



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:39 PM UTC

PDB ID : 2ZL0 / pdb_00002zl0
Title : Crystal structure of H.pylori ClpP
Authors : Kim, D.Y.; Kim, K.K.
Deposited on : 2008-04-02
Resolution : 2.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

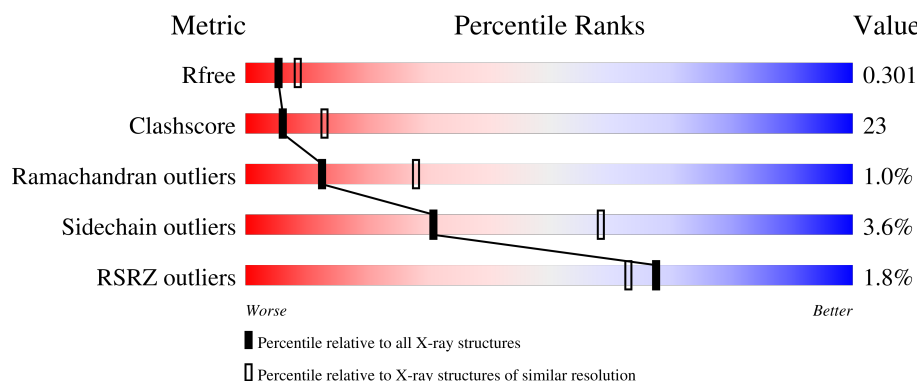
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



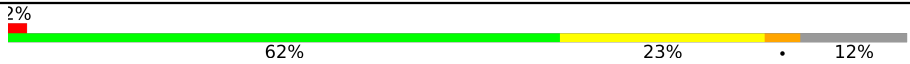
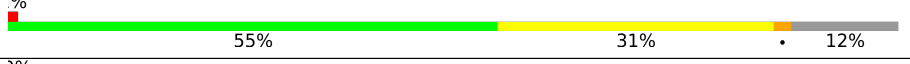
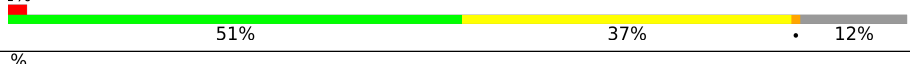
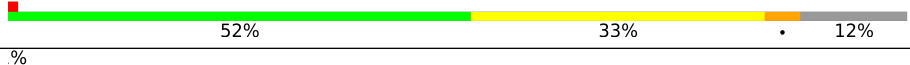
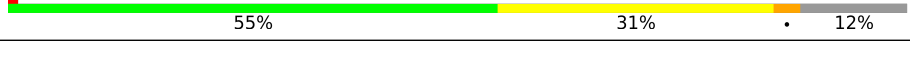
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	196	3% 46% 37% 5% 12%
1	B	196	2% 38% 44% 6% 12%
1	C	196	4% 47% 37% 12%
1	D	196	0% 45% 37% 6% 12%
1	E	196	3% 51% 36% 12%

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Mol	Chain	Length	Quality of chain
1	F	196	
1	G	196	
1	H	196	
1	I	196	
1	J	196	
1	K	196	
1	L	196	
1	M	196	
1	N	196	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18919 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 ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	B	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	C	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	D	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	E	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	F	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	G	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	H	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	I	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	J	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	K	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	L	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	M	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			
1	N	173	Total	C	N	O	S	0	0	0
			1315	828	222	258	7			

