



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 15, 2016 – 08:17 AM EST

PDB ID : 5F4H  
Title : Archaeal RuvB-like Holiday junction helicase  
Authors : Zhai, B.; DuPrez, K.T.; Doukov, T.I.; Shen, Y.; Fan, L.  
Deposited on : 2015-12-03  
Resolution : 2.70 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  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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-20028442

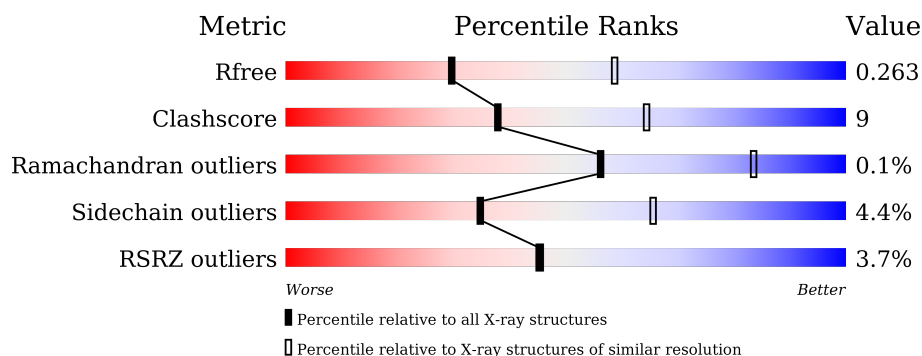
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	505	<div> <div>2%</div> <div>69% 15% • 13%</div> </div>
1	B	505	<div> <div>2%</div> <div>68% 16% • 14%</div> </div>
1	C	505	<div> <div>6%</div> <div>70% 13% • 14%</div> </div>
1	D	505	<div> <div>2%</div> <div>67% 17% • 14%</div> </div>
1	E	505	<div> <div>3%</div> <div>67% 17% •• 14%</div> </div>
1	F	505	<div> <div>3%</div> <div>67% 17% • 14%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	601	-	-	-	X
2	GOL	B	601	-	-	-	X
2	GOL	B	602	-	-	-	X
2	GOL	C	601	-	-	X	X
2	GOL	D	601	-	-	-	X
2	GOL	D	604	-	-	-	X
2	GOL	E	601	-	-	-	X
2	GOL	E	603	-	-	-	X
2	GOL	E	604	-	-	-	X
2	GOL	E	605	-	-	-	X
2	GOL	F	601	-	-	-	X
2	GOL	F	602	-	-	-	X
2	GOL	F	604	-	-	-	X
3	EDO	A	605	-	-	-	X
3	EDO	B	605	-	-	-	X
3	EDO	F	605	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20358 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 Nucleotide binding protein PINc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3329	2118	556	639	16			
1	B	435	Total	C	N	O	S	0	0	0
			3347	2132	556	644	15			
1	C	436	Total	C	N	O	S	0	0	0
			3274	2071	554	635	14			
1	D	436	Total	C	N	O	S	0	0	0
			3324	2110	557	642	15			
1	E	436	Total	C	N	O	S	0	0	0
			3334	2115	561	644	14			
1	F	436	Total	C	N	O	S	0	0	0
			3350	2131	565	638	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	261	ALA	LYS	engineered mutation	UNP C3MQK6
B	261	ALA	LYS	engineered mutation	UNP C3MQK6
C	261	ALA	LYS	engineered mutation	UNP C3MQK6
D	261	ALA	LYS	engineered mutation	UNP C3MQK6
E	261	ALA	LYS	engineered mutation	UNP C3MQK6
F	261	ALA	LYS	engineered mutation	UNP C3MQK6

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

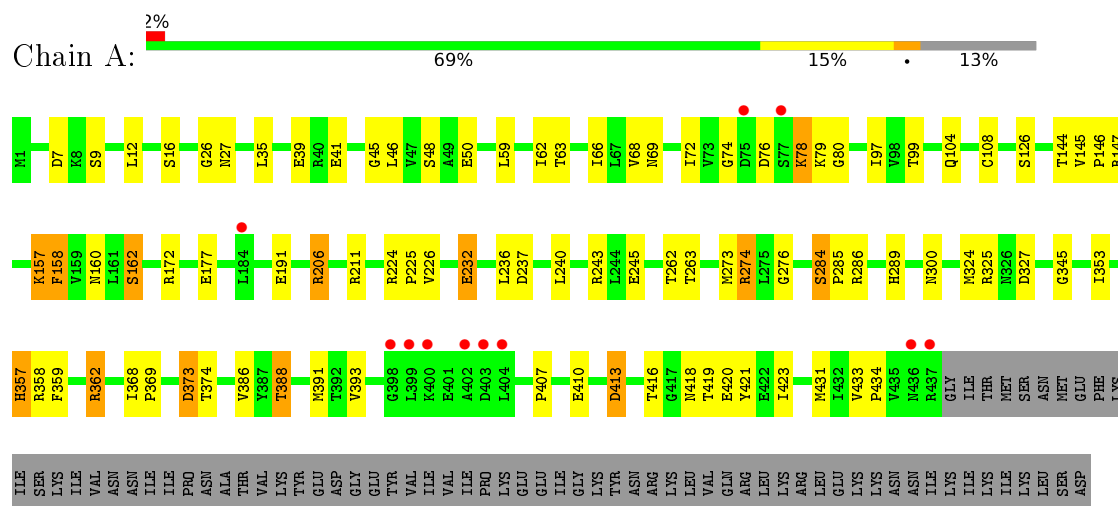
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	49	Total O 49 49	0	0
4	B	28	Total O 28 28	0	0
4	C	19	Total O 19 19	0	0
4	D	38	Total O 38 38	0	0
4	E	56	Total O 56 56	0	0
4	F	40	Total O 40 40	0	0

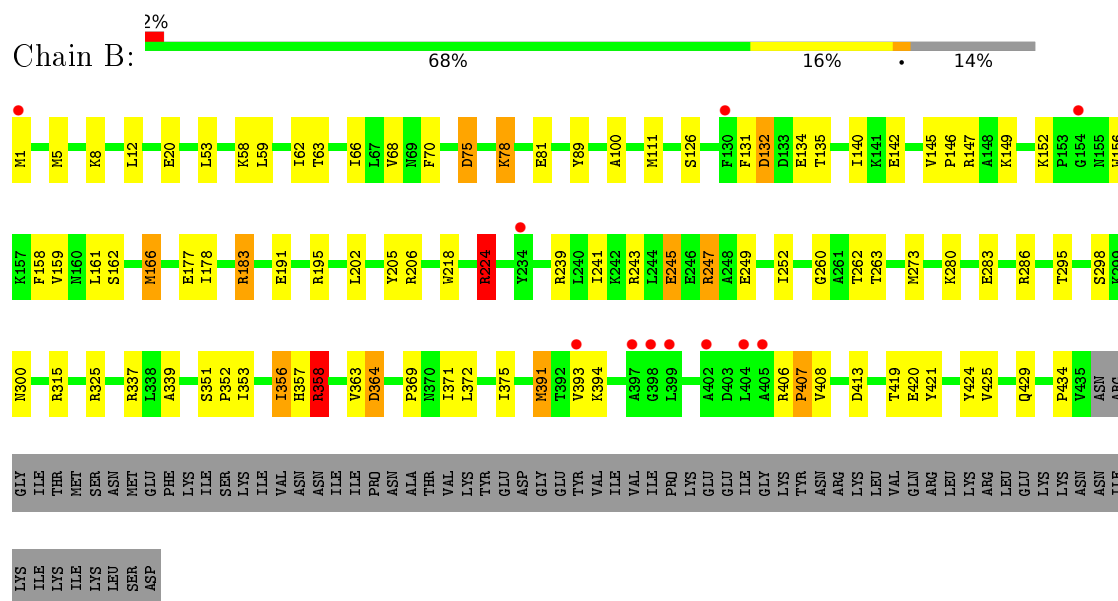
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Nucleotide binding protein PINc



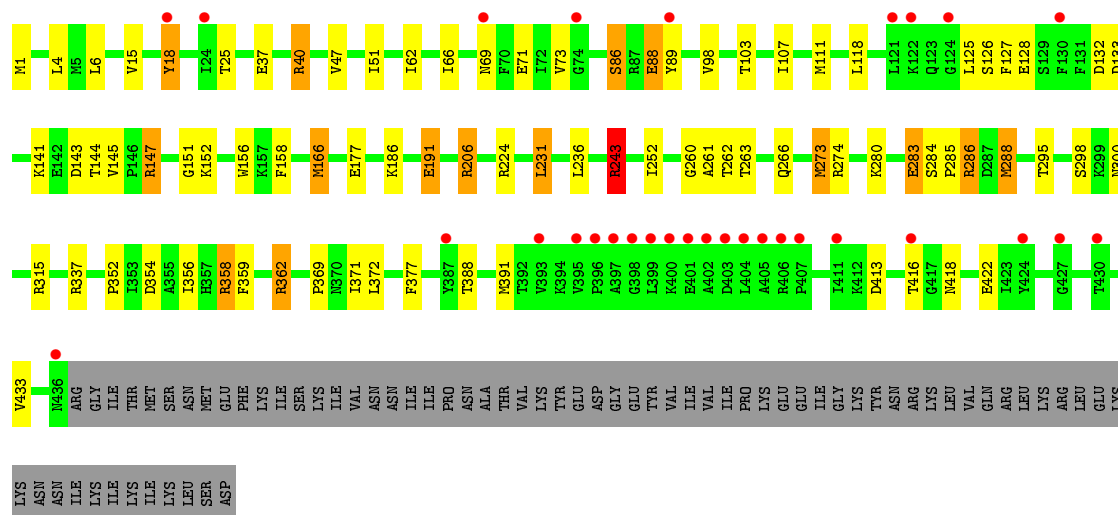
#### • Molecule 1: Nucleotide binding protein PINc



