



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:28 PM UTC

PDB ID : 4CBM / pdb_00004cbm
Title : Pestivirus NS3 helicase
Authors : Tortorici, M.A.; Duquerroy, S.; Kwok, J.; Vonnrhein, C.; Perez, J.; Lamp, B.;
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Deposited on : 2013-10-14
Resolution : 3.27 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

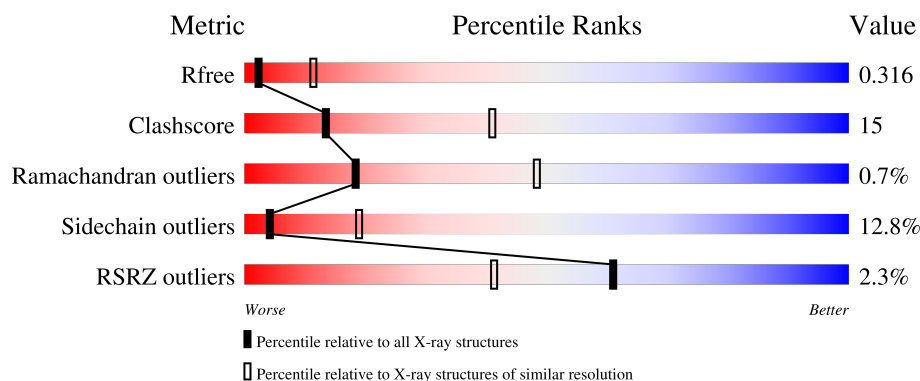
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.27 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1303 (3.30-3.26)
Clashscore	190562	1354 (3.30-3.26)
Ramachandran outliers	187476	1334 (3.30-3.26)
Sidechain outliers	187428	1333 (3.30-3.26)
RSRZ outliers	180081	1303 (3.30-3.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	516	
1	B	516	
1	C	516	
1	D	516	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14616 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 SERINE PROTEASE NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3704	2349	632	702	21			
1	B	458	Total	C	N	O	S	0	0	0
			3641	2310	622	688	21			
1	C	461	Total	C	N	O	S	0	0	0
			3672	2331	624	695	22			
1	D	453	Total	C	N	O	S	0	0	0
			3598	2282	611	683	22			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	176	MET	-	expression tag	UNP P19712
A	177	ALA	-	expression tag	UNP P19712
A	178	SER	-	expression tag	UNP P19712
A	179	HIS	-	expression tag	UNP P19712
A	180	HIS	-	expression tag	UNP P19712
A	181	HIS	-	expression tag	UNP P19712
A	182	HIS	-	expression tag	UNP P19712
A	183	HIS	-	expression tag	UNP P19712
A	184	HIS	-	expression tag	UNP P19712
A	185	HIS	-	expression tag	UNP P19712
A	186	GLU	-	expression tag	UNP P19712
A	187	ASN	-	expression tag	UNP P19712
A	188	LEU	-	expression tag	UNP P19712
A	189	TYR	-	expression tag	UNP P19712
A	190	PHE	-	expression tag	UNP P19712
A	191	GLN	-	expression tag	UNP P19712
A	192	GLY	-	expression tag	UNP P19712
A	600	LYS	GLN	engineered mutation	UNP P19712
B	176	MET	-	expression tag	UNP P19712
B	177	ALA	-	expression tag	UNP P19712
B	178	SER	-	expression tag	UNP P19712

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Chain	Residue	Modelled	Actual	Comment	Reference
B	179	HIS	-	expression tag	UNP P19712
B	180	HIS	-	expression tag	UNP P19712
B	181	HIS	-	expression tag	UNP P19712
B	182	HIS	-	expression tag	UNP P19712
B	183	HIS	-	expression tag	UNP P19712
B	184	HIS	-	expression tag	UNP P19712
B	185	HIS	-	expression tag	UNP P19712
B	186	GLU	-	expression tag	UNP P19712
B	187	ASN	-	expression tag	UNP P19712
B	188	LEU	-	expression tag	UNP P19712
B	189	TYR	-	expression tag	UNP P19712
B	190	PHE	-	expression tag	UNP P19712
B	191	GLN	-	expression tag	UNP P19712
B	192	GLY	-	expression tag	UNP P19712
B	600	LYS	GLN	engineered mutation	UNP P19712
C	176	MET	-	expression tag	UNP P19712
C	177	ALA	-	expression tag	UNP P19712
C	178	SER	-	expression tag	UNP P19712
C	179	HIS	-	expression tag	UNP P19712
C	180	HIS	-	expression tag	UNP P19712
C	181	HIS	-	expression tag	UNP P19712
C	182	HIS	-	expression tag	UNP P19712
C	183	HIS	-	expression tag	UNP P19712
C	184	HIS	-	expression tag	UNP P19712
C	185	HIS	-	expression tag	UNP P19712
C	186	GLU	-	expression tag	UNP P19712
C	187	ASN	-	expression tag	UNP P19712
C	188	LEU	-	expression tag	UNP P19712
C	189	TYR	-	expression tag	UNP P19712
C	190	PHE	-	expression tag	UNP P19712
C	191	GLN	-	expression tag	UNP P19712
C	192	GLY	-	expression tag	UNP P19712
C	600	LYS	GLN	engineered mutation	UNP P19712
D	176	MET	-	expression tag	UNP P19712
D	177	ALA	-	expression tag	UNP P19712
D	178	SER	-	expression tag	UNP P19712
D	179	HIS	-	expression tag	UNP P19712
D	180	HIS	-	expression tag	UNP P19712
D	181	HIS	-	expression tag	UNP P19712
D	182	HIS	-	expression tag	UNP P19712
D	183	HIS	-	expression tag	UNP P19712
D	184	HIS	-	expression tag	UNP P19712

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Chain	Residue	Modelled	Actual	Comment	Reference
D	185	HIS	-	expression tag	UNP P19712
D	186	GLU	-	expression tag	UNP P19712
D	187	ASN	-	expression tag	UNP P19712
D	188	LEU	-	expression tag	UNP P19712
D	189	TYR	-	expression tag	UNP P19712
D	190	PHE	-	expression tag	UNP P19712
D	191	GLN	-	expression tag	UNP P19712
D	192	GLY	-	expression tag	UNP P19712
D	600	LYS	GLN	engineered mutation	UNP P19712

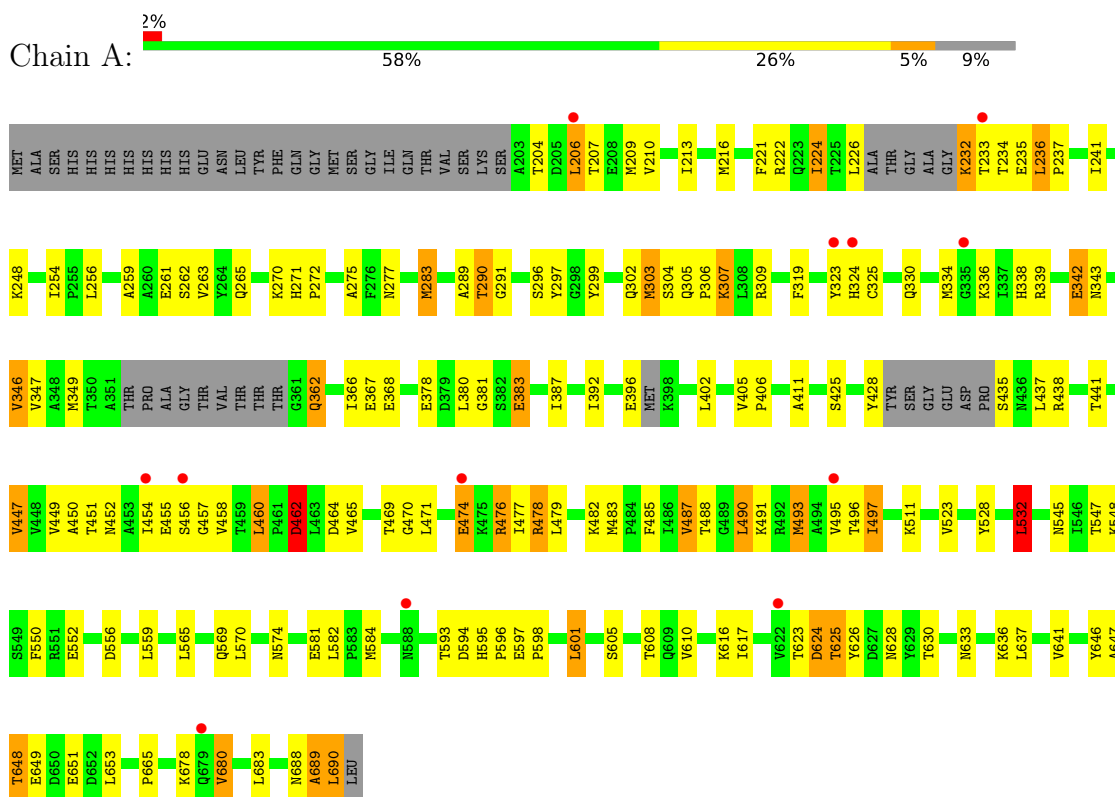
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O 1 1	0	0