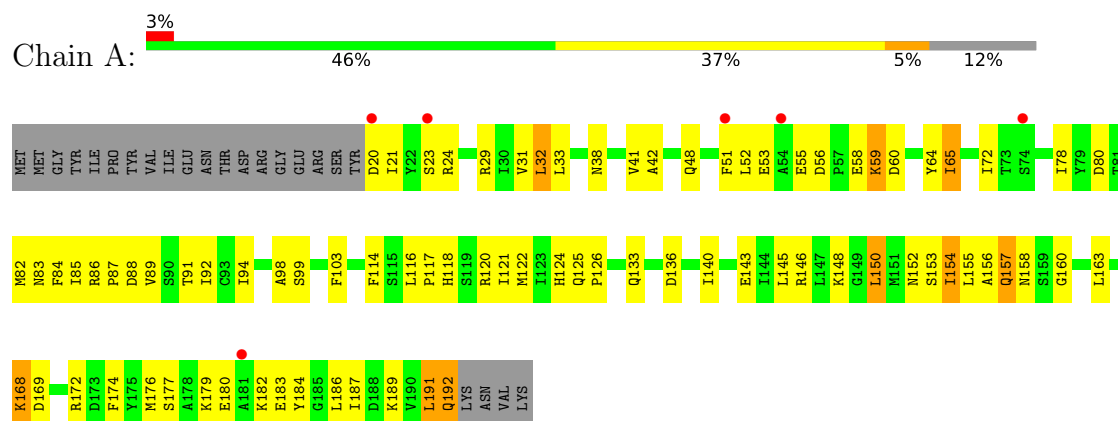
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	51	Total 51	O 51	0	0
2	B	41	Total 41	O 41	0	0
2	C	28	Total 28	O 28	0	0
2	D	28	Total 28	O 28	0	0
2	E	27	Total 27	O 27	0	0
2	F	33	Total 33	O 33	0	0
2	G	43	Total 43	O 43	0	0
2	H	38	Total 38	O 38	0	0
2	I	40	Total 40	O 40	0	0
2	J	27	Total 27	O 27	0	0
2	K	31	Total 31	O 31	0	0
2	L	27	Total 27	O 27	0	0
2	M	47	Total 47	O 47	0	0
2	N	48	Total 48	O 48	0	0

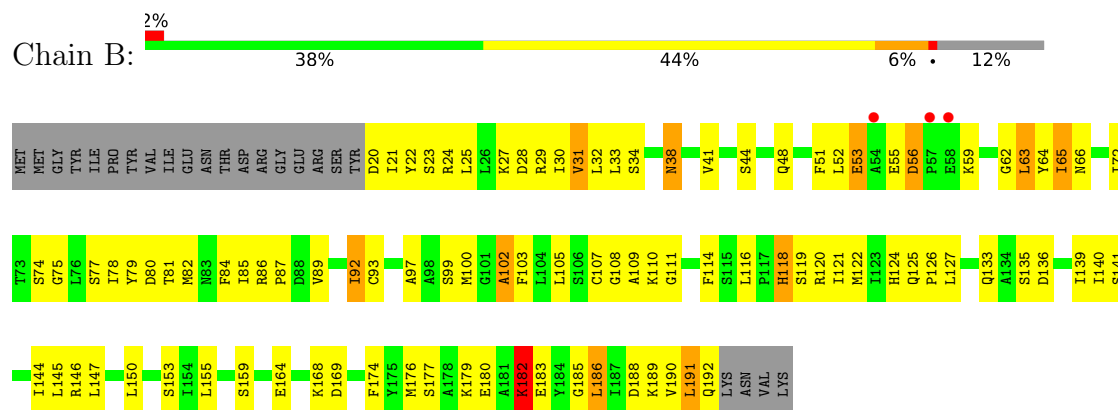
3 Residue-property plots

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.

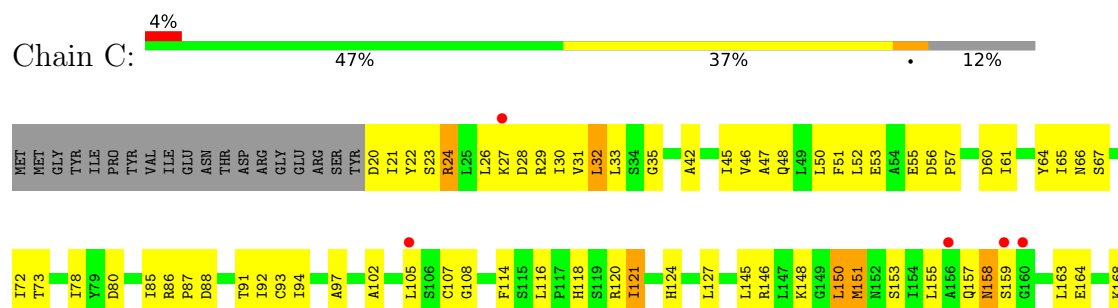
• Molecule 1: ATP-dependent Clp protease proteolytic subunit

