41
1:H:89:TYR:CZ	1:H:92:PRO:HA	2.55	0.41
1:J:93:LYS:HB3	1:J:93:LYS:HE2	1.68	0.41
1:K:117:ILE:CD1	3:K:164:HOH:O	2.64	0.41
1:E:107:GLU:OE2	3:E:182:HOH:O	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:152:LYS:HA	1:H:152:LYS:HD3	1.91	0.41
1:I:21:ASN:O	1:I:24:THR:HG22	2.21	0.41
1:J:94:THR:CG2	3:J:189:HOH:O	2.69	0.41
1:B:126:ASP:OD2	1:G:114:LYS:NZ	2.46	0.41
1:D:35:ARG:NE	3:D:166:HOH:O	2.38	0.41
1:F:7:VAL:CG1	1:F:11:GLU:CB	2.99	0.41
1:I:120:THR:HG22	1:I:129:ASN:ND2	2.32	0.41
1:K:42:LEU:HA	1:K:42:LEU:HD12	1.81	0.41
1:F:79:LEU:HA	1:F:79:LEU:HD23	1.47	0.41
1:H:21:ASN:O	1:H:24:THR:HG22	2.20	0.41
1:F:147:LYS:HD2	1:F:154:PRO:O	2.22	0.40
1:I:8:ASP:C	1:I:8:ASP:OD1	2.59	0.40
1:J:113:TYR:O	1:J:117:ILE:N	2.48	0.40
1:G:155:LEU:O	1:G:156:GLU:C	2.58	0.40
1:I:118:GLU:O	1:I:121:ASP:HB3	2.21	0.40
1:K:94:THR:HG23	1:K:96:ASP:H	1.84	0.40
1:C:89:TYR:CZ	1:C:92:PRO:HA	2.57	0.40
1:D:7:VAL:CG1	1:D:8:ASP:H	2.30	0.40
1:E:14:ASN:OD1	1:E:71:PRO:HA	2.21	0.40
1:K:114:LYS:CA	3:K:164:HOH:O	2.42	0.40
1:E:94:THR:CG2	1:E:96:ASP:HB2	2.51	0.40
1:F:126:ASP:O	1:F:129:ASN:HB3	2.22	0.40
1:I:8:ASP:OD1	1:I:11:GLU:HB2	2.21	0.40
1:J:15:HIS:HE1	1:J:83:SER:OG	2.05	0.40
1:K:92:PRO:HG2	1:K:92:PRO:O	2.21	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	148/156 (95%)	145 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	148/156 (95%)	146 (99%)	2 (1%)	0	100	100
1	C	148/156 (95%)	146 (99%)	2 (1%)	0	100	100
1	D	148/156 (95%)	142 (96%)	6 (4%)	0	100	100
1	E	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
1	F	148/156 (95%)	143 (97%)	5 (3%)	0	100	100
1	G	148/156 (95%)	146 (99%)	2 (1%)	0	100	100
1	H	148/156 (95%)	146 (99%)	2 (1%)	0	100	100
1	I	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
1	J	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
1	K	148/156 (95%)	144 (97%)	4 (3%)	0	100	100
1	L	148/156 (95%)	143 (97%)	5 (3%)	0	100	100
All	All	1776/1872 (95%)	1736 (98%)	40 (2%)	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	133/139 (96%)	121 (91%)	12 (9%)	11	11
1	B	133/139 (96%)	123 (92%)	10 (8%)	16	17
1	C	133/139 (96%)	123 (92%)	10 (8%)	16	17
1	D	133/139 (96%)	121 (91%)	12 (9%)	11	11
1	E	133/139 (96%)	122 (92%)	11 (8%)	13	14
1	F	133/139 (96%)	121 (91%)	12 (9%)	11	11
1	G	133/139 (96%)	120 (90%)	13 (10%)	9	8
1	H	133/139 (96%)	119 (90%)	14 (10%)	8	7
1	I	133/139 (96%)	121 (91%)	12 (9%)	11	11
1	J	133/139 (96%)	124 (93%)	9 (7%)	18	20

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	133/139 (96%)	120 (90%)	13 (10%)	9	8
1	L	133/139 (96%)	123 (92%)	10 (8%)	16	17
All	All	1596/1668 (96%)	1458 (91%)	138 (9%)	12	12