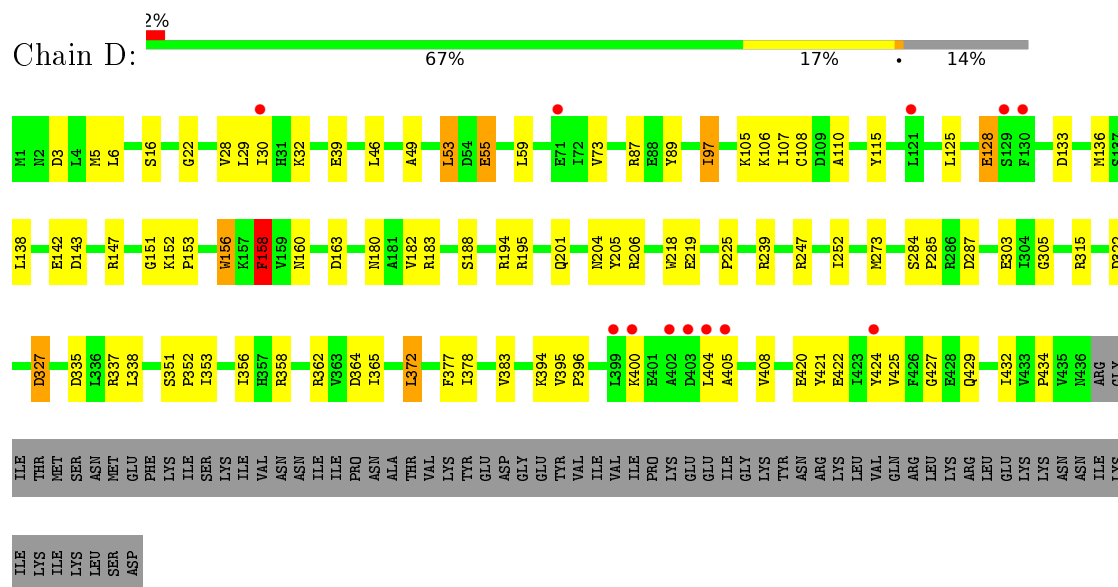
#### • Molecule 1: Nucleotide binding protein PINc



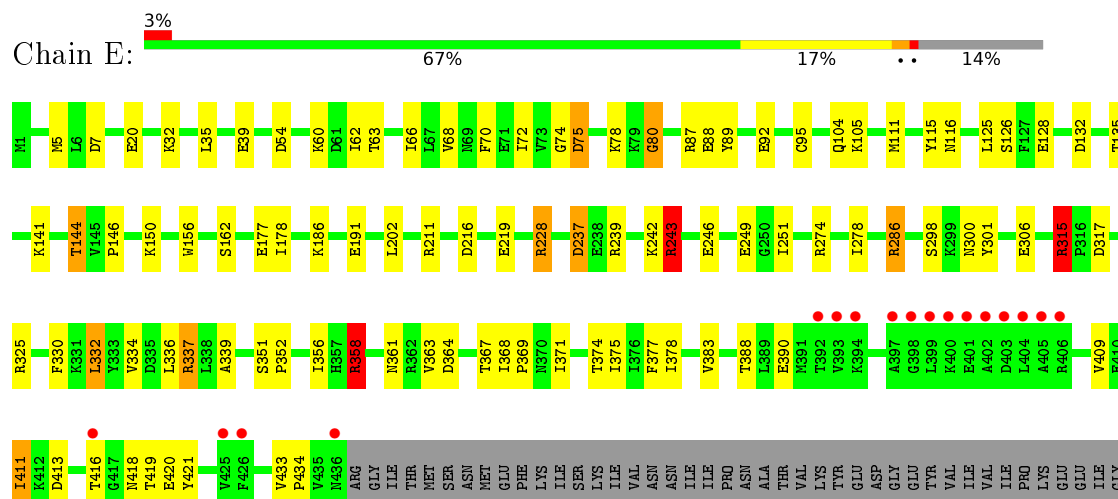




• Molecule 1: Nucleotide binding protein PINc

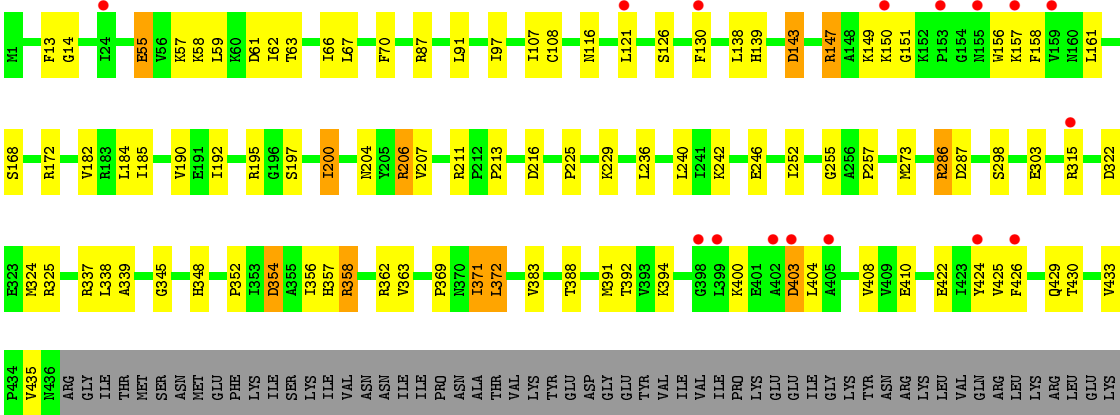


• Molecule 1: Nucleotide binding protein PINc



LYS
TYR
ASN
ARG
LYS
LEU
VAL
GLN
ARG
LEU
LYS
ARG
LEU
GLU
LYS
LYS
ASN
ASN
ILE
LYS
ILE
LYS
LYS
LYS
LEU
SER
ASP

• Molecule 1: Nucleotide binding protein PINc



LYS
ASN
ILE
LYS
ILE
LYS
ILE
LEU
SER
ASP

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.72Å 148.98Å 122.13Å 90.00° 104.07° 90.00°	Depositor
Resolution (Å)	39.19 – 2.70 39.19 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.6 (39.19-2.70) 97.7 (39.19-2.70)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.05 (at 2.69Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.227 , 0.265 0.227 , 0.263	Depositor DCC
$R_{free}$ test set	4732 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	75.5	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 51.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20358	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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 ⓘ

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

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	0.95	2/3381 (0.1%)	1.04	10/4585 (0.2%)
1	B	0.91	2/3401 (0.1%)	1.01	16/4610 (0.3%)
1	C	0.90	4/3326 (0.1%)	1.05	18/4515 (0.4%)
1	D	0.91	5/3376 (0.1%)	1.08	19/4577 (0.4%)
1	E	0.96	4/3384 (0.1%)	1.04	17/4587 (0.4%)
1	F	0.98	3/3402 (0.1%)	1.07	18/4604 (0.4%)
All	All	0.94	20/20270 (0.1%)	1.05	98/27478 (0.4%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	219	GLU	CD-OE1	10.55	1.37	1.25
1	F	55	GLU	CD-OE1	-7.73	1.17	1.25
1	C	86	SER	CB-OG	-7.43	1.32	1.42
1	F	354	ASP	CB-CG	6.40	1.65	1.51
1	D	55	GLU	CD-OE2	-6.38	1.18	1.25
1	E	219	GLU	CD-OE2	6.32	1.32	1.25
1	C	191	GLU	CD-OE2	-6.13	1.19	1.25
1	C	298	SER	CB-OG	-6.09	1.34	1.42
1	D	39	GLU	CD-OE2	6.04	1.32	1.25
1	A	162	SER	CB-OG	-6.04	1.34	1.42
1	D	219	GLU	CD-OE2	-5.88	1.19	1.25
1	E	298	SER	CB-OG	-5.80	1.34	1.42
1	D	427	GLY	N-CA	5.49	1.54	1.46
1	C	283	GLU	CD-OE2	5.45	1.31	1.25
1	E	95	CYS	CB-SG	-5.38	1.73	1.81
1	A	16	SER	CB-OG	-5.37	1.35	1.42
1	B	134	GLU	CB-CG	5.21	1.62	1.52
1	B	298	SER	CB-OG	-5.17	1.35	1.42
1	D	39	GLU	CG-CD	5.13	1.59	1.51
1	F	55	GLU	CD-OE2	-5.10	1.20	1.25