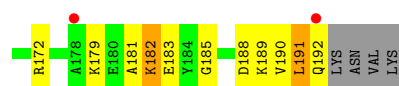


• Molecule 1: ATP-dependent Clp protease proteolytic subunit

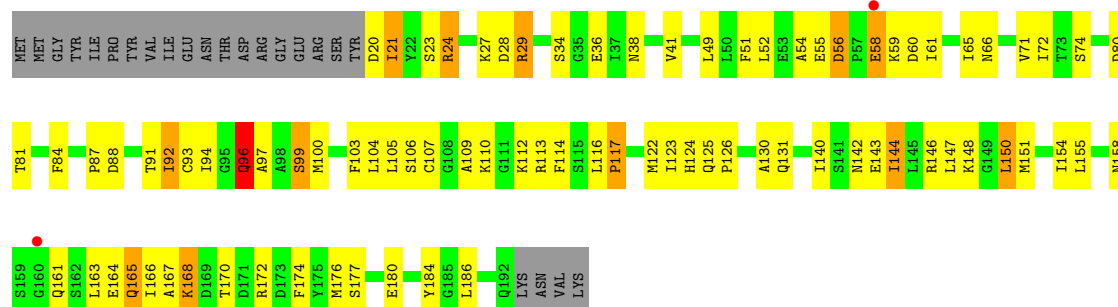
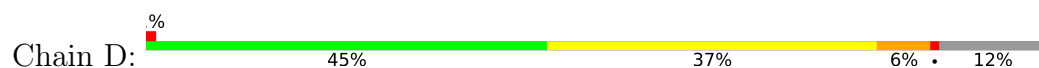


• Molecule 1: ATP-dependent Clp protease proteolytic subunit

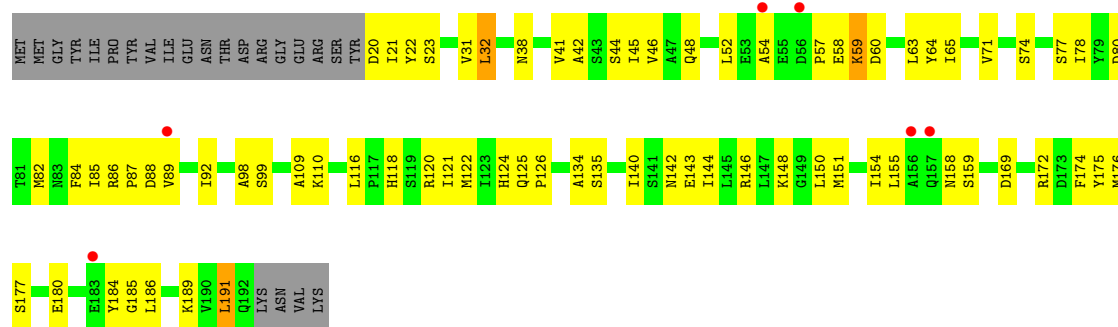




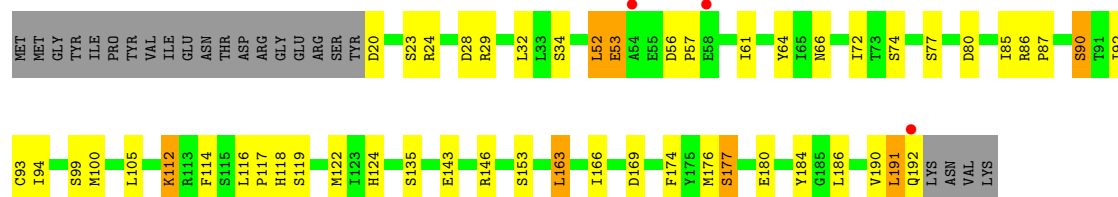
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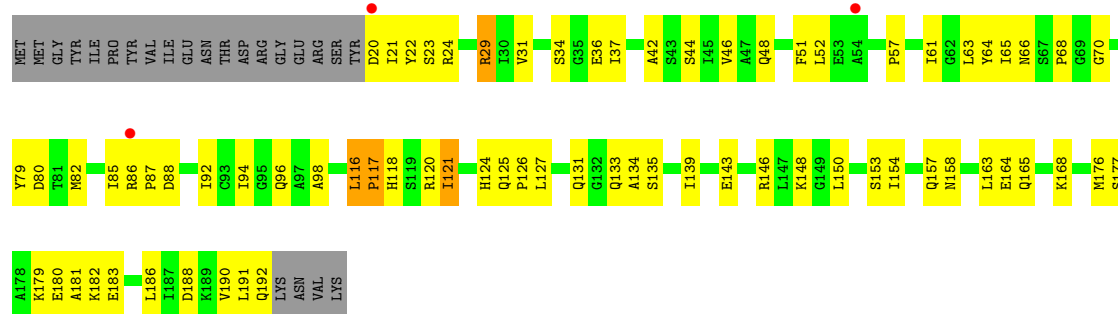