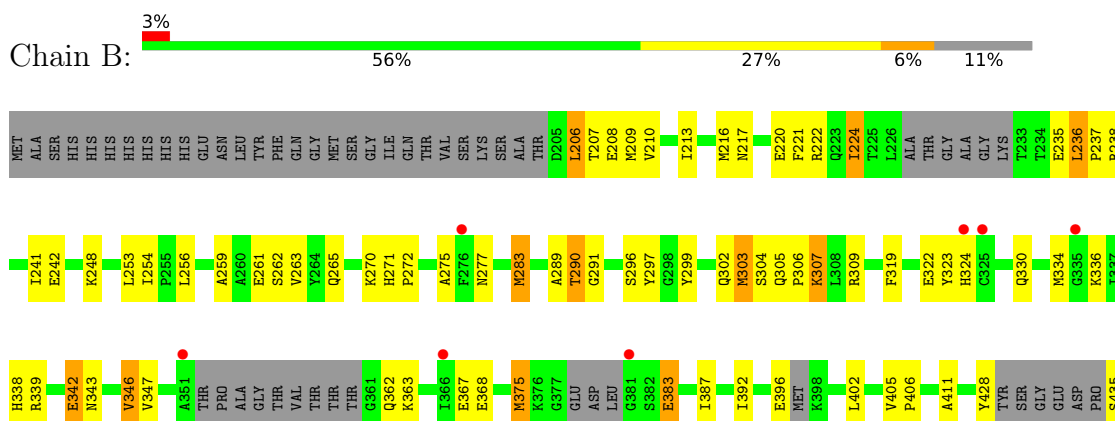
3 Residue-property plots

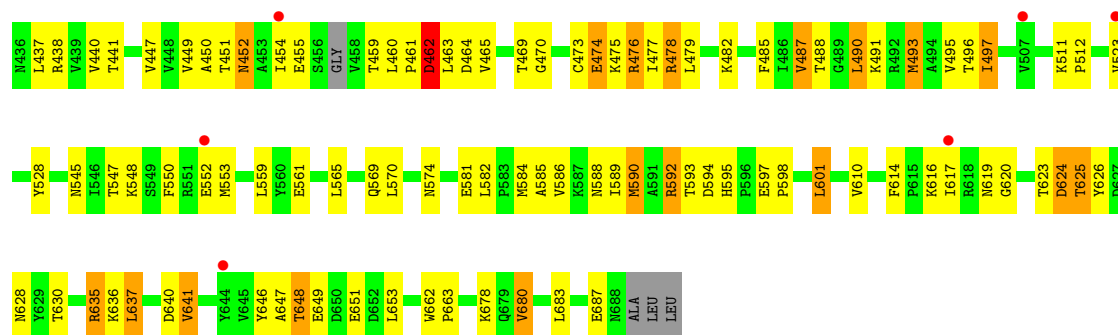
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: SERINE PROTEASE NS3

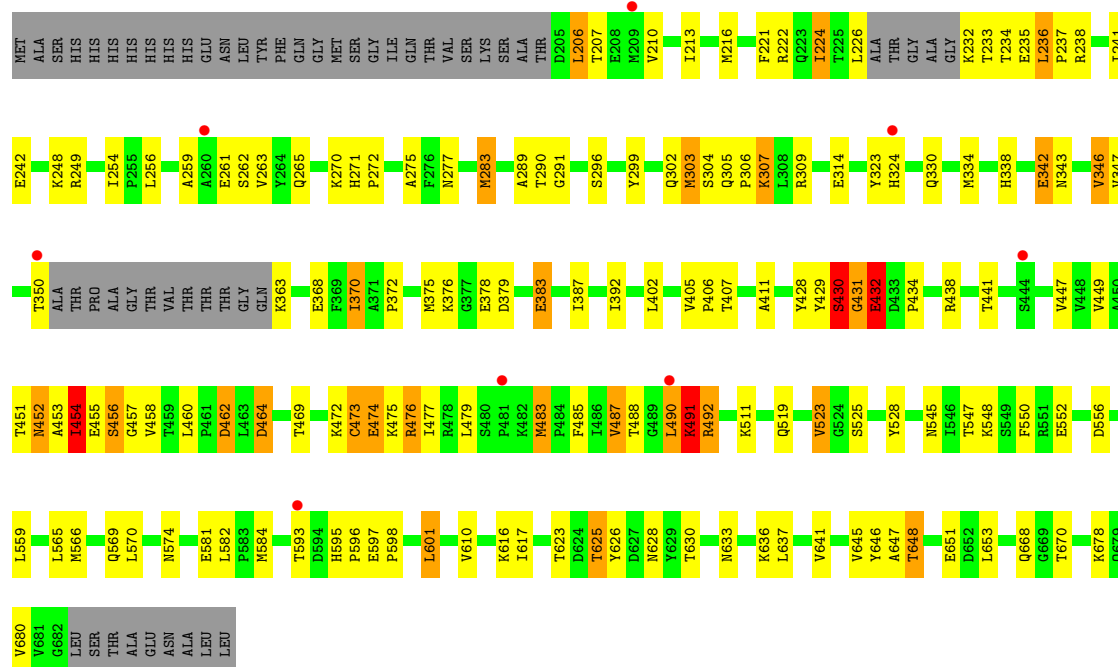


• Molecule 1: SERINE PROTEASE NS3

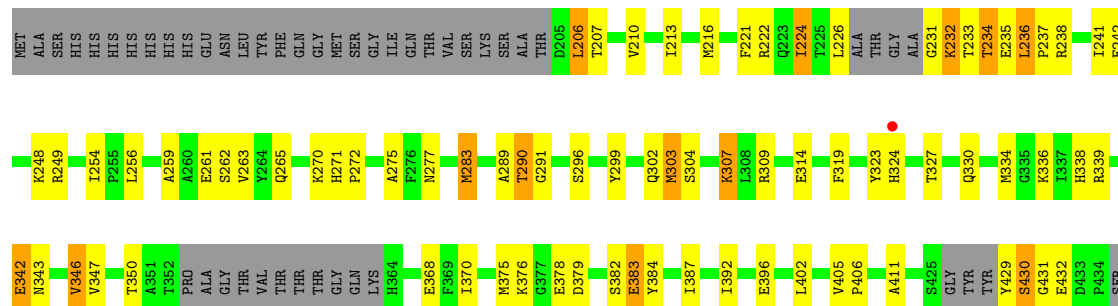


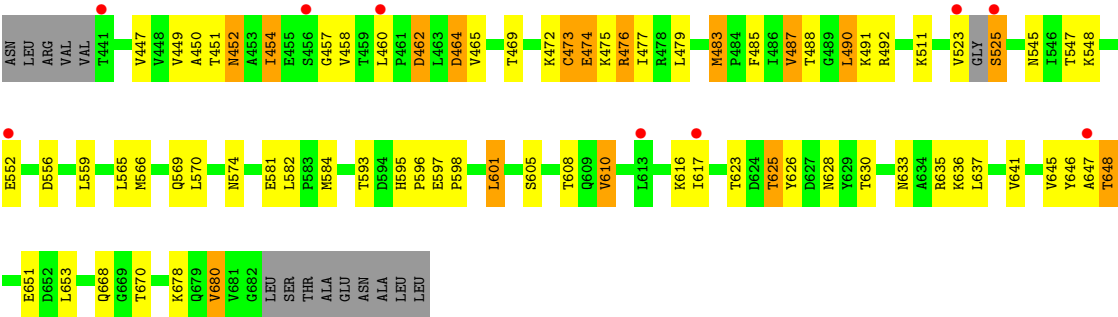


• Molecule 1: SERINE PROTEASE NS3



• Molecule 1: SERINE PROTEASE NS3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.10Å 159.59Å 99.23Å 90.00° 97.24° 90.00°	Depositor
Resolution (Å)	20.00 – 3.27 20.00 – 3.27	Depositor EDS
% Data completeness (in resolution range)	94.0 (20.00-3.27) 93.6 (20.00-3.27)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 3.29Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.233 , 0.283 0.264 , 0.316	Depositor DCC
R_{free} test set	1585 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	51.2	Xtriage
Anisotropy	1.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 60.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	14616	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.80	2/3771 (0.1%)	1.25	20/5098 (0.4%)
1	B	0.83	1/3706 (0.0%)	1.24	18/5007 (0.4%)
1	C	0.84	4/3743 (0.1%)	1.27	23/5062 (0.5%)
1	D	0.79	2/3664 (0.1%)	1.19	11/4951 (0.2%)
All	All	0.81	9/14884 (0.1%)	1.24	72/20118 (0.4%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	483	MET	SD-CE	-9.60	1.55	1.79
1	C	454	ILE	CA-C	8.39	1.63	1.52
1	C	483	MET	SD-CE	-7.48	1.60	1.79
1	B	493	MET	SD-CE	-6.98	1.62	1.79
1	A	493	MET	SD-CE	-6.18	1.64	1.79
1	D	231	GLY	C-N	5.81	1.41	1.33
1	C	456	SER	CA-C	5.70	1.60	1.52
1	C	491	LYS	CA-C	5.66	1.59	1.52
1	A	366	ILE	CA-CB	5.23	1.60	1.54