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	211	ARG	NE-CZ-NH1	10.90	125.75	120.30
1	A	373	ASP	CB-CG-OD2	-10.89	108.50	118.30
1	E	274	ARG	NE-CZ-NH2	10.03	125.31	120.30
1	A	413	ASP	CB-CG-OD2	9.72	127.05	118.30
1	F	211	ARG	NE-CZ-NH2	9.36	124.98	120.30
1	F	206	ARG	NE-CZ-NH1	-9.10	115.75	120.30
1	D	337	ARG	NE-CZ-NH2	8.93	124.77	120.30
1	C	206	ARG	NE-CZ-NH1	-8.91	115.84	120.30
1	D	239	ARG	NE-CZ-NH2	8.70	124.65	120.30
1	A	373	ASP	CB-CG-OD1	8.64	126.07	118.30
1	D	133	ASP	CB-CG-OD2	8.54	125.99	118.30
1	E	211	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	A	274	ARG	NE-CZ-NH2	8.38	124.49	120.30
1	B	183	ARG	NE-CZ-NH2	8.33	124.47	120.30
1	B	286	ARG	NE-CZ-NH1	-8.26	116.17	120.30
1	C	166	MET	CG-SD-CE	-8.09	87.25	100.20
1	C	288	MET	CG-SD-CE	8.05	113.09	100.20
1	F	206	ARG	NE-CZ-NH2	8.03	124.31	120.30
1	C	206	ARG	NE-CZ-NH2	7.95	124.28	120.30
1	B	364	ASP	CB-CG-OD1	7.86	125.37	118.30
1	F	322	ASP	CB-CG-OD1	-7.85	111.24	118.30
1	B	337	ARG	NE-CZ-NH2	7.60	124.10	120.30
1	C	243	ARG	NE-CZ-NH2	7.56	124.08	120.30
1	E	274	ARG	NE-CZ-NH1	-7.56	116.52	120.30
1	E	300	ASN	N-CA-CB	-7.53	97.05	110.60
1	B	224	ARG	NE-CZ-NH2	-7.50	116.55	120.30
1	D	322	ASP	CB-CG-OD2	-7.40	111.64	118.30
1	B	286	ARG	NE-CZ-NH2	7.38	123.99	120.30
1	F	286	ARG	NE-CZ-NH1	-7.33	116.63	120.30
1	B	132	ASP	CB-CG-OD1	7.23	124.81	118.30
1	D	143	ASP	CB-CG-OD1	-7.16	111.85	118.30
1	F	195	ARG	NE-CZ-NH1	7.16	123.88	120.30
1	B	364	ASP	CB-CG-OD2	-7.15	111.86	118.30
1	F	286	ARG	NE-CZ-NH2	7.10	123.85	120.30
1	C	315	ARG	NE-CZ-NH2	7.00	123.80	120.30
1	F	337	ARG	NE-CZ-NH2	6.91	123.75	120.30
1	C	243	ARG	NE-CZ-NH1	-6.78	116.91	120.30
1	A	413	ASP	CB-CG-OD1	-6.71	112.26	118.30
1	A	80	GLY	N-CA-C	-6.62	96.56	113.10
1	D	133	ASP	CB-CG-OD1	-6.60	112.36	118.30
1	F	354	ASP	CB-CG-OD1	6.55	124.20	118.30
1	D	55	GLU	OE1-CD-OE2	-6.54	115.46	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	315	ARG	NE-CZ-NH1	-6.47	117.06	120.30
1	E	243	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	E	315	ARG	NE-CZ-NH2	6.41	123.50	120.30
1	F	322	ASP	CB-CG-OD2	6.36	124.02	118.30
1	E	413	ASP	CB-CG-OD1	6.35	124.01	118.30
1	C	286	ARG	NE-CZ-NH1	-6.32	117.14	120.30
1	C	147	ARG	NE-CZ-NH1	-6.30	117.15	120.30
1	A	74	GLY	N-CA-C	-6.29	97.38	113.10
1	B	239	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	F	211	ARG	NE-CZ-NH1	-6.24	117.18	120.30
1	F	216	ASP	CB-CG-OD2	6.21	123.89	118.30
1	E	228	ARG	NE-CZ-NH2	6.10	123.35	120.30
1	F	371	ILE	CG1-CB-CG2	-6.09	98.01	111.40
1	C	231	LEU	CA-CB-CG	6.03	129.16	115.30
1	C	337	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	E	337	ARG	NE-CZ-NH2	5.99	123.30	120.30
1	B	183	ARG	NE-CZ-NH1	-5.87	117.36	120.30
1	D	364	ASP	CB-CG-OD1	5.87	123.59	118.30
1	E	358	ARG	NE-CZ-NH2	5.81	123.21	120.30
1	D	337	ARG	NE-CZ-NH1	-5.78	117.41	120.30
1	A	274	ARG	NE-CZ-NH1	-5.76	117.42	120.30
1	B	358	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	F	372	LEU	CB-CA-C	-5.76	99.26	110.20
1	E	239	ARG	NE-CZ-NH2	5.75	123.18	120.30
1	D	239	ARG	NE-CZ-NH1	-5.75	117.43	120.30
1	E	87	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	E	239	ARG	NE-CZ-NH1	-5.71	117.44	120.30
1	C	147	ARG	NE-CZ-NH2	5.69	123.15	120.30
1	D	87	ARG	NE-CZ-NH2	5.67	123.14	120.30
1	D	158	PHE	CB-CG-CD2	-5.61	116.87	120.80
1	D	87	ARG	NE-CZ-NH1	-5.60	117.50	120.30
1	D	219	GLU	OE1-CD-OE2	-5.59	116.59	123.30
1	B	224	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	E	286	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	F	87	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	E	80	GLY	N-CA-C	-5.50	99.36	113.10
1	C	286	ARG	NE-CZ-NH2	5.46	123.03	120.30
1	D	315	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	C	18	TYR	CB-CG-CD1	5.39	124.23	121.00
1	A	373	ASP	CB-CA-C	-5.38	99.65	110.40
1	B	161	LEU	CA-CB-CG	5.37	127.64	115.30
1	F	55	GLU	OE1-CD-OE2	-5.32	116.91	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	232	GLU	OE1-CD-OE2	-5.27	116.97	123.30
1	D	195	ARG	NE-CZ-NH2	5.25	122.92	120.30
1	C	86	SER	CA-CB-OG	-5.17	97.24	111.20
1	D	322	ASP	CB-CG-OD1	5.17	122.95	118.30
1	B	413	ASP	CB-CG-OD1	5.16	122.94	118.30
1	C	191	GLU	CG-CD-OE1	5.15	128.60	118.30
1	B	249	GLU	OE1-CD-OE2	-5.14	117.13	123.30
1	D	372	LEU	CB-CA-C	-5.11	100.48	110.20
1	F	337	ARG	NE-CZ-NH1	-5.09	117.76	120.30
1	C	362	ARG	NE-CZ-NH1	5.07	122.84	120.30
1	E	332	LEU	CB-CG-CD1	5.06	119.61	111.00
1	F	358	ARG	NE-CZ-NH1	-5.04	117.78	120.30
1	D	39	GLU	OE1-CD-OE2	-5.04	117.25	123.30
1	B	75	ASP	CB-CG-OD1	5.00	122.80	118.30