All (138) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	11	GLU
1	A	13	LEU
1	A	20	LEU
1	A	24	THR
1	A	41	THR
1	A	42	LEU
1	A	93	LYS
1	A	102	LEU
1	A	119	LEU
1	A	131	MET
1	A	132	LEU
1	B	8	ASP
1	B	11	GLU
1	B	13	LEU
1	B	20	LEU
1	B	24	THR
1	B	41	THR
1	B	42	LEU
1	B	102	LEU
1	B	132	LEU
1	B	156	GLU
1	C	11	GLU
1	C	13	LEU
1	C	20	LEU
1	C	24	THR
1	C	41	THR
1	C	42	LEU
1	C	49	LEU
1	C	102	LEU
1	C	132	LEU
1	C	156	GLU
1	D	11	GLU
1	D	13	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	20	LEU
1	D	24	THR
1	D	42	LEU
1	D	49	LEU
1	D	91	LYS
1	D	94	THR
1	D	102	LEU
1	D	130	ASP
1	D	131	MET
1	D	132	LEU
1	E	8	ASP
1	E	11	GLU
1	E	13	LEU
1	E	20	LEU
1	E	24	THR
1	E	41	THR
1	E	42	LEU
1	E	94	THR
1	E	102	LEU
1	E	132	LEU
1	E	156	GLU
1	F	11	GLU
1	F	13	LEU
1	F	20	LEU
1	F	24	THR
1	F	28	HIS
1	F	41	THR
1	F	42	LEU
1	F	49	LEU
1	F	102	LEU
1	F	119	LEU
1	F	123	GLU
1	F	132	LEU
1	G	7	VAL
1	G	11	GLU
1	G	13	LEU
1	G	20	LEU
1	G	24	THR
1	G	28	HIS
1	G	41	THR
1	G	42	LEU
1	G	94	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	102	LEU
1	G	119	LEU
1	G	121	ASP
1	G	132	LEU
1	H	8	ASP
1	H	11	GLU
1	H	13	LEU
1	H	20	LEU
1	H	24	THR
1	H	41	THR
1	H	42	LEU
1	H	49	LEU
1	H	65	LEU
1	H	94	THR
1	H	102	LEU
1	H	119	LEU
1	H	132	LEU
1	H	156	GLU
1	I	8	ASP
1	I	11	GLU
1	I	13	LEU
1	I	20	LEU
1	I	24	THR
1	I	41	THR
1	I	42	LEU
1	I	49	LEU
1	I	102	LEU
1	I	120	THR
1	I	132	LEU
1	I	156	GLU
1	J	11	GLU
1	J	13	LEU
1	J	20	LEU
1	J	24	THR
1	J	42	LEU
1	J	65	LEU
1	J	102	LEU
1	J	132	LEU
1	J	156	GLU
1	K	7	VAL
1	K	11	GLU
1	K	13	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	20	LEU
1	K	24	THR
1	K	41	THR
1	K	42	LEU
1	K	49	LEU
1	K	65	LEU
1	K	102	LEU
1	K	120	THR
1	K	132	LEU
1	K	156	GLU
1	L	7	VAL
1	L	11	GLU
1	L	13	LEU
1	L	20	LEU
1	L	24	THR
1	L	41	THR
1	L	42	LEU
1	L	102	LEU
1	L	132	LEU
1	L	156	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	28	HIS
1	A	37	HIS
1	A	81	ASN
1	B	15	HIS
1	B	37	HIS
1	B	43	HIS
1	B	81	ASN
1	B	129	ASN
1	C	15	HIS
1	C	28	HIS
1	C	81	ASN
1	C	129	ASN
1	D	15	HIS
1	D	29	GLN
1	D	37	HIS
1	E	15	HIS
1	E	28	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	81	ASN
1	E	129	ASN
1	F	15	HIS
1	F	37	HIS
1	F	81	ASN
1	F	97	GLN
1	G	15	HIS
1	G	28	HIS
1	G	81	ASN
1	H	15	HIS
1	H	37	HIS
1	H	81	ASN
1	H	129	ASN
1	I	15	HIS
1	I	28	HIS
1	I	31	HIS
1	I	37	HIS
1	I	43	HIS
1	I	81	ASN
1	I	129	ASN
1	J	15	HIS
1	J	28	HIS
1	J	29	GLN
1	J	37	HIS
1	J	81	ASN
1	J	129	ASN
1	K	15	HIS
1	K	28	HIS
1	K	37	HIS
1	K	43	HIS
1	K	81	ASN
1	K	129	ASN
1	L	15	HIS
1	L	28	HIS
1	L	43	HIS
1	L	81	ASN
1	L	129	ASN

5.3.3 RNA ⓘ

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](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.