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	497	ILE	N-CA-C	-15.07	89.00	108.89
1	A	462	ASP	CA-CB-CG	15.02	127.62	112.60
1	B	497	ILE	N-CA-C	-14.82	89.33	108.89
1	B	462	ASP	CA-CB-CG	14.48	127.08	112.60
1	C	454	ILE	CA-C-N	11.14	141.76	121.70
1	C	454	ILE	C-N-CA	11.14	141.76	121.70
1	C	431	GLY	CA-C-N	9.53	139.74	121.54
1	C	431	GLY	C-N-CA	9.53	139.74	121.54
1	B	322	GLU	CB-CA-C	-9.19	98.16	111.95
1	B	561	GLU	CB-CG-CD	-9.02	97.26	112.60
1	C	432	GLU	CA-C-N	-8.87	109.97	122.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	432	GLU	C-N-CA	-8.87	109.97	122.66
1	A	457	GLY	CA-C-N	8.20	136.73	121.97
1	A	457	GLY	C-N-CA	8.20	136.73	121.97
1	D	457	GLY	CA-C-N	7.67	135.78	121.97
1	D	457	GLY	C-N-CA	7.67	135.78	121.97
1	A	325	CYS	N-CA-C	-7.36	102.63	111.69
1	A	624	ASP	CA-CB-CG	-7.01	105.59	112.60
1	C	457	GLY	CA-C-N	6.93	134.45	121.97
1	C	457	GLY	C-N-CA	6.93	134.45	121.97
1	A	378	GLU	CA-C-N	-6.90	112.20	122.56
1	A	378	GLU	C-N-CA	-6.90	112.20	122.56
1	A	235	GLU	N-CA-C	-6.84	104.94	113.28
1	A	204	THR	N-CA-C	-6.74	103.74	112.23
1	B	235	GLU	N-CA-C	-6.58	105.25	113.28
1	C	523	VAL	CA-C-N	6.53	128.51	120.22
1	C	523	VAL	C-N-CA	6.53	128.51	120.22
1	C	235	GLU	N-CA-C	-6.48	105.37	113.28
1	D	235	GLU	N-CA-C	-6.47	105.39	113.28
1	B	624	ASP	CA-CB-CG	-6.40	106.20	112.60
1	B	383	GLU	N-CA-C	-6.23	106.22	113.88
1	C	452	ASN	CA-CB-CG	6.13	118.73	112.60
1	A	452	ASN	CA-CB-CG	6.12	118.72	112.60
1	B	637	LEU	CD1-CG-CD2	-6.10	97.38	110.80
1	B	272	PRO	N-CA-C	6.04	121.77	113.98
1	A	383	GLU	N-CA-C	-5.97	106.53	113.88
1	C	462	ASP	CA-CB-CG	5.94	118.54	112.60
1	D	452	ASN	CA-CB-CG	5.91	118.51	112.60
1	D	272	PRO	N-CA-C	5.90	121.51	113.84
1	D	383	GLU	N-CA-C	-5.90	106.63	113.88
1	C	453	ALA	CA-C-N	5.89	132.57	121.97
1	C	453	ALA	C-N-CA	5.89	132.57	121.97
1	A	272	PRO	N-CA-C	5.85	121.53	113.98
1	C	261	GLU	CB-CG-CD	-5.73	102.86	112.60
1	B	452	ASN	CA-CB-CG	5.71	118.31	112.60
1	C	272	PRO	N-CA-C	5.69	121.24	113.84
1	C	383	GLU	N-CA-C	-5.68	106.89	113.88
1	A	367	GLU	CB-CG-CD	5.66	122.22	112.60
1	B	367	GLU	CB-CG-CD	5.66	122.21	112.60
1	D	462	ASP	CA-CB-CG	5.53	118.13	112.60
1	C	581	GLU	CB-CG-CD	5.52	121.98	112.60
1	C	430	SER	CA-C-N	5.45	132.10	121.41
1	C	430	SER	C-N-CA	5.45	132.10	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	290	THR	N-CA-C	5.45	119.19	112.54
1	A	581	GLU	CB-CG-CD	5.41	121.79	112.60
1	A	261	GLU	CB-CG-CD	-5.28	103.63	112.60
1	B	461	PRO	CA-C-N	5.27	130.30	122.82
1	B	461	PRO	C-N-CA	5.27	130.30	122.82
1	B	261	GLU	CB-CG-CD	-5.26	103.65	112.60
1	A	532	LEU	CD1-CG-CD2	5.26	122.37	110.80
1	C	523	VAL	CB-CA-C	5.25	117.26	110.12
1	D	581	GLU	CB-CG-CD	5.22	121.48	112.60
1	A	689	ALA	CA-C-N	5.21	131.08	121.70
1	A	689	ALA	C-N-CA	5.21	131.08	121.70
1	B	440	VAL	CA-C-N	5.17	127.73	120.28
1	B	440	VAL	C-N-CA	5.17	127.73	120.28
1	D	464	ASP	CA-CB-CG	5.17	117.77	112.60
1	A	290	THR	N-CA-C	5.16	118.84	112.54
1	D	232	LYS	N-CA-CB	5.14	117.51	110.57
1	D	290	THR	N-CA-C	5.05	119.16	112.89
1	B	581	GLU	CB-CG-CD	5.01	121.12	112.60
1	C	464	ASP	CA-CB-CG	5.01	117.61	112.60

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	3704	0	3724	122	0
1	B	3641	0	3657	122	0
1	C	3672	0	3685	104	0
1	D	3598	0	3602	102	0
2	A	1	0	0	2	0
All	All	14616	0	14668	430	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 15.