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	3329	0	3283	65	0
1	B	3347	0	3303	64	0
1	C	3274	0	3126	61	0
1	D	3324	0	3234	63	1
1	E	3334	0	3295	73	0
1	F	3350	0	3334	65	1
2	A	18	0	24	3	0
2	B	12	0	16	2	0
2	C	6	0	8	6	0
2	D	36	0	48	3	0
2	E	30	0	40	0	0
2	F	24	0	32	0	0
3	A	8	0	12	3	0
3	B	16	0	24	0	0
3	C	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	8	0	12	0	0
3	F	8	0	12	0	0
4	A	49	0	0	0	0
4	B	28	0	0	0	0
4	C	19	0	0	0	0
4	D	38	0	0	0	0
4	E	56	0	0	0	0
4	F	40	0	0	0	0
All	All	20358	0	19809	369	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (369) 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:191:GLU:OE1	1:A:206:ARG:NH1	1.63	1.32
1:F:394:LYS:NZ	1:F:422:GLU:OE2	1.65	1.29
1:B:325:ARG:O	1:B:358:ARG:NH2	1.76	1.18
1:D:206:ARG:NH1	1:D:287:ASP:OD2	1.78	1.16
1:A:243:ARG:HH12	1:A:388:THR:HB	0.97	1.13
1:F:57:LYS:NZ	1:F:61:ASP:OD1	1.89	1.05
1:A:206:ARG:NH2	1:A:286:ARG:O	1.93	1.01
1:A:243:ARG:NH1	1:A:388:THR:HB	1.76	1.00
1:F:425:VAL:HA	1:F:430:THR:HA	1.48	0.95
1:A:99:THR:HG21	1:A:104:GLN:HG2	1.49	0.93
1:E:243:ARG:NH2	1:E:388:THR:HB	1.88	0.87
1:D:55:GLU:O	1:D:59:LEU:HD13	1.76	0.85
1:A:369:PRO:HG2	1:A:391:MET:HB2	1.57	0.84
1:D:421:TYR:HA	1:D:434:PRO:HD3	1.60	0.84
1:A:243:ARG:HH12	1:A:388:THR:CB	1.89	0.81
1:D:305:GLY:H	2:D:604:GOL:H2	1.46	0.81
1:F:66:ILE:HG22	1:F:66:ILE:O	1.82	0.78
1:F:149:LYS:HG3	1:F:158:PHE:CZ	2.20	0.77
1:C:369:PRO:HG2	1:C:391:MET:CB	2.16	0.76
1:B:146:PRO:HD2	1:B:162:SER:HB3	1.68	0.75
1:F:190:VAL:HA	1:F:200:ILE:HG22	1.69	0.74
1:E:390:GLU:O	1:E:409:VAL:HB	1.87	0.73
1:A:126:SER:HB3	1:A:177:GLU:OE1	1.89	0.73
1:C:352:PRO:HG3	1:C:377:PHE:CD1	2.23	0.73
1:B:352:PRO:HG2	1:B:421:TYR:CE2	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:150:LYS:O	1:F:157:LYS:N	2.22	0.72
1:F:13:PHE:HE1	1:F:184:LEU:CD1	2.03	0.71
1:E:63:THR:HG23	1:E:68:VAL:O	1.91	0.71
1:E:243:ARG:HH21	1:E:388:THR:HB	1.55	0.71
1:F:168:SER:OG	1:F:172:ARG:NH2	2.24	0.70
1:B:100:ALA:O	1:B:183:ARG:NH2	2.26	0.69
1:B:262:THR:HB	2:B:601:GOL:H31	1.74	0.69
1:D:425:VAL:HA	1:D:429:GLN:HA	1.75	0.69
1:F:138:LEU:HD11	1:F:161:LEU:HD21	1.73	0.69
1:A:27:ASN:HA	1:A:68:VAL:CG1	2.23	0.69
1:D:204:ASN:O	1:D:225:PRO:HD3	1.94	0.68
1:D:351:SER:HB2	1:D:353:ILE:CD1	2.24	0.68
1:E:278:ILE:HG12	1:F:147:ARG:HH12	1.58	0.68
1:D:338:LEU:HD12	1:E:325:ARG:HD2	1.74	0.67
1:F:14:GLY:HA2	1:F:55:GLU:OE2	1.93	0.67
1:F:139:HIS:HB3	1:F:147:ARG:HE	1.60	0.66
1:A:324:MET:HE2	1:A:345:GLY:HA3	1.78	0.66
1:C:62:ILE:O	1:C:66:ILE:HG12	1.96	0.66
1:E:35:LEU:HD22	1:E:72:ILE:HD13	1.76	0.65
1:B:280:LYS:HE2	1:B:295:THR:HG21	1.79	0.65
1:E:278:ILE:HD11	1:F:158:PHE:CE2	2.31	0.65
1:F:151:GLY:HA3	1:F:156:TRP:HA	1.77	0.65
1:A:35:LEU:HD22	1:A:72:ILE:HD13	1.79	0.65
1:B:394:LYS:N	1:B:406:ARG:O	2.29	0.65
1:F:206:ARG:NH2	1:F:287:ASP:OD2	2.30	0.65
1:C:263:THR:H	2:C:601:GOL:H31	1.60	0.64
1:B:59:LEU:O	1:B:63:THR:HG23	1.98	0.64
1:B:241:ILE:HG22	1:B:245:GLU:OE1	1.97	0.64
1:F:13:PHE:CE1	1:F:184:LEU:CD1	2.80	0.64
1:C:145:VAL:O	1:C:147:ARG:HD2	1.98	0.63
1:B:352:PRO:HG2	1:B:421:TYR:HE2	1.62	0.63
1:C:416:THR:HG22	1:C:418:ASN:CB	2.29	0.63
1:A:232:GLU:CD	1:A:274:ARG:HH12	2.01	0.63
1:B:280:LYS:CE	1:B:295:THR:HG21	2.27	0.63
1:D:305:GLY:N	2:D:604:GOL:H2	2.12	0.63
1:B:408:VAL:HG12	1:B:424:TYR:HB3	1.78	0.62
1:A:240:LEU:HD12	1:A:386:VAL:HG21	1.81	0.62
1:C:260:GLY:H	2:C:601:GOL:H12	1.63	0.62
1:F:149:LYS:HG3	1:F:158:PHE:CE1	2.34	0.62
1:E:63:THR:HG21	1:E:70:PHE:HB2	1.82	0.61
1:E:32:LYS:HD2	1:E:75:ASP:HA	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:GLU:HG3	1:B:62:ILE:HD12	1.83	0.60
1:D:97:ILE:HG21	1:D:108:CYS:SG	2.40	0.60
1:C:6:LEU:CD2	1:C:15:VAL:HG21	2.32	0.60
1:A:327:ASP:HB3	1:A:362:ARG:HH22	1.67	0.60
1:A:410:GLU:CD	1:A:419:THR:HG21	2.23	0.59
1:B:295:THR:HB	1:C:141:LYS:HE2	1.85	0.59
1:B:369:PRO:HG2	1:B:391:MET:HB2	1.84	0.59
1:F:286:ARG:HH21	1:F:298:SER:HB2	1.68	0.59
1:A:97:ILE:HG12	1:A:108:CYS:SG	2.42	0.59
1:D:420:GLU:O	1:D:434:PRO:HD2	2.03	0.59
1:C:191:GLU:CD	1:C:206:ARG:HH11	2.06	0.59
1:B:135:THR:HG23	1:B:135:THR:O	2.03	0.59
1:E:356:ILE:HG22	1:E:356:ILE:O	2.03	0.58
1:C:126:SER:HB3	1:C:177:GLU:OE2	2.02	0.58
1:A:97:ILE:HD12	1:A:99:THR:HG23	1.85	0.58
1:D:335:ASP:OD1	1:E:325:ARG:NH2	2.30	0.58
1:F:13:PHE:HE1	1:F:184:LEU:HD11	1.66	0.58
1:C:422:GLU:N	1:C:433:VAL:O	2.36	0.58
1:C:260:GLY:HA2	2:C:601:GOL:H32	1.86	0.58
1:D:147:ARG:HD3	1:D:160:ASN:OD1	2.04	0.58
1:D:351:SER:HB2	1:D:353:ILE:HD13	1.86	0.57
1:F:59:LEU:O	1:F:63:THR:HG23	2.04	0.57
1:F:13:PHE:CE1	1:F:184:LEU:HD13	2.39	0.57
1:C:358:ARG:HG3	1:C:358:ARG:HH11	1.69	0.57
1:D:394:LYS:HE3	1:D:395:VAL:O	2.05	0.57
1:B:131:PHE:CD1	1:B:135:THR:CG2	2.88	0.57
1:B:363:VAL:HG11	1:B:371:ILE:HD12	1.85	0.57
1:D:201:GLN:OE1	1:D:201:GLN:HA	2.05	0.57
1:D:394:LYS:C	1:D:405:ALA:HB1	2.26	0.57
1:A:39:GLU:HB2	1:F:107:ILE:HD11	1.87	0.56
1:C:206:ARG:NH2	1:C:286:ARG:O	2.38	0.56
1:A:410:GLU:OE1	1:A:419:THR:HG21	2.05	0.56
1:C:356:ILE:CD1	1:C:372:LEU:HD22	2.35	0.56
1:B:63:THR:HG21	1:B:70:PHE:HB2	1.87	0.56
1:D:156:TRP:O	1:D:156:TRP:HE3	1.87	0.56
1:B:66:ILE:O	1:B:66:ILE:HG12	2.05	0.56
1:B:260:GLY:HA2	2:B:601:GOL:H32	1.88	0.56
1:B:243:ARG:NH1	1:B:247:ARG:HE	2.03	0.56
1:C:141:LYS:O	1:C:144:THR:HB	2.05	0.56
1:D:6:LEU:CD1	1:D:28:VAL:HG13	2.36	0.56
1:C:37:GLU:HA	1:C:40:ARG:HD2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:324:MET:HE1	1:F:345:GLY:HA3	1.88	0.55
1:B:371:ILE:HG22	1:B:372:LEU:HD12	1.88	0.55
1:D:396:PRO:HB3	1:D:424:TYR:CE2	2.40	0.55
1:D:394:LYS:HE2	1:D:422:GLU:OE2	2.07	0.55
1:E:334:VAL:HG13	1:E:371:ILE:HD12	1.89	0.55
1:C:125:LEU:HD13	1:C:127:PHE:CE1	2.42	0.55
1:A:76:ASP:OD1	1:A:78:LYS:HB3	2.07	0.54
1:B:145:VAL:O	1:B:147:ARG:HG3	2.07	0.54
1:C:252:ILE:HD11	1:C:359:PHE:CE2	2.42	0.54
1:B:280:LYS:CE	1:B:295:THR:CG2	2.85	0.54
1:C:18:TYR:CE2	1:C:118:LEU:HG	2.43	0.54
1:E:126:SER:HB3	1:E:177:GLU:OE1	2.08	0.54
1:F:236:LEU:CD2	1:F:383:VAL:HG21	2.37	0.54
1:F:58:LYS:O	1:F:62:ILE:HG12	2.08	0.54
1:B:353:ILE:O	1:B:357:HIS:HB3	2.07	0.54
1:C:4:LEU:HD23	1:C:98:VAL:HG21	1.90	0.54
1:F:139:HIS:CB	1:F:147:ARG:HH21	2.21	0.54
1:C:266:GLN:HA	1:C:288:MET:CE	2.38	0.54
1:F:426:PHE:N	1:F:429:GLN:O	2.41	0.54
1:C:88:GLU:OE2	1:D:32:LYS:NZ	2.42	0.54
1:E:186:LYS:HE3	1:F:143:ASP:OD2	2.08	0.53
1:E:334:VAL:HG13	1:E:371:ILE:CD1	2.38	0.53
1:D:16:SER:CB	1:D:55:GLU:OE1	2.56	0.53
1:F:13:PHE:CE1	1:F:184:LEU:HD11	2.43	0.53
1:B:75:ASP:OD1	1:B:78:LYS:HB2	2.08	0.53
1:F:67:LEU:HD12	1:F:67:LEU:N	2.23	0.53
1:C:69:ASN:HB3	1:C:71:GLU:OE1	2.08	0.53
1:F:358:ARG:O	1:F:362:ARG:HG3	2.09	0.53
1:A:324:MET:CE	1:A:345:GLY:HA3	2.38	0.53
1:A:353:ILE:O	1:A:357:HIS:HB3	2.08	0.53
1:D:353:ILE:HD12	1:D:353:ILE:H	1.73	0.53
1:D:358:ARG:O	1:D:362:ARG:HG3	2.09	0.52
1:E:332:LEU:HD21	1:E:336:LEU:HD11	1.92	0.52
1:E:251:ILE:HG12	1:E:374:THR:CG2	2.38	0.52
1:D:49:ALA:O	1:D:53:LEU:HB2	2.09	0.52
1:B:295:THR:HB	1:C:141:LYS:CE	2.40	0.52
1:A:7:ASP:OD1	1:A:9:SER:HB3	2.09	0.52
1:B:131:PHE:HD1	1:B:135:THR:CG2	2.22	0.52
1:E:146:PRO:HD2	1:E:162:SER:HB3	1.92	0.52
1:E:286:ARG:NH2	1:F:213:PRO:O	2.43	0.52
1:E:7:ASP:OD2	1:E:104:GLN:OE1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:ILE:CD1	1:C:359:PHE:CE2	2.93	0.51
1:D:106:LYS:HE2	1:E:54:ASP:OD1	2.09	0.51
1:E:332:LEU:O	1:E:332:LEU:HD23	2.10	0.51
1:A:41:GLU:HB3	1:A:46:LEU:HD12	1.90	0.51
1:A:7:ASP:OD2	1:A:99:THR:HB	2.10	0.51
1:C:191:GLU:CD	1:C:206:ARG:NH1	2.63	0.51
1:E:278:ILE:HD11	1:F:158:PHE:CZ	2.45	0.51
1:D:16:SER:HB2	1:D:55:GLU:OE1	2.10	0.51
1:F:252:ILE:CG1	1:F:372:LEU:HD21	2.41	0.51
1:D:421:TYR:CA	1:D:434:PRO:HD3	2.38	0.51
1:E:20:GLU:HB2	1:E:62:ILE:HD13	1.91	0.51
1:C:273:MET:HG3	1:C:274:ARG:N	2.22	0.51
1:E:141:LYS:O	1:E:144:THR:HG22	2.10	0.51
1:E:243:ARG:NH1	1:E:374:THR:HB	2.25	0.51
1:E:351:SER:C	1:E:377:PHE:HZ	2.14	0.51
1:C:262:THR:HB	2:C:601:GOL:H31	1.93	0.51
1:A:368:ILE:HB	1:A:369:PRO:HD3	1.93	0.50
1:F:66:ILE:CG2	1:F:66:ILE:O	2.52	0.50
1:A:224:ARG:HG3	1:A:225:PRO:HD2	1.93	0.50
1:A:423:ILE:HG12	1:A:431:MET:HG3	1.92	0.50
1:E:141:LYS:NZ	1:E:216:ASP:OD1	2.44	0.50
1:E:5:MET:HE1	1:E:89:TYR:CD1	2.46	0.50
1:D:395:VAL:HA	1:D:405:ALA:HA	1.93	0.50
1:F:57:LYS:NZ	1:F:61:ASP:CG	2.63	0.50
1:D:125:LEU:HD12	1:D:128:GLU:OE1	2.11	0.50
1:B:241:ILE:CG2	1:B:245:GLU:OE1	2.60	0.50
1:F:315:ARG:NH1	1:F:339:ALA:O	2.45	0.50
1:A:263:THR:CB	2:A:601:GOL:HO1	2.25	0.49
1:A:7:ASP:OD2	1:A:99:THR:CG2	2.60	0.49
1:B:252:ILE:HD11	1:B:356:ILE:HG22	1.92	0.49