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

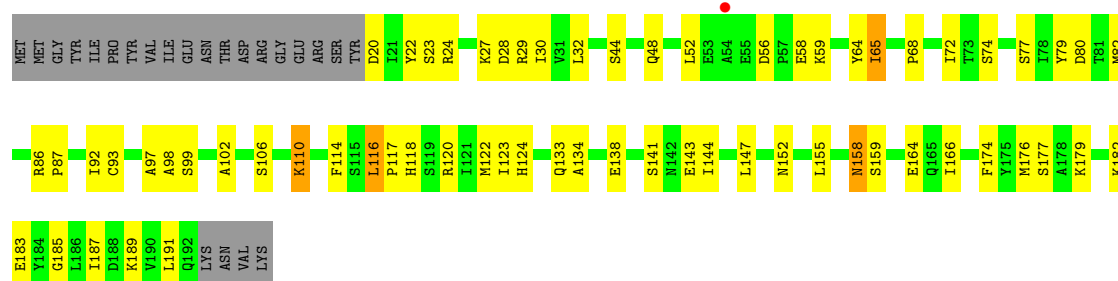




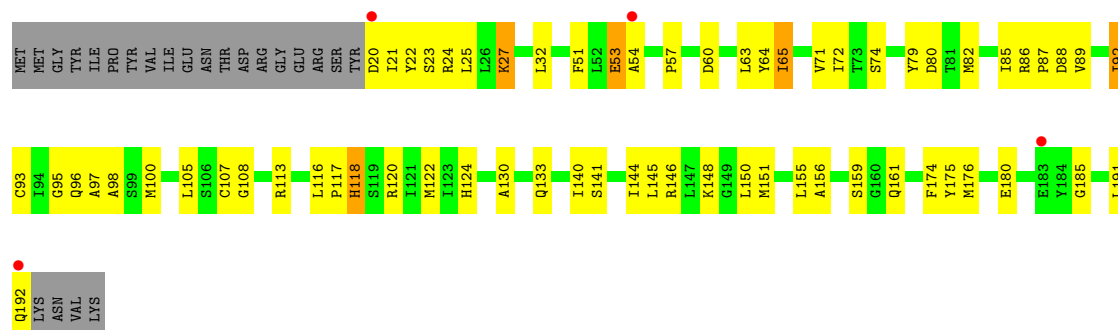
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



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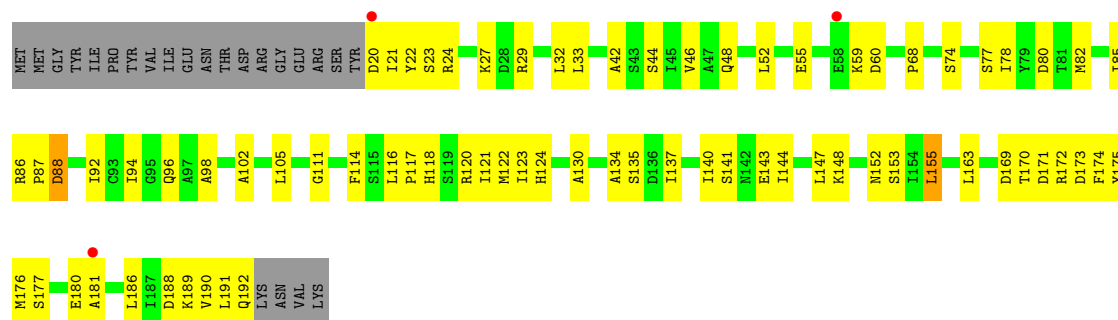


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