All (430) 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:450:ALA:CB	1:A:454:ILE:HG21	1.46	1.44
1:A:450:ALA:HB1	1:A:454:ILE:CG2	1.47	1.43
1:B:450:ALA:CB	1:B:454:ILE:HG21	1.48	1.42
1:B:450:ALA:HB1	1:B:454:ILE:CG2	1.49	1.41
1:C:324:HIS:HD2	1:C:350:THR:OG1	1.10	1.33
1:C:324:HIS:CD2	1:C:350:THR:OG1	1.88	1.24
1:D:324:HIS:HD2	1:D:350:THR:OG1	1.11	1.23
1:D:324:HIS:CD2	1:D:350:THR:OG1	1.90	1.23
1:A:323:TYR:CE1	1:A:324:HIS:CE1	2.28	1.22
1:A:323:TYR:CZ	1:A:324:HIS:CE1	2.36	1.14
1:B:428:TYR:CD1	1:B:454:ILE:HG22	1.98	0.99
1:A:428:TYR:CD1	1:A:454:ILE:HG22	1.98	0.98
1:A:428:TYR:HD1	1:A:454:ILE:HG22	1.25	0.96
1:B:428:TYR:HD1	1:B:454:ILE:HG22	1.26	0.94
1:D:323:TYR:CE1	1:D:324:HIS:CE1	2.55	0.93
1:C:323:TYR:CE1	1:C:324:HIS:CE1	2.57	0.93
1:B:641:VAL:HG22	1:B:663:PRO:HD3	1.48	0.93
1:D:450:ALA:HB1	1:D:454:ILE:HG13	1.48	0.92
1:B:323:TYR:HA	1:B:330:GLN:NE2	1.83	0.92
1:B:428:TYR:HB2	1:B:437:LEU:HD11	1.54	0.89
1:B:402:LEU:HD12	1:B:460:LEU:HD22	1.55	0.86
1:A:428:TYR:HB2	1:A:437:LEU:HD11	1.57	0.86
1:A:323:TYR:CZ	1:A:324:HIS:HE1	1.87	0.86
1:A:283:MET:HE1	1:A:307:LYS:HD2	1.61	0.83
1:C:593:THR:HG22	1:C:595:HIS:H	1.44	0.82
1:C:454:ILE:HA	1:C:456:SER:N	1.95	0.82
1:D:593:THR:HG22	1:D:595:HIS:H	1.46	0.81
1:C:283:MET:HE1	1:C:307:LYS:HD2	1.62	0.81
1:B:593:THR:HG22	1:B:595:HIS:H	1.46	0.80
1:B:283:MET:HE1	1:B:307:LYS:HD2	1.63	0.79
1:A:593:THR:HG22	1:A:595:HIS:H	1.45	0.79
1:D:283:MET:HE1	1:D:307:LYS:HD2	1.63	0.78
1:A:593:THR:HG23	1:A:630:THR:O	1.85	0.77
1:C:593:THR:HG23	1:C:630:THR:O	1.85	0.77
1:D:593:THR:HG23	1:D:630:THR:O	1.85	0.76
1:B:402:LEU:HD12	1:B:460:LEU:CD2	2.16	0.76
1:C:259:ALA:O	1:C:263:VAL:HG23	1.86	0.76
1:B:236:LEU:HB3	1:B:237:PRO:HD3	1.68	0.76
1:A:236:LEU:HB3	1:A:237:PRO:HD3	1.68	0.75
1:D:595:HIS:CD2	1:D:597:GLU:H	2.05	0.74
1:B:593:THR:HG23	1:B:630:THR:O	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:595:HIS:CD2	1:B:597:GLU:H	2.05	0.74
1:A:259:ALA:O	1:A:263:VAL:HG23	1.88	0.73
1:A:595:HIS:CD2	1:A:597:GLU:H	2.06	0.73
1:A:323:TYR:OH	1:A:324:HIS:HE1	1.71	0.73
1:C:595:HIS:CD2	1:C:597:GLU:H	2.05	0.73
1:B:259:ALA:O	1:B:263:VAL:HG23	1.89	0.72
1:B:595:HIS:HD2	1:B:597:GLU:H	1.38	0.72
1:D:259:ALA:O	1:D:263:VAL:HG23	1.88	0.72
1:B:406:PRO:HD3	1:B:469:THR:HG21	1.72	0.71
1:A:406:PRO:HD3	1:A:469:THR:HG21	1.71	0.71
1:C:595:HIS:HD2	1:C:597:GLU:H	1.39	0.71
1:A:595:HIS:HD2	1:A:597:GLU:H	1.39	0.71
1:C:236:LEU:HB3	1:C:237:PRO:HD3	1.71	0.71
1:D:236:LEU:HB3	1:D:237:PRO:HD3	1.73	0.71
1:D:595:HIS:HD2	1:D:597:GLU:H	1.38	0.70
1:B:299:TYR:O	1:B:302:GLN:HG3	1.90	0.70
1:D:406:PRO:HD3	1:D:469:THR:HG21	1.74	0.69
1:C:406:PRO:HD3	1:C:469:THR:HG21	1.72	0.69
1:D:226:LEU:CD2	1:D:233:THR:HG22	2.22	0.69
1:C:226:LEU:CD2	1:C:233:THR:HG22	2.23	0.69
1:C:324:HIS:HD2	1:C:350:THR:HG1	1.38	0.69
1:A:342:GLU:HG2	1:D:545:ASN:CB	2.22	0.69
1:B:323:TYR:CE1	1:B:559:LEU:HD22	2.27	0.69
1:B:585:ALA:HA	1:B:588:ASN:HD22	1.58	0.69
1:A:323:TYR:OH	1:A:324:HIS:CE1	2.44	0.68
1:B:309:ARG:HH21	1:B:343:ASN:HD21	1.39	0.68
1:D:490:LEU:O	1:D:491:LYS:HG2	1.93	0.68
1:D:450:ALA:HB1	1:D:454:ILE:CG1	2.21	0.68
1:A:299:TYR:O	1:A:302:GLN:HG3	1.94	0.67
1:B:614:PHE:CD2	1:B:637:LEU:HD12	2.29	0.67
1:C:324:HIS:NE2	1:C:350:THR:HG21	2.09	0.67
1:A:616:LYS:HE3	1:A:625:THR:CG2	2.25	0.67
1:B:342:GLU:HG2	1:C:545:ASN:CB	2.26	0.66
1:B:585:ALA:O	1:B:589:ILE:HG13	1.96	0.66
1:C:324:HIS:CD2	1:C:350:THR:CB	2.78	0.66
1:D:324:HIS:CD2	1:D:350:THR:CB	2.78	0.66
1:D:299:TYR:O	1:D:302:GLN:HG3	1.96	0.66
1:B:616:LYS:HE3	1:B:625:THR:CG2	2.25	0.66
1:A:226:LEU:CD2	1:A:233:THR:HG22	2.25	0.66
1:D:323:TYR:HE1	1:D:324:HIS:CE1	2.10	0.66
1:A:213:ILE:HD11	1:A:224:ILE:HD11	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:616:LYS:HE3	1:C:625:THR:CG2	2.26	0.65
1:A:309:ARG:HH21	1:A:343:ASN:HD21	1.45	0.65
1:A:487:VAL:HA	1:A:647:ALA:O	1.96	0.65
1:C:299:TYR:O	1:C:302:GLN:HG3	1.97	0.65
1:B:487:VAL:HA	1:B:647:ALA:O	1.97	0.65
1:B:478:ARG:HD3	1:B:649:GLU:OE2	1.96	0.65
1:D:324:HIS:NE2	1:D:350:THR:HG21	2.11	0.64
1:A:478:ARG:HD3	1:A:649:GLU:OE2	1.97	0.64
1:B:375:MET:HE3	1:B:375:MET:HA	1.79	0.64
1:D:464:ASP:OD1	1:D:511:LYS:HE2	1.97	0.64
1:A:428:TYR:HB2	1:A:437:LEU:CD1	2.28	0.64
1:C:487:VAL:HA	1:C:647:ALA:O	1.98	0.64
1:B:586:VAL:O	1:B:590:MET:HG3	1.97	0.63
1:D:487:VAL:HA	1:D:647:ALA:O	1.97	0.63
1:C:454:ILE:HA	1:C:456:SER:H	1.61	0.63
1:D:616:LYS:HE3	1:D:625:THR:CG2	2.28	0.63
1:B:213:ILE:HD11	1:B:224:ILE:HD11	1.79	0.63
1:C:438:ARG:HA	1:C:441:THR:OG1	1.99	0.62
1:B:428:TYR:HB2	1:B:437:LEU:CD1	2.27	0.62
1:B:641:VAL:CG2	1:B:663:PRO:HD3	2.25	0.62
1:B:451:THR:HG22	1:B:452:ASN:N	2.14	0.62
1:C:309:ARG:HH21	1:C:343:ASN:HD21	1.48	0.62
1:B:476:ARG:HE	1:B:493:MET:HE1	1.64	0.62
1:D:324:HIS:HD2	1:D:350:THR:HG1	1.41	0.62
1:C:213:ILE:HD11	1:C:224:ILE:HD11	1.81	0.61
1:A:342:GLU:HG2	1:D:545:ASN:HB3	1.82	0.61