1:F:352:PRO:O	1:F:356:ILE:HG13	2.12	0.49
1:A:369:PRO:CG	1:A:391:MET:HB2	2.38	0.49
1:A:240:LEU:CD1	1:A:386:VAL:HG21	2.43	0.49
1:E:363:VAL:HG23	1:E:368:ILE:CD1	2.42	0.49
1:A:262:THR:HB	2:A:601:GOL:H11	1.95	0.49
1:A:420:GLU:O	1:A:434:PRO:HD2	2.12	0.49
1:B:149:LYS:HG2	1:B:156:TRP:CD1	2.48	0.49
1:B:191:GLU:OE2	1:B:206:ARG:NH2	2.46	0.49
1:B:146:PRO:HG3	1:B:166:MET:CE	2.42	0.49
1:C:371:ILE:HG22	1:C:372:LEU:HD12	1.95	0.49
1:D:182:VAL:HA	1:D:188:SER:OG	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:425:VAL:CA	1:D:429:GLN:HA	2.43	0.48
1:B:420:GLU:O	1:B:434:PRO:HD2	2.14	0.48
1:D:105:LYS:HG3	1:D:115:TYR:CE2	2.49	0.48
1:B:126:SER:HB3	1:B:177:GLU:OE1	2.13	0.48
1:D:152:LYS:CB	1:D:153:PRO:HD2	2.43	0.48
1:F:408:VAL:HG12	1:F:424:TYR:HB3	1.93	0.48
1:C:263:THR:N	2:C:601:GOL:H31	2.27	0.48
1:C:152:LYS:O	1:C:156:TRP:HD1	1.96	0.48
1:E:278:ILE:HD12	1:E:317:ASP:OD2	2.12	0.48
1:E:420:GLU:O	1:E:433:VAL:HG23	2.14	0.48
1:A:157:LYS:HE2	3:A:604:EDO:C1	2.44	0.48
1:E:191:GLU:OE1	1:E:301:TYR:OH	2.19	0.48
1:F:139:HIS:HB2	1:F:147:ARG:HH21	1.77	0.48
1:F:424:TYR:CE1	1:F:433:VAL:HG11	2.49	0.48
1:D:352:PRO:O	1:D:356:ILE:HG13	2.13	0.47
1:E:352:PRO:HB3	1:E:377:PHE:HE2	1.79	0.47
1:D:424:TYR:OH	1:D:432:ILE:HG21	2.14	0.47
1:E:390:GLU:O	1:E:409:VAL:CB	2.59	0.47
1:C:158:PHE:CD1	1:C:158:PHE:C	2.88	0.47
1:D:136:MET:HG3	1:D:151:GLY:O	2.14	0.47
1:D:378:ILE:HD13	1:D:383:VAL:HG12	1.96	0.47
1:B:152:LYS:O	1:B:156:TRP:N	2.47	0.47
1:C:4:LEU:HD11	1:C:25:THR:O	2.15	0.47
1:D:252:ILE:CG1	1:D:372:LEU:HD21	2.45	0.47
1:B:260:GLY:O	1:B:263:THR:HG22	2.15	0.47
1:B:364:ASP:OD2	1:C:354:ASP:HB3	2.14	0.47
1:E:411:ILE:N	1:E:411:ILE:HD12	2.30	0.47
1:E:416:THR:CG2	1:E:418:ASN:CB	2.93	0.47
1:A:12:LEU:HD22	1:A:48:SER:HB3	1.96	0.47
1:D:107:ILE:HD11	1:E:39:GLU:HB2	1.96	0.47
1:B:419:THR:O	1:B:419:THR:HG23	2.15	0.47
1:E:332:LEU:C	1:E:332:LEU:HD23	2.36	0.47
1:A:26:GLY:O	1:A:68:VAL:HG11	2.14	0.46
1:B:205:TYR:CE1	1:B:224:ARG:HG3	2.50	0.46
1:B:75:ASP:OD1	1:B:78:LYS:N	2.46	0.46
1:D:73:VAL:HG21	1:D:89:TYR:CE2	2.50	0.46
1:F:130:PHE:N	1:F:130:PHE:CD1	2.83	0.46
1:E:306:GLU:OE2	1:F:197:SER:CB	2.63	0.46
1:A:324:MET:HE1	1:A:359:PHE:HZ	1.79	0.46
1:B:132:ASP:O	1:B:135:THR:HG22	2.16	0.46
1:A:50:GLU:CB	1:A:172:ARG:HH12	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:LYS:O	1:B:62:ILE:HG12	2.14	0.46
1:C:266:GLN:HA	1:C:288:MET:HE2	1.97	0.46
1:E:63:THR:CG2	1:E:68:VAL:O	2.61	0.46
1:E:105:LYS:HG3	1:E:115:TYR:CE2	2.51	0.46
1:E:78:LYS:HG2	1:E:80:GLY:CA	2.46	0.46
1:A:146:PRO:HD2	1:A:162:SER:HB3	1.98	0.46
1:E:242:LYS:O	1:E:246:GLU:HB2	2.15	0.45
1:E:330:PHE:CD2	1:E:358:ARG:HG2	2.51	0.45
1:E:74:GLY:O	1:E:75:ASP:C	2.54	0.45
1:B:280:LYS:HE3	1:B:295:THR:CG2	2.46	0.45
1:B:140:ILE:HG23	1:B:166:MET:CE	2.47	0.45
1:C:261:ALA:N	2:C:601:GOL:H11	2.31	0.45
1:C:352:PRO:HG3	1:C:377:PHE:CG	2.51	0.45
1:E:315:ARG:NH2	1:E:315:ARG:HG2	2.31	0.45
1:E:416:THR:HG22	1:E:418:ASN:CB	2.47	0.45
1:F:369:PRO:HG2	1:F:391:MET:HB2	1.98	0.45
1:F:63:THR:HG21	1:F:70:PHE:HB2	1.97	0.45
1:B:135:THR:O	1:B:135:THR:CG2	2.65	0.45
1:C:151:GLY:HA3	1:C:156:TRP:HA	1.98	0.45
1:B:8:LYS:HE3	1:B:12:LEU:HD11	1.98	0.45
1:C:252:ILE:HD11	1:C:359:PHE:CZ	2.52	0.45
1:D:142:GLU:OE2	1:D:218:TRP:HD1	2.00	0.45
1:D:352:PRO:HD3	1:D:377:PHE:CE2	2.52	0.45
1:E:315:ARG:HH21	1:E:315:ARG:CG	2.30	0.45
1:E:421:TYR:CE2	1:E:433:VAL:HB	2.52	0.45
1:E:178:ILE:HG23	1:E:202:LEU:HD22	1.97	0.45
1:E:332:LEU:CD2	1:E:336:LEU:HD11	2.47	0.45
1:A:39:GLU:HB2	1:F:107:ILE:CD1	2.47	0.45
1:C:103:THR:O	1:C:107:ILE:HD13	2.17	0.45
1:A:157:LYS:HE2	3:A:604:EDO:H12	1.99	0.45
1:B:66:ILE:HG23	1:B:68:VAL:HG13	1.99	0.44
1:D:284:SER:HA	1:D:285:PRO:HA	1.69	0.44
1:B:363:VAL:CG1	1:B:371:ILE:HD12	2.48	0.44
1:A:243:ARG:NH1	1:A:374:THR:HG22	2.32	0.44
1:C:132:ASP:O	1:C:224:ARG:NH2	2.49	0.44
1:C:358:ARG:HG3	1:C:358:ARG:NH1	2.33	0.44
1:E:62:ILE:O	1:E:66:ILE:HG12	2.17	0.44
1:F:236:LEU:HD23	1:F:383:VAL:HG21	2.00	0.44
1:B:131:PHE:CD1	1:B:135:THR:HG21	2.52	0.44
1:A:126:SER:CB	1:A:177:GLU:OE1	2.62	0.44
1:A:325:ARG:HD3	1:F:338:LEU:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:THR:O	1:C:107:ILE:CD1	2.66	0.44
1:A:62:ILE:O	1:A:66:ILE:HG12	2.18	0.43
1:C:125:LEU:HD13	1:C:127:PHE:HE1	1.83	0.43
1:E:249:GLU:HG3	1:E:337:ARG:NH2	2.33	0.43
1:A:158:PHE:C	1:A:158:PHE:CD1	2.91	0.43
1:A:144:THR:HG22	1:A:145:VAL:O	2.19	0.43
1:C:191:GLU:OE1	1:C:206:ARG:NH1	2.51	0.43
1:D:147:ARG:NH1	1:D:158:PHE:CD2	2.87	0.43
1:D:252:ILE:HG13	1:D:372:LEU:HD21	2.00	0.43
1:F:400:LYS:O	1:F:403:ASP:N	2.50	0.43
1:B:131:PHE:CD1	1:B:135:THR:HG23	2.52	0.43
1:B:425:VAL:HG23	1:B:429:GLN:CA	2.48	0.43
1:C:280:LYS:HD3	1:C:295:THR:HB	2.01	0.43
1:E:132:ASP:OD2	1:E:150:LYS:NZ	2.40	0.43
1:F:182:VAL:O	1:F:185:ILE:O	2.37	0.43
1:A:393:VAL:HA	1:A:407:PRO:HA	2.00	0.43
1:C:126:SER:HB2	1:C:177:GLU:OE1	2.17	0.43
1:D:408:VAL:CG1	1:D:422:GLU:HG2	2.48	0.43
1:A:160:ASN:OD1	1:A:160:ASN:N	2.52	0.43
1:A:68:VAL:HG12	1:A:69:ASN:N	2.33	0.43
1:C:243:ARG:HH22	1:C:388:THR:CB	2.31	0.43
1:A:276:GLY:O	1:B:158:PHE:HB3	2.19	0.43
1:A:421:TYR:HA	1:A:433:VAL:HA	1.99	0.43
1:D:147:ARG:CZ	1:D:158:PHE:CD2	3.02	0.43
1:C:6:LEU:HD23	1:C:15:VAL:HG21	2.00	0.43
1:E:306:GLU:OE2	1:F:197:SER:HB2	2.19	0.43
1:B:356:ILE:HG21	1:B:375:ILE:HD11	2.00	0.43
1:D:5:MET:HE2	1:D:30:ILE:HA	2.01	0.43
1:E:332:LEU:CD2	1:E:336:LEU:CD1	2.97	0.43
1:E:339:ALA:HB2	1:F:257:PRO:HB2	1.99	0.43
1:F:204:ASN:O	1:F:225:PRO:HD3	2.18	0.43
1:C:4:LEU:HD23	1:C:98:VAL:CG2	2.48	0.43
1:E:132:ASP:HB2	1:E:135:THR:OG1	2.18	0.43
1:E:364:ASP:O	1:E:367:THR:HB	2.19	0.43
1:D:110:ALA:HB1	1:E:72:ILE:HD11	2.00	0.43
1:E:421:TYR:HA	1:E:434:PRO:HD2	2.00	0.42
1:A:262:THR:HB	2:A:601:GOL:H31	2.00	0.42
1:C:47:VAL:O	1:C:51:ILE:HD12	2.19	0.42
1:D:5:MET:HE3	1:D:29:LEU:HB2	2.01	0.42
1:E:368:ILE:HB	1:E:369:PRO:HD3	2.00	0.42
1:F:242:LYS:HG2	1:F:246:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:VAL:O	1:A:289:HIS:ND1	2.52	0.42
1:D:3:ASP:HB3	1:D:29:LEU:HD11	2.02	0.42
1:E:60:LYS:O	1:E:63:THR:HB	2.19	0.42
1:E:88:GLU:O	1:E:92:GLU:HG3	2.20	0.42
1:F:424:TYR:CZ	1:F:433:VAL:HG11	2.55	0.42
1:B:315:ARG:NH1	1:B:339:ALA:O	2.52	0.42
1:F:252:ILE:HG12	1:F:372:LEU:HD21	2.02	0.42
1:A:59:LEU:O	1:A:63:THR:HG23	2.20	0.42
1:C:284:SER:HA	1:C:285:PRO:HA	1.71	0.42
1:E:378:ILE:HD13	1:E:383:VAL:HG12	2.01	0.42
1:B:5:MET:HE1	1:B:89:TYR:CD2	2.55	0.42
1:D:147:ARG:NH1	1:D:158:PHE:HB3	2.35	0.42
1:B:178:ILE:HG23	1:B:202:LEU:HD22	2.01	0.41
1:A:97:ILE:CD1	1:A:99:THR:HG23	2.50	0.41
1:D:105:LYS:HE3	1:D:115:TYR:OH	2.20	0.41
1:C:73:VAL:HG21	1:C:89:TYR:CZ	2.55	0.41
1:D:247:ARG:HB3	2:D:605:GOL:O2	2.20	0.41
1:E:125:LEU:HB2	1:E:128:GLU:HG3	2.00	0.41
1:F:392:THR:HG21	1:F:410:GLU:OE1	2.20	0.41
1:A:144:THR:HG21	1:A:147:ARG:NH2	2.35	0.41
1:C:422:GLU:O	1:C:433:VAL:N	2.40	0.41
1:D:180:ASN:O	1:D:183:ARG:HG3	2.20	0.41
1:D:138:LEU:HA	1:D:138:LEU:HD12	1.84	0.41
1:D:46:LEU:HD23	1:D:46:LEU:HA	1.90	0.41
1:E:156:TRP:C	1:E:156:TRP:CD1	2.94	0.41
1:B:142:GLU:OE2	1:B:218:TRP:HD1	2.03	0.41
1:D:201:GLN:OE1	1:D:205:TYR:O	2.39	0.41
1:E:315:ARG:NH2	1:E:315:ARG:CG	2.84	0.41
1:A:416:THR:CG2	1:A:418:ASN:CB	2.99	0.41
1:A:7:ASP:CG	1:A:99:THR:HG22	2.41	0.41
1:C:358:ARG:CD	1:C:358:ARG:H	2.34	0.41
1:F:236:LEU:HD22	1:F:240:LEU:HD23	2.02	0.41
1:C:266:GLN:HA	1:C:288:MET:HE3	2.03	0.41
1:A:145:VAL:HG12	1:A:146:PRO:O	2.20	0.41
1:C:88:GLU:HA	1:C:88:GLU:OE1	2.20	0.41
1:F:91:LEU:HA	1:F:91:LEU:HD23	1.91	0.41
1:B:53:LEU:HA	1:B:53:LEU:HD23	1.87	0.40
1:E:237:ASP:N	1:E:237:ASP:OD1	2.52	0.40
1:D:107:ILE:CD1	1:E:39:GLU:HB2	2.51	0.40
1:F:255:GLY:O	1:F:348:HIS:HA	2.20	0.40
1:A:284:SER:O	3:A:605:EDO:H12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:LYS:O	1:A:79:LYS:C	2.58	0.40
1:E:356:ILE:HD11	1:E:375:ILE:CD1	2.51	0.40
1:F:200:ILE:HG13	1:F:207:VAL:HB	2.03	0.40
1:A:284:SER:HA	1:A:285:PRO:HA	1.73	0.40
1:C:273:MET:CG	1:C:274:ARG:N	2.82	0.40
1:F:13:PHE:CZ	1:F:184:LEU:HD13	2.56	0.40
1:A:45:GLY:O	1:A:211:ARG:NH2	2.42	0.40
1:F:97:ILE:HD12	1:F:108:CYS:SG	2.61	0.40
1:B:132:ASP:OD1	1:B:135:THR:HB	2.21	0.40
1:B:140:ILE:HG23	1:B:166:MET:HE3	2.03	0.40
1:B:146:PRO:HG3	1:B:166:MET:HE1	2.03	0.40
1:B:393:VAL:HA	1:B:407:PRO:HA	2.03	0.40
1:C:413:ASP:HB3	1:C:416:THR:HB	2.03	0.40
1:D:327:ASP:OD1	1:D:358:ARG:NH2	2.54	0.40
1:D:5:MET:HE3	1:D:29:LEU:CB	2.51	0.40
1:F:363:VAL:HG11	1:F:371:ILE:HD13	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:GLY:O	1:F:121:LEU:O[2_356]	2.17	0.03