1:B:545:ASN:CB	1:C:342:GLU:HG2	2.29	0.61
1:C:323:TYR:HE1	1:C:324:HIS:CE1	2.13	0.61
1:A:476:ARG:HE	1:A:493:MET:HE1	1.64	0.61
1:C:464:ASP:OD1	1:C:511:LYS:HE2	1.99	0.61
1:B:464:ASP:OD1	1:B:511:LYS:HE2	2.01	0.60
1:C:429:TYR:C	1:C:431:GLY:H	2.10	0.59
1:D:309:ARG:HH21	1:D:343:ASN:HD21	1.50	0.59
1:B:283:MET:CE	1:B:307:LYS:HD2	2.32	0.59
1:C:226:LEU:HD21	1:C:233:THR:HG22	1.82	0.59
1:B:342:GLU:HG2	1:C:545:ASN:HB2	1.83	0.59
1:C:428:TYR:CE2	1:C:454:ILE:O	2.56	0.59
1:C:221:PHE:HD1	1:C:346:VAL:HG22	1.67	0.59
1:A:323:TYR:CE1	1:A:324:HIS:NE2	2.69	0.58
1:A:342:GLU:HG2	1:D:545:ASN:HB2	1.83	0.58
1:D:213:ILE:HD11	1:D:224:ILE:HD11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:221:PHE:HD1	1:D:346:VAL:HG22	1.68	0.58
1:D:226:LEU:HD21	1:D:233:THR:HG22	1.84	0.58
1:A:283:MET:CE	1:A:307:LYS:HD2	2.32	0.58
1:B:594:ASP:OD2	1:B:630:THR:HG23	2.04	0.58
1:A:464:ASP:OD1	1:A:511:LYS:HE2	2.03	0.58
1:A:665:PRO:HD3	2:A:2001:HOH:O	2.03	0.58
1:B:221:PHE:HD1	1:B:346:VAL:HG22	1.69	0.57
1:A:226:LEU:HD21	1:A:233:THR:HG22	1.86	0.57
1:C:623:THR:OG1	1:C:625:THR:HB	2.04	0.57
1:C:473:CYS:SG	1:C:492:ARG:HG3	2.44	0.57
1:D:451:THR:HG22	1:D:452:ASN:N	2.20	0.57
1:B:342:GLU:HG2	1:C:545:ASN:HB3	1.87	0.57
1:B:635:ARG:NH2	1:B:640:ASP:O	2.34	0.57
1:C:277:ASN:CG	1:C:289:ALA:HB1	2.30	0.57
1:A:283:MET:HE1	1:A:307:LYS:CD	2.34	0.56
1:B:545:ASN:HB3	1:C:342:GLU:HG2	1.87	0.56
1:A:213:ILE:O	1:A:216:MET:HB2	2.06	0.56
1:A:221:PHE:HD1	1:A:346:VAL:HG22	1.70	0.56
1:B:476:ARG:NE	1:B:493:MET:CE	2.69	0.56
1:A:689:ALA:O	1:A:690:LEU:HB2	2.06	0.56
1:D:450:ALA:CB	1:D:454:ILE:HG13	2.32	0.56
1:A:476:ARG:NE	1:A:493:MET:HE1	2.21	0.56
1:D:277:ASN:CG	1:D:289:ALA:HB1	2.31	0.56
1:B:476:ARG:HE	1:B:493:MET:CE	2.19	0.55
1:A:545:ASN:CB	1:D:342:GLU:HG2	2.36	0.55
1:B:490:LEU:O	1:B:491:LYS:HG2	2.07	0.55
1:D:623:THR:OG1	1:D:625:THR:HB	2.06	0.55
1:A:593:THR:HG22	1:A:595:HIS:N	2.19	0.55
1:B:275:ALA:O	1:B:291:GLY:HA3	2.07	0.55
1:D:248:LYS:O	1:D:290:THR:O	2.25	0.55
1:D:275:ALA:O	1:D:291:GLY:HA3	2.07	0.55
1:A:248:LYS:O	1:A:290:THR:O	2.23	0.55
1:A:623:THR:OG1	1:A:625:THR:HB	2.07	0.55
1:B:277:ASN:CG	1:B:289:ALA:HB1	2.31	0.55
1:B:623:THR:OG1	1:B:625:THR:HB	2.07	0.55
1:C:275:ALA:O	1:C:291:GLY:HA3	2.07	0.54
1:D:429:TYR:C	1:D:431:GLY:H	2.15	0.54
1:D:450:ALA:HB1	1:D:454:ILE:CB	2.38	0.54
1:D:617:ILE:HD13	1:D:653:LEU:HD23	1.90	0.54
1:B:476:ARG:NE	1:B:493:MET:HE1	2.23	0.54
1:B:283:MET:HE1	1:B:307:LYS:CD	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ASN:CG	1:A:289:ALA:HB1	2.32	0.54
1:B:248:LYS:O	1:B:290:THR:O	2.25	0.54
1:A:594:ASP:OD2	1:A:630:THR:HG23	2.08	0.53
1:C:407:THR:HG22	1:C:492:ARG:HH11	1.72	0.53
1:C:593:THR:HG21	1:C:595:HIS:HB2	1.90	0.53
1:D:593:THR:HG22	1:D:595:HIS:N	2.19	0.53
1:D:593:THR:HG21	1:D:595:HIS:HB2	1.90	0.53
1:A:490:LEU:O	1:A:491:LYS:HG2	2.07	0.53
1:B:545:ASN:HB2	1:C:342:GLU:HG2	1.90	0.53
1:B:593:THR:HG22	1:B:595:HIS:N	2.19	0.53
1:D:213:ILE:O	1:D:216:MET:HB2	2.08	0.53
1:B:614:PHE:CG	1:B:637:LEU:HD12	2.43	0.53
1:D:475:LYS:HG2	1:D:490:LEU:HD13	1.89	0.53
1:A:477:ILE:HG22	1:A:488:THR:HG22	1.91	0.53
1:C:451:THR:HG22	1:C:452:ASN:N	2.23	0.53
1:D:309:ARG:HH21	1:D:343:ASN:ND2	2.06	0.53
1:D:323:TYR:CZ	1:D:324:HIS:CE1	2.96	0.53
1:C:617:ILE:HD13	1:C:653:LEU:HD23	1.89	0.53
1:C:309:ARG:HH21	1:C:343:ASN:ND2	2.06	0.53
1:C:323:TYR:CZ	1:C:324:HIS:CE1	2.97	0.53
1:C:477:ILE:HG22	1:C:488:THR:HG22	1.92	0.52
1:A:275:ALA:O	1:A:291:GLY:HA3	2.10	0.52
1:A:309:ARG:HH21	1:A:343:ASN:ND2	2.08	0.52
1:A:593:THR:HG21	1:A:595:HIS:HB2	1.90	0.52
1:C:476:ARG:HG2	1:C:491:LYS:HD2	1.91	0.52
1:D:598:PRO:O	1:D:601:LEU:HB2	2.09	0.52
1:A:362:GLN:HG2	1:C:372:PRO:HB3	1.90	0.52
1:B:593:THR:HG21	1:B:595:HIS:HB2	1.91	0.52
1:B:213:ILE:O	1:B:216:MET:HB2	2.09	0.51
1:C:248:LYS:O	1:C:290:THR:O	2.27	0.51
1:A:476:ARG:NE	1:A:493:MET:CE	2.72	0.51
1:A:648:THR:HG22	1:A:651:GLU:H	1.75	0.51
1:B:451:THR:O	1:B:454:ILE:HG23	2.10	0.51
1:C:213:ILE:O	1:C:216:MET:HB2	2.09	0.51
1:B:648:THR:HG22	1:B:651:GLU:H	1.75	0.51
1:C:475:LYS:HG2	1:C:490:LEU:HD13	1.92	0.51
1:D:476:ARG:HG3	1:D:476:ARG:HH11	1.75	0.51
1:C:598:PRO:O	1:C:601:LEU:HB2	2.11	0.51
1:B:451:THR:CG2	1:B:452:ASN:N	2.74	0.51
1:C:593:THR:HG22	1:C:595:HIS:N	2.18	0.51
1:D:304:SER:H	1:D:307:LYS:HZ1	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:477:ILE:HG22	1:D:488:THR:HG22	1.93	0.51
1:A:598:PRO:O	1:A:601:LEU:HB2	2.11	0.50
1:C:648:THR:HG22	1:C:651:GLU:H	1.76	0.50
1:A:362:GLN:CG	1:C:372:PRO:HB3	2.41	0.50
1:A:483:MET:HB2	2:A:2001:HOH:O	2.11	0.50
1:A:617:ILE:HD13	1:A:653:LEU:HD23	1.94	0.50
1:B:334:MET:HE1	1:B:559:LEU:HD13	1.93	0.50
1:A:532:LEU:O	1:A:532:LEU:HD22	2.12	0.50
1:A:222:ARG:O	1:A:347:VAL:HA	2.12	0.50
1:A:545:ASN:HB2	1:D:342:GLU:HG2	1.94	0.50
1:D:523:VAL:HG22	1:D:525:SER:HB3	1.92	0.50
1:A:304:SER:H	1:A:307:LYS:HZ1	1.60	0.50