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	435/505 (86%)	426 (98%)	9 (2%)	0	100	100
1	B	433/505 (86%)	423 (98%)	9 (2%)	1 (0%)	52	80
1	C	434/505 (86%)	428 (99%)	6 (1%)	0	100	100
1	D	434/505 (86%)	423 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	434/505 (86%)	426 (98%)	7 (2%)	1 (0%)	52	80
1	F	434/505 (86%)	425 (98%)	9 (2%)	0	100	100
All	All	2604/3030 (86%)	2551 (98%)	51 (2%)	2 (0%)	56	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	75	ASP
1	B	407	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	348/447 (78%)	332 (95%)	16 (5%)	33	64
1	B	351/447 (78%)	334 (95%)	17 (5%)	31	62
1	C	328/447 (73%)	310 (94%)	18 (6%)	27	55
1	D	340/447 (76%)	327 (96%)	13 (4%)	40	71
1	E	350/447 (78%)	339 (97%)	11 (3%)	47	78
1	F	352/447 (79%)	336 (96%)	16 (4%)	34	65
All	All	2069/2682 (77%)	1978 (96%)	91 (4%)	35	65

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LYS
1	A	157	LYS
1	A	158	PHE
1	A	206	ARG
1	A	236	LEU
1	A	237	ASP
1	A	245	GLU
1	A	273	MET