1:A:338:HIS:HE1	1:A:556:ASP:OD2	1.95	0.50
1:B:206:LEU:O	1:B:210:VAL:HG23	2.11	0.50
1:B:477:ILE:HG22	1:B:488:THR:HG22	1.94	0.50
1:B:277:ASN:OD1	1:B:289:ALA:HB1	2.12	0.49
1:A:451:THR:O	1:A:454:ILE:HG23	2.11	0.49
1:B:462:ASP:OD2	1:B:511:LYS:NZ	2.45	0.49
1:A:236:LEU:HD23	1:A:319:PHE:HE2	1.77	0.49
1:B:304:SER:H	1:B:307:LYS:HZ1	1.59	0.49
1:C:338:HIS:HE1	1:C:556:ASP:OD2	1.95	0.49
1:C:476:ARG:HH11	1:C:476:ARG:HG3	1.76	0.49
1:B:334:MET:CE	1:B:559:LEU:HD13	2.42	0.49
1:D:323:TYR:CZ	1:D:324:HIS:NE2	2.80	0.49
1:A:206:LEU:O	1:A:210:VAL:HG23	2.12	0.49
1:A:323:TYR:CE1	1:A:324:HIS:ND1	2.75	0.49
1:B:435:SER:O	1:B:438:ARG:HB2	2.13	0.49
1:C:454:ILE:HG23	1:C:456:SER:HB3	1.94	0.49
1:D:483:MET:HE2	1:D:645:VAL:HG22	1.94	0.49
1:B:309:ARG:HH21	1:B:343:ASN:ND2	2.09	0.49
1:C:472:LYS:HD2	1:C:474:GLU:HG2	1.94	0.49
1:B:338:HIS:CD2	1:B:553:MET:HA	2.48	0.48
1:B:236:LEU:HD23	1:B:319:PHE:HE2	1.78	0.48
1:D:222:ARG:O	1:D:347:VAL:HA	2.13	0.48
1:B:222:ARG:O	1:B:347:VAL:HA	2.12	0.48
1:C:304:SER:H	1:C:307:LYS:HZ1	1.61	0.48
1:B:323:TYR:CZ	1:B:559:LEU:HD22	2.49	0.48
1:D:616:LYS:HB2	1:D:625:THR:HG22	1.96	0.48
1:A:323:TYR:HE1	1:A:324:HIS:NE2	2.12	0.48
1:B:588:ASN:O	1:B:592:ARG:HG3	2.13	0.48
1:C:206:LEU:O	1:C:210:VAL:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:648:THR:HG22	1:D:651:GLU:H	1.77	0.48
1:B:496:THR:HG22	1:B:523:VAL:HG13	1.96	0.48
1:B:598:PRO:O	1:B:601:LEU:HB2	2.14	0.48
1:C:523:VAL:HG22	1:C:525:SER:HB2	1.95	0.48
1:A:435:SER:O	1:A:438:ARG:HB2	2.14	0.47
1:B:236:LEU:HB3	1:B:237:PRO:CD	2.41	0.47
1:C:483:MET:HE2	1:C:645:VAL:HG22	1.95	0.47
1:A:277:ASN:OD1	1:A:289:ALA:HB1	2.14	0.47
1:D:206:LEU:O	1:D:210:VAL:HG23	2.14	0.47
1:D:226:LEU:HD23	1:D:233:THR:HG22	1.95	0.47
1:D:472:LYS:HD2	1:D:474:GLU:HG2	1.96	0.47
1:D:490:LEU:C	1:D:491:LYS:HG2	2.39	0.47
1:A:334:MET:CE	1:A:559:LEU:HD13	2.45	0.47
1:A:462:ASP:OD2	1:A:511:LYS:NZ	2.45	0.47
1:A:476:ARG:HE	1:A:493:MET:CE	2.27	0.47
1:A:683:LEU:HD21	1:B:687:GLU:HA	1.95	0.47
1:C:277:ASN:OD1	1:C:289:ALA:HB1	2.15	0.47
1:A:428:TYR:CE1	1:A:454:ILE:HA	2.50	0.47
1:C:236:LEU:HB3	1:C:237:PRO:CD	2.44	0.47
1:B:548:LYS:O	1:B:552:GLU:HG3	2.14	0.47
1:D:277:ASN:OD1	1:D:289:ALA:HB1	2.15	0.47
1:D:304:SER:OG	1:D:307:LYS:HE3	2.15	0.47
1:A:496:THR:HG22	1:A:523:VAL:HG13	1.96	0.46
1:A:548:LYS:O	1:A:552:GLU:HG3	2.15	0.46
1:C:548:LYS:O	1:C:552:GLU:HG3	2.14	0.46
1:C:616:LYS:HB2	1:C:625:THR:HG22	1.97	0.46
1:A:411:ALA:HA	1:A:449:VAL:CG1	2.46	0.46
1:A:474:GLU:HB2	1:A:493:MET:SD	2.55	0.46
1:A:545:ASN:HB3	1:D:342:GLU:HG2	1.96	0.46
1:B:474:GLU:HB2	1:B:493:MET:SD	2.55	0.46
1:C:270:LYS:HG2	1:C:271:HIS:CD2	2.51	0.46
1:C:411:ALA:HA	1:C:449:VAL:CG1	2.46	0.46
1:D:236:LEU:HD23	1:D:319:PHE:HE2	1.80	0.46
1:D:338:HIS:HE1	1:D:556:ASP:OD2	1.97	0.46
1:D:451:THR:CG2	1:D:452:ASN:N	2.78	0.46
1:B:411:ALA:HA	1:B:449:VAL:CG1	2.46	0.46
1:B:616:LYS:HG3	1:B:625:THR:HG22	1.96	0.46
1:A:616:LYS:HG3	1:A:625:THR:HG22	1.98	0.46
1:D:283:MET:CE	1:D:307:LYS:HD2	2.39	0.46
1:D:334:MET:CE	1:D:559:LEU:HD13	2.46	0.46
1:D:334:MET:HE1	1:D:559:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:626:TYR:CZ	1:D:636:LYS:HD3	2.51	0.46
1:B:428:TYR:HD1	1:B:454:ILE:CG2	2.13	0.46
1:B:512:PRO:HG3	1:D:384:TYR:OH	2.16	0.46
1:C:334:MET:CE	1:C:559:LEU:HD13	2.46	0.46
1:D:411:ALA:HA	1:D:449:VAL:CG1	2.46	0.46
1:A:402:LEU:HD12	1:A:460:LEU:HD12	1.99	0.45
1:A:323:TYR:HA	1:A:330:GLN:NE2	2.32	0.45
1:A:428:TYR:HD1	1:A:454:ILE:CG2	2.13	0.45
1:A:334:MET:HE1	1:A:559:LEU:HD13	1.97	0.45
1:A:470:GLY:O	1:A:495:VAL:HG22	2.17	0.45
1:C:304:SER:OG	1:C:307:LYS:HE3	2.15	0.45
1:B:265:GLN:OE1	1:B:265:GLN:HA	2.15	0.45
1:A:265:GLN:OE1	1:A:265:GLN:HA	2.16	0.45
1:C:323:TYR:CZ	1:C:324:HIS:NE2	2.84	0.45
1:B:438:ARG:HA	1:B:441:THR:OG1	2.17	0.45
1:D:548:LYS:O	1:D:552:GLU:HG3	2.16	0.45
1:C:222:ARG:O	1:C:347:VAL:HA	2.16	0.45
1:C:451:THR:CG2	1:C:452:ASN:N	2.80	0.45
1:C:565:LEU:O	1:C:569:GLN:HG3	2.17	0.45
1:D:323:TYR:HA	1:D:330:GLN:NE2	2.32	0.45
1:A:362:GLN:HE21	1:C:519:GLN:CD	2.24	0.44
1:A:565:LEU:O	1:A:569:GLN:HG3	2.17	0.44
1:B:428:TYR:CE1	1:B:454:ILE:HA	2.51	0.44
1:B:451:THR:CG2	1:B:452:ASN:H	2.30	0.44
1:A:616:LYS:HB2	1:A:625:THR:HG22	1.99	0.44
1:C:254:ILE:O	1:C:296:SER:HA	2.18	0.44
1:A:222:ARG:HB2	1:A:347:VAL:HG22	1.99	0.44
1:A:304:SER:OG	1:A:307:LYS:HE3	2.18	0.44
1:B:547:THR:H	1:B:574:ASN:ND2	2.16	0.44
1:D:565:LEU:O	1:D:569:GLN:HG3	2.17	0.44
1:B:305:GLN:N	1:B:306:PRO:HD2	2.33	0.44
1:B:460:LEU:HD23	1:B:463:LEU:HD13	1.99	0.44
1:B:565:LEU:O	1:B:569:GLN:HG3	2.17	0.44
1:A:305:GLN:N	1:A:306:PRO:HD2	2.32	0.44
1:D:610:VAL:CG2	1:D:635:ARG:HG2	2.48	0.44
1:D:270:LYS:HG2	1:D:271:HIS:CD2	2.53	0.44
1:B:470:GLY:O	1:B:495:VAL:HG22	2.18	0.43
1:A:236:LEU:HB3	1:A:237:PRO:CD	2.41	0.43
1:A:690:LEU:O	1:B:683:LEU:HD11	2.18	0.43
1:C:303:MET:HB3	1:C:307:LYS:HB3	2.00	0.43
1:B:336:LYS:O	1:B:339:ARG:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:LYS:C	1:C:234:THR:H	2.27	0.43
1:C:547:THR:H	1:C:574:ASN:ND2	2.16	0.43
1:A:226:LEU:HD23	1:A:233:THR:HG22	1.98	0.43
1:B:584:MET:O	1:B:588:ASN:ND2	2.51	0.43
1:B:614:PHE:CD2	1:B:637:LEU:CD1	3.00	0.43
1:A:303:MET:HB3	1:A:307:LYS:HB3	2.01	0.43
1:B:254:ILE:O	1:B:296:SER:HA	2.18	0.43
1:B:303:MET:HB3	1:B:307:LYS:HB3	2.00	0.43
1:C:283:MET:HE1	1:C:307:LYS:CD	2.41	0.43
1:C:334:MET:HE1	1:C:559:LEU:HD13	1.99	0.43
1:C:595:HIS:CD2	1:C:596:PRO:HD2	2.53	0.43
1:C:626:TYR:CZ	1:C:636:LYS:HD3	2.53	0.43
1:A:438:ARG:HA	1:A:441:THR:OG1	2.18	0.43
1:B:222:ARG:HB2	1:B:347:VAL:HG22	2.00	0.43
1:B:565:LEU:HD12	1:B:680:VAL:HG13	2.00	0.43
1:B:616:LYS:HB2	1:B:625:THR:HG22	1.99	0.43
1:C:249:ARG:HD2	1:C:289:ALA:O	2.19	0.43
1:C:483:MET:HE1	1:C:670:THR:HB	2.00	0.43
1:C:238:ARG:NH1	1:C:242:GLU:OE1	2.51	0.43
1:C:323:TYR:HA	1:C:330:GLN:NE2	2.33	0.43
1:D:616:LYS:HG3	1:D:625:THR:HG22	2.00	0.43
1:B:641:VAL:HG21	1:B:662:TRP:HA	2.01	0.43
1:D:396:GLU:HG3	1:D:465:VAL:HG11	2.01	0.43
1:D:483:MET:HE1	1:D:670:THR:HB	2.01	0.43
1:A:254:ILE:O	1:A:296:SER:HA	2.19	0.42
1:A:547:THR:H	1:A:574:ASN:ND2	2.17	0.42
1:B:304:SER:OG	1:B:307:LYS:HE3	2.18	0.42
1:C:283:MET:CE	1:C:307:LYS:HD2	2.40	0.42
1:C:370:ILE:HD11	1:C:519:GLN:HA	2.00	0.42
1:A:565:LEU:HD12	1:A:680:VAL:HG13	2.00	0.42
1:B:396:GLU:HG3	1:B:465:VAL:HG11	2.01	0.42
1:B:619:ASN:HB3	1:B:620:GLY:H	1.57	0.42
1:C:324:HIS:NE2	1:C:350:THR:CB	2.82	0.42
1:D:238:ARG:NH1	1:D:242:GLU:OE1	2.52	0.42
1:D:547:THR:H	1:D:574:ASN:ND2	2.16	0.42
1:D:595:HIS:CD2	1:D:596:PRO:HD2	2.53	0.42
1:C:222:ARG:HB2	1:C:347:VAL:HG22	2.02	0.42
1:D:473:CYS:SG	1:D:492:ARG:HG2	2.59	0.42
1:B:209:MET:O	1:B:213:ILE:HG12	2.19	0.42
1:B:528:TYR:CE2	1:B:550:PHE:CZ	3.08	0.42
1:D:254:ILE:O	1:D:296:SER:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:411:ALA:HA	1:D:449:VAL:HG12	2.02	0.42
1:B:435:SER:HB3	1:B:438:ARG:HG3	2.02	0.42
1:D:283:MET:HE1	1:D:307:LYS:CD	2.41	0.42
1:D:475:LYS:O	1:D:476:ARG:HD3	2.20	0.42
1:A:435:SER:HB3	1:A:438:ARG:HG3	2.00	0.42
1:C:249:ARG:HH21	1:C:314:GLU:CB	2.33	0.42
1:C:411:ALA:HA	1:C:449:VAL:HG12	2.02	0.42
1:B:617:ILE:HD13	1:B:653:LEU:HD23	2.02	0.42
1:A:209:MET:O	1:A:213:ILE:HG12	2.20	0.42
1:D:249:ARG:HD2	1:D:289:ALA:O	2.20	0.42
1:D:565:LEU:HD12	1:D:680:VAL:HG13	2.01	0.42
1:D:605:SER:HA	1:D:608:THR:O	2.20	0.42
1:A:626:TYR:CZ	1:A:636:LYS:HD3	2.55	0.41
1:A:690:LEU:O	1:B:683:LEU:CD1	2.68	0.41
1:B:238:ARG:NH1	1:B:242:GLU:OE1	2.52	0.41
1:B:626:TYR:CZ	1:B:636:LYS:HD3	2.54	0.41
1:C:324:HIS:NE2	1:C:350:THR:CG2	2.81	0.41
1:C:479:LEU:HA	1:C:485:PHE:O	2.19	0.41
1:A:232:LYS:C	1:A:234:THR:H	2.28	0.41
1:A:362:GLN:HE22	1:C:370:ILE:HG12	1.85	0.41
1:A:396:GLU:HG3	1:A:465:VAL:HG11	2.01	0.41
1:C:593:THR:CG2	1:C:595:HIS:H	2.25	0.41
1:D:249:ARG:HH21	1:D:314:GLU:CB	2.34	0.41
1:D:303:MET:HB3	1:D:307:LYS:HB3	2.01	0.41
1:D:479:LEU:HA	1:D:485:PHE:O	2.21	0.41
1:A:336:LYS:O	1:A:339:ARG:HB2	2.20	0.41
1:A:411:ALA:HA	1:A:449:VAL:HG12	2.01	0.41
1:A:595:HIS:CD2	1:A:596:PRO:HD2	2.55	0.41
1:B:475:LYS:O	1:B:476:ARG:HD3	2.20	0.41
1:C:434:PRO:O	1:C:438:ARG:HG2	2.19	0.41
1:C:265:GLN:OE1	1:C:265:GLN:HA	2.21	0.41
1:D:222:ARG:HB2	1:D:347:VAL:HG22	2.03	0.41
1:A:593:THR:CG2	1:A:595:HIS:H	2.26	0.41
1:A:528:TYR:CE2	1:A:550:PHE:CZ	3.09	0.41
1:A:593:THR:CG2	1:A:595:HIS:HB2	2.51	0.41
1:B:253:LEU:HD22	1:B:297:TYR:HA	2.03	0.41
1:B:411:ALA:HA	1:B:449:VAL:HG12	2.03	0.41
1:C:528:TYR:CE2	1:C:550:PHE:CZ	3.09	0.41
1:D:221:PHE:CD1	1:D:346:VAL:HG22	2.52	0.41
1:D:224:ILE:HG22	1:D:226:LEU:HD22	2.02	0.41
1:A:221:PHE:CD1	1:A:346:VAL:HG22	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:476:ARG:HG3	1:A:476:ARG:HH11	1.86	0.41
1:B:476:ARG:HG3	1:B:476:ARG:HH11	1.87	0.41
1:C:305:GLN:N	1:C:306:PRO:HD2	2.36	0.41
1:C:429:TYR:O	1:C:431:GLY:N	2.51	0.41
1:B:593:THR:CG2	1:B:595:HIS:HB2	2.51	0.40
1:C:221:PHE:CD1	1:C:346:VAL:HG22	2.52	0.40
1:A:270:LYS:HG2	1:A:271:HIS:CD2	2.57	0.40
1:B:217:ASN:HB2	1:B:220:GLU:OE2	2.21	0.40
1:A:349:MET:HE3	1:A:349:MET:HB2	1.89	0.40
1:A:479:LEU:HA	1:A:485:PHE:O	2.22	0.40
1:A:425:SER:HA	1:A:447:VAL:O	2.22	0.40
1:A:605:SER:HA	1:A:608:THR:O	2.21	0.40
1:B:270:LYS:HG2	1:B:271:HIS:CD2	2.56	0.40
1:B:479:LEU:HA	1:B:485:PHE:O	2.20	0.40
1:D:265:GLN:OE1	1:D:265:GLN:HA	2.20	0.40
1:D:336:LYS:O	1:D:339:ARG:HB2	2.21	0.40
1:A:297:TYR:CZ	1:A:330:GLN:HG3	2.57	0.40
1:B:297:TYR:CZ	1:B:330:GLN:HG3	2.56	0.40
1:D:232:LYS:C	1:D:234:THR:H	2.29	0.40
1:D:477:ILE:HD12	1:D:479:LEU:HD21	2.03	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	457/516 (89%)	437 (96%)	17 (4%)	3 (1%)	18	48
1	B	444/516 (86%)	432 (97%)	12 (3%)	0	100	100
1	C	455/516 (88%)	434 (95%)	15 (3%)	6 (1%)	9	35
1	D	441/516 (86%)	422 (96%)	15 (3%)	4 (1%)	14	43
All	All	1797/2064 (87%)	1725 (96%)	59 (3%)	13 (1%)	18	48