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Mol	Chain	Res	Type
1	A	284	SER
1	A	300	ASN
1	A	357	HIS
1	A	358	ARG
1	A	362	ARG
1	A	373	ASP
1	A	388	THR
1	A	413	ASP
1	B	1	MET
1	B	78	LYS
1	B	81	GLU
1	B	111	MET
1	B	159	VAL
1	B	166	MET
1	B	195	ARG
1	B	224	ARG
1	B	245	GLU
1	B	247	ARG
1	B	273	MET
1	B	283	GLU
1	B	300	ASN
1	B	351	SER
1	B	356	ILE
1	B	358	ARG
1	B	391	MET
1	C	1	MET
1	C	40	ARG
1	C	86	SER
1	C	88	GLU
1	C	111	MET
1	C	128	GLU
1	C	133	ASP
1	C	143	ASP
1	C	166	MET
1	C	186	LYS
1	C	231	LEU
1	C	236	LEU
1	C	243	ARG
1	C	273	MET
1	C	283	GLU
1	C	300	ASN
1	C	358	ARG

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Mol	Chain	Res	Type
1	C	362	ARG
1	D	53	LEU
1	D	97	ILE
1	D	128	GLU
1	D	156	TRP
1	D	158	PHE
1	D	163	ASP
1	D	194	ARG
1	D	273	MET
1	D	303	GLU
1	D	327	ASP
1	D	365	ILE
1	D	400	LYS
1	D	404	LEU
1	E	111	MET
1	E	116	ASN
1	E	144	THR
1	E	228	ARG
1	E	237	ASP
1	E	243	ARG
1	E	315	ARG
1	E	358	ARG
1	E	361	ASN
1	E	411	ILE
1	E	419	THR
1	F	116	ASN
1	F	126	SER
1	F	143	ASP
1	F	147	ARG
1	F	192	ILE
1	F	200	ILE
1	F	229	LYS
1	F	273	MET
1	F	303	GLU
1	F	325	ARG
1	F	354	ASP
1	F	357	HIS
1	F	388	THR
1	F	403	ASP
1	F	404	LEU
1	F	435	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	300	ASN
1	B	379	ASN
1	C	123	GLN
1	D	27	ASN
1	D	180	ASN
1	E	104	GLN
1	E	116	ASN
1	E	361	ASN
1	E	370	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	GOL	A	601	-	5,5,5	0.36	0	5,5,5	0.79	0
2	GOL	A	602	-	5,5,5	0.66	0	5,5,5	0.62	0
2	GOL	A	603	-	5,5,5	0.74	0	5,5,5	0.64	0
3	EDO	A	604	-	3,3,3	0.64	0	2,2,2	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	A	605	-	3,3,3	0.70	0	2,2,2	0.09	0
2	GOL	B	601	-	5,5,5	0.15	0	5,5,5	1.03	0
2	GOL	B	602	-	5,5,5	0.73	0	5,5,5	0.71	0
3	EDO	B	603	-	3,3,3	0.59	0	2,2,2	0.34	0
3	EDO	B	604	-	3,3,3	0.65	0	2,2,2	0.19	0
3	EDO	B	605	-	3,3,3	0.60	0	2,2,2	0.81	0
3	EDO	B	606	-	3,3,3	0.53	0	2,2,2	0.16	0
2	GOL	C	601	-	5,5,5	0.54	0	5,5,5	0.74	0
3	EDO	C	602	-	3,3,3	0.59	0	2,2,2	0.38	0
2	GOL	D	601	-	5,5,5	0.27	0	5,5,5	0.27	0
2	GOL	D	602	-	5,5,5	0.78	0	5,5,5	0.88	0
2	GOL	D	603	-	5,5,5	0.55	0	5,5,5	0.78	0
2	GOL	D	604	-	5,5,5	0.68	0	5,5,5	0.76	0
2	GOL	D	605	-	5,5,5	0.40	0	5,5,5	0.32	0
2	GOL	D	606	-	5,5,5	0.67	0	5,5,5	0.36	0
3	EDO	D	607	-	3,3,3	0.51	0	2,2,2	0.32	0
3	EDO	D	608	-	3,3,3	0.75	0	2,2,2	0.37	0
2	GOL	E	601	-	5,5,5	0.50	0	5,5,5	0.40	0
2	GOL	E	602	-	5,5,5	0.38	0	5,5,5	0.55	0
2	GOL	E	603	-	5,5,5	0.67	0	5,5,5	0.41	0
2	GOL	E	604	-	5,5,5	0.80	0	5,5,5	0.90	0
2	GOL	E	605	-	5,5,5	0.72	0	5,5,5	0.76	0
2	GOL	F	601	-	5,5,5	0.50	0	5,5,5	0.94	1 (20%)
2	GOL	F	602	-	5,5,5	0.79	0	5,5,5	0.80	0
2	GOL	F	603	-	5,5,5	0.70	0	5,5,5	0.53	0
2	GOL	F	604	-	5,5,5	0.76	0	5,5,5	0.59	0
3	EDO	F	605	-	3,3,3	0.79	0	2,2,2	0.16	0
3	EDO	F	606	-	3,3,3	0.66	0	2,2,2	0.19	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	601	-	-	0/4/4/4	0/0/0/0
2	GOL	A	602	-	-	0/4/4/4	0/0/0/0
2	GOL	A	603	-	-	0/4/4/4	0/0/0/0
3	EDO	A	604	-	-	0/1/1/1	0/0/0/0
3	EDO	A	605	-	-	0/1/1/1	0/0/0/0
2	GOL	B	601	-	-	0/4/4/4	0/0/0/0
2	GOL	B	602	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	603	-	-	0/1/1/1	0/0/0/0
3	EDO	B	604	-	-	0/1/1/1	0/0/0/0
3	EDO	B	605	-	-	0/1/1/1	0/0/0/0
3	EDO	B	606	-	-	0/1/1/1	0/0/0/0
2	GOL	C	601	-	-	0/4/4/4	0/0/0/0
3	EDO	C	602	-	-	0/1/1/1	0/0/0/0
2	GOL	D	601	-	-	0/4/4/4	0/0/0/0
2	GOL	D	602	-	-	0/4/4/4	0/0/0/0
2	GOL	D	603	-	-	0/4/4/4	0/0/0/0
2	GOL	D	604	-	-	0/4/4/4	0/0/0/0
2	GOL	D	605	-	-	0/4/4/4	0/0/0/0
2	GOL	D	606	-	-	0/4/4/4	0/0/0/0
3	EDO	D	607	-	-	0/1/1/1	0/0/0/0
3	EDO	D	608	-	-	0/1/1/1	0/0/0/0
2	GOL	E	601	-	-	0/4/4/4	0/0/0/0
2	GOL	E	602	-	-	0/4/4/4	0/0/0/0
2	GOL	E	603	-	-	0/4/4/4	0/0/0/0
2	GOL	E	604	-	-	0/4/4/4	0/0/0/0
2	GOL	E	605	-	-	0/4/4/4	0/0/0/0
2	GOL	F	601	-	-	0/4/4/4	0/0/0/0
2	GOL	F	602	-	-	0/4/4/4	0/0/0/0
2	GOL	F	603	-	-	0/4/4/4	0/0/0/0
2	GOL	F	604	-	-	0/4/4/4	0/0/0/0
3	EDO	F	605	-	-	0/1/1/1	0/0/0/0
3	EDO	F	606	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	601	GOL	O2-C2-C1	2.00	118.08	108.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	GOL	3	0
3	A	604	EDO	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	605	EDO	1	0
2	B	601	GOL	2	0
2	C	601	GOL	6	0
2	D	604	GOL	2	0
2	D	605	GOL	1	0