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	458	VAL
1	C	432	GLU
1	C	454	ILE
1	C	455	GLU
1	C	458	VAL
1	D	432	GLU
1	D	458	VAL
1	C	430	SER
1	D	430	SER
1	A	381	GLY
1	A	456	SER
1	C	376	LYS
1	D	376	LYS

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	403/442 (91%)	353 (88%)	50 (12%)	4	20
1	B	397/442 (90%)	348 (88%)	49 (12%)	4	20
1	C	401/442 (91%)	349 (87%)	52 (13%)	4	18
1	D	392/442 (89%)	339 (86%)	53 (14%)	4	17
All	All	1593/1768 (90%)	1389 (87%)	204 (13%)	4	19

All (204) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	206	LEU
1	A	207	THR
1	A	224	ILE
1	A	232	LYS
1	A	236	LEU
1	A	241	ILE
1	A	256	LEU

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Mol	Chain	Res	Type
1	A	262	SER
1	A	283	MET
1	A	303	MET
1	A	307	LYS
1	A	342	GLU
1	A	346	VAL
1	A	362	GLN
1	A	368	GLU
1	A	380	LEU
1	A	383	GLU
1	A	387	ILE
1	A	392	ILE
1	A	405	VAL
1	A	447	VAL
1	A	455	GLU
1	A	460	LEU
1	A	462	ASP
1	A	471	LEU
1	A	474	GLU
1	A	476	ARG
1	A	478	ARG
1	A	482	LYS
1	A	487	VAL
1	A	490	LEU
1	A	497	ILE
1	A	532	LEU
1	A	570	LEU
1	A	582	LEU
1	A	584	MET
1	A	601	LEU
1	A	610	VAL
1	A	624	ASP
1	A	625	THR
1	A	628	ASN
1	A	633	ASN
1	A	637	LEU
1	A	641	VAL
1	A	646	TYR
1	A	648	THR
1	A	678	LYS
1	A	680	VAL
1	A	688	ASN

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Mol	Chain	Res	Type
1	A	690	LEU
1	B	206	LEU
1	B	207	THR
1	B	208	GLU
1	B	224	ILE
1	B	236	LEU
1	B	241	ILE
1	B	256	LEU
1	B	262	SER
1	B	283	MET
1	B	303	MET
1	B	307	LYS
1	B	324	HIS
1	B	342	GLU
1	B	346	VAL
1	B	362	GLN
1	B	363	LYS
1	B	368	GLU
1	B	375	MET
1	B	383	GLU
1	B	387	ILE
1	B	392	ILE
1	B	405	VAL
1	B	447	VAL
1	B	455	GLU
1	B	459	THR
1	B	462	ASP
1	B	473	CYS
1	B	474	GLU
1	B	476	ARG
1	B	478	ARG
1	B	482	LYS
1	B	487	VAL
1	B	490	LEU
1	B	497	ILE
1	B	570	LEU
1	B	582	LEU
1	B	590	MET
1	B	592	ARG
1	B	601	LEU
1	B	610	VAL
1	B	624	ASP

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Mol	Chain	Res	Type
1	B	625	THR
1	B	628	ASN
1	B	635	ARG
1	B	641	VAL
1	B	646	TYR
1	B	648	THR
1	B	678	LYS
1	B	680	VAL
1	C	206	LEU
1	C	207	THR
1	C	224	ILE
1	C	236	LEU
1	C	241	ILE
1	C	256	LEU
1	C	262	SER
1	C	283	MET
1	C	303	MET
1	C	307	LYS
1	C	342	GLU
1	C	346	VAL
1	C	363	LYS
1	C	368	GLU
1	C	370	ILE
1	C	375	MET
1	C	378	GLU
1	C	379	ASP
1	C	383	GLU
1	C	387	ILE
1	C	392	ILE
1	C	402	LEU
1	C	405	VAL
1	C	430	SER
1	C	432	GLU
1	C	447	VAL
1	C	454	ILE
1	C	460	LEU
1	C	462	ASP
1	C	473	CYS
1	C	474	GLU
1	C	476	ARG
1	C	487	VAL
1	C	490	LEU

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Mol	Chain	Res	Type
1	C	491	LYS
1	C	492	ARG
1	C	566	MET
1	C	570	LEU
1	C	582	LEU
1	C	584	MET
1	C	601	LEU
1	C	610	VAL
1	C	625	THR
1	C	628	ASN
1	C	633	ASN
1	C	637	LEU
1	C	641	VAL
1	C	646	TYR
1	C	648	THR
1	C	668	GLN
1	C	678	LYS
1	C	680	VAL
1	D	206	LEU
1	D	207	THR
1	D	224	ILE
1	D	234	THR
1	D	236	LEU
1	D	241	ILE
1	D	256	LEU
1	D	261	GLU
1	D	262	SER
1	D	283	MET
1	D	303	MET
1	D	307	LYS
1	D	327	THR
1	D	342	GLU
1	D	346	VAL
1	D	368	GLU
1	D	370	ILE
1	D	375	MET
1	D	378	GLU
1	D	379	ASP
1	D	382	SER
1	D	383	GLU
1	D	387	ILE
1	D	392	ILE

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Mol	Chain	Res	Type
1	D	402	LEU
1	D	405	VAL
1	D	430	SER
1	D	447	VAL
1	D	454	ILE
1	D	460	LEU
1	D	462	ASP
1	D	473	CYS
1	D	474	GLU
1	D	476	ARG
1	D	487	VAL
1	D	490	LEU
1	D	525	SER
1	D	566	MET
1	D	570	LEU
1	D	582	LEU
1	D	584	MET
1	D	601	LEU
1	D	610	VAL
1	D	625	THR
1	D	628	ASN
1	D	633	ASN
1	D	637	LEU
1	D	641	VAL
1	D	646	TYR
1	D	648	THR
1	D	668	GLN
1	D	678	LYS
1	D	680	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	302	GLN
1	A	305	GLN
1	A	324	HIS
1	A	338	HIS
1	A	343	ASN
1	A	362	GLN
1	A	424	ASN
1	A	574	ASN
1	A	595	HIS

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Mol	Chain	Res	Type
1	A	668	GLN
1	B	223	GLN
1	B	302	GLN
1	B	343	ASN
1	B	424	ASN
1	B	574	ASN
1	B	588	ASN
1	B	595	HIS
1	B	668	GLN
1	B	688	ASN
1	C	223	GLN
1	C	302	GLN
1	C	324	HIS
1	C	338	HIS
1	C	343	ASN
1	C	424	ASN
1	C	443	GLN
1	C	519	GLN
1	C	574	ASN
1	C	595	HIS
1	C	668	GLN
1	D	223	GLN
1	D	302	GLN
1	D	324	HIS
1	D	338	HIS
1	D	343	ASN
1	D	424	ASN
1	D	443	GLN
1	D	519	GLN
1	D	574	ASN
1	D	595	HIS
1	D	668	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	467/516 (90%)	0.59	12 (2%) 57 38	23, 58, 96, 119	0
1	B	458/516 (88%)	0.58	13 (2%) 55 36	15, 60, 89, 116	0
1	C	461/516 (89%)	0.57	8 (1%) 69 50	25, 63, 96, 126	0
1	D	453/516 (87%)	0.61	10 (2%) 62 43	25, 67, 106, 135	0
All	All	1839/2064 (89%)	0.59	43 (2%) 61 41	15, 62, 98, 135	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	324	HIS	4.4
1	A	233	THR	3.6
1	A	588	ASN	3.3
1	B	325	CYS	3.0
1	C	209	MET	3.0
1	C	324	HIS	2.9
1	A	622	VAL	2.9
1	A	323	TYR	2.7
1	B	644	TYR	2.7
1	C	350	THR	2.6
1	B	276	PHE	2.5
1	B	324	HIS	2.5
1	D	647	ALA	2.4
1	D	456	SER	2.4
1	B	335	GLY	2.4
1	B	351	ALA	2.3
1	C	481	PRO	2.3
1	A	324	HIS	2.3
1	C	593	THR	2.3
1	D	613	LEU	2.3
1	D	523	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	260	ALA	2.3
1	A	206	LEU	2.3
1	B	454	ILE	2.2
1	A	456	SER	2.2
1	A	495	VAL	2.2
1	A	335	GLY	2.2
1	D	460	LEU	2.2
1	B	523	VAL	2.2
1	A	679	GLN	2.2
1	B	366	ILE	2.2
1	B	617	ILE	2.2
1	D	617	ILE	2.1
1	D	441	THR	2.1
1	A	454	ILE	2.1
1	C	444	SER	2.1
1	B	507	VAL	2.1
1	C	490	LEU	2.1
1	D	552	GLU	2.1
1	D	525	SER	2.1
1	B	381	GLY	2.1
1	A	474	GLU	2.0
1	B	552	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.