## 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	437/505 (86%)	-0.15	11 (2%) 61 61	44, 72, 130, 185	0
1	B	435/505 (86%)	-0.15	11 (2%) 61 61	47, 81, 147, 192	0
1	C	436/505 (86%)	-0.02	30 (6%) 20 18	58, 95, 147, 179	0
1	D	436/505 (86%)	-0.09	12 (2%) 56 57	40, 86, 136, 163	0
1	E	436/505 (86%)	-0.04	17 (3%) 43 43	42, 71, 143, 213	0
1	F	436/505 (86%)	-0.11	16 (3%) 45 45	42, 74, 127, 162	0
All	All	2616/3030 (86%)	-0.09	97 (3%) 45 45	40, 80, 139, 213	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	404	LEU	8.7
1	E	403	ASP	7.7
1	B	405	ALA	6.7
1	B	399	LEU	6.4
1	B	402	ALA	6.0
1	E	397	ALA	5.9
1	E	402	ALA	5.8
1	B	154	GLY	5.5
1	B	398	GLY	5.1
1	F	121	LEU	4.7
1	E	398	GLY	4.7
1	C	405	ALA	4.6
1	C	393	VAL	4.5
1	E	399	LEU	4.4
1	F	405	ALA	4.2
1	E	405	ALA	4.2
1	B	397	ALA	4.1
1	F	399	LEU	4.0
1	D	399	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	403	ASP	3.8
1	A	404	LEU	3.7
1	E	392	THR	3.7
1	C	404	LEU	3.6
1	D	129	SER	3.6
1	B	130	PHE	3.6
1	C	427	GLY	3.6
1	A	402	ALA	3.5
1	E	393	VAL	3.4
1	E	425	VAL	3.4
1	C	387	TYR	3.4
1	F	159	VAL	3.3
1	E	401	GLU	3.3
1	A	398	GLY	3.3
1	A	400	LYS	3.3
1	C	416	THR	3.2
1	F	426	PHE	3.2
1	E	416	THR	3.2
1	D	402	ALA	3.2
1	D	400	LYS	3.1
1	F	424	TYR	3.0
1	C	406	ARG	3.0
1	C	407	PRO	3.0
1	E	406	ARG	2.9
1	A	403	ASP	2.9
1	A	436	ASN	2.9
1	D	30	ILE	2.8
1	C	430	THR	2.8
1	C	402	ALA	2.8
1	D	405	ALA	2.8
1	F	130	PHE	2.8
1	B	393	VAL	2.7
1	F	153	PRO	2.7
1	C	401	GLU	2.7
1	A	437	ARG	2.6
1	C	424	TYR	2.6
1	C	130	PHE	2.6
1	F	24	ILE	2.6
1	A	77	SER	2.6
1	A	399	LEU	2.6
1	D	403	ASP	2.6
1	F	155	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	402	ALA	2.5
1	C	396	PRO	2.5
1	E	394	LYS	2.5
1	C	397	ALA	2.5
1	A	75	ASP	2.4
1	C	122	LYS	2.4
1	C	400	LYS	2.4
1	C	89	TYR	2.4
1	C	399	LEU	2.4
1	F	403	ASP	2.4
1	D	130	PHE	2.4
1	E	436	ASN	2.3
1	D	71	GLU	2.3
1	E	400	LYS	2.3
1	C	436	ASN	2.3
1	E	426	PHE	2.3
1	F	157	LYS	2.2
1	F	315	ARG	2.2
1	B	234	TYR	2.2
1	C	124	GLY	2.2
1	C	121	LEU	2.2
1	A	184	LEU	2.1
1	D	121	LEU	2.1
1	D	404	LEU	2.1
1	C	398	GLY	2.1
1	C	74	GLY	2.1
1	C	69	ASN	2.1
1	C	411	ILE	2.1
1	C	24	ILE	2.0
1	B	1	MET	2.0
1	B	404	LEU	2.0
1	C	18	TYR	2.0
1	D	424	TYR	2.0
1	C	395	VAL	2.0
1	F	150	LYS	2.0
1	F	398	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	GOL	E	604	6/6	0.72	0.39	10.81	96,105,111,114	0
2	GOL	F	604	6/6	0.70	0.36	10.29	86,104,111,111	0
3	EDO	A	605	4/4	0.87	0.58	8.30	68,75,77,81	0
2	GOL	A	601	6/6	0.86	0.37	7.38	63,74,82,95	0
2	GOL	D	601	6/6	0.86	0.32	7.13	83,87,90,91	0
2	GOL	B	602	6/6	0.84	0.42	6.89	85,91,95,98	0
2	GOL	E	603	6/6	0.78	0.32	5.22	93,95,104,105	0
2	GOL	E	601	6/6	0.93	0.42	4.91	64,79,86,88	0
2	GOL	E	605	6/6	0.79	0.27	3.75	78,90,92,97	0
2	GOL	B	601	6/6	0.89	0.28	3.26	86,88,91,109	0
2	GOL	C	601	6/6	0.91	0.24	3.23	73,77,86,99	0
2	GOL	F	602	6/6	0.80	0.22	2.94	74,88,93,95	0
3	EDO	B	605	4/4	0.90	0.21	2.80	67,75,76,76	0
3	EDO	F	605	4/4	0.87	0.41	2.70	72,79,81,84	0
2	GOL	F	601	6/6	0.87	0.22	2.53	71,80,84,88	0
2	GOL	D	604	6/6	0.87	0.20	2.30	70,86,94,95	0
2	GOL	E	602	6/6	0.76	0.17	1.19	96,102,105,106	0
2	GOL	D	605	6/6	0.86	0.21	0.87	97,103,111,111	0
2	GOL	D	606	6/6	0.86	0.17	0.62	88,101,104,106	0
3	EDO	B	604	4/4	0.82	0.18	0.61	88,90,91,93	0
2	GOL	D	603	6/6	0.88	0.24	0.54	96,101,105,108	0
3	EDO	B	603	4/4	0.91	0.14	-0.29	70,72,75,77	0
3	EDO	C	602	4/4	0.83	0.14	-0.69	89,96,100,103	0
2	GOL	D	602	6/6	0.65	0.45	-	107,109,114,119	0
2	GOL	F	603	6/6	0.87	0.36	-	95,101,103,107	0
2	GOL	A	602	6/6	0.51	0.24	-	94,103,108,109	0
3	EDO	B	606	4/4	0.82	0.28	-	90,97,100,105	0
2	GOL	A	603	6/6	0.71	0.35	-	86,94,102,102	0
3	EDO	D	608	4/4	0.85	0.18	-	73,82,84,85	0
3	EDO	A	604	4/4	0.83	0.35	-	83,85,85,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	D	607	4/4	0.89	0.19	-	92,92,93,94	0
3	EDO	F	606	4/4	0.81	0.21	-	78,84,89,90	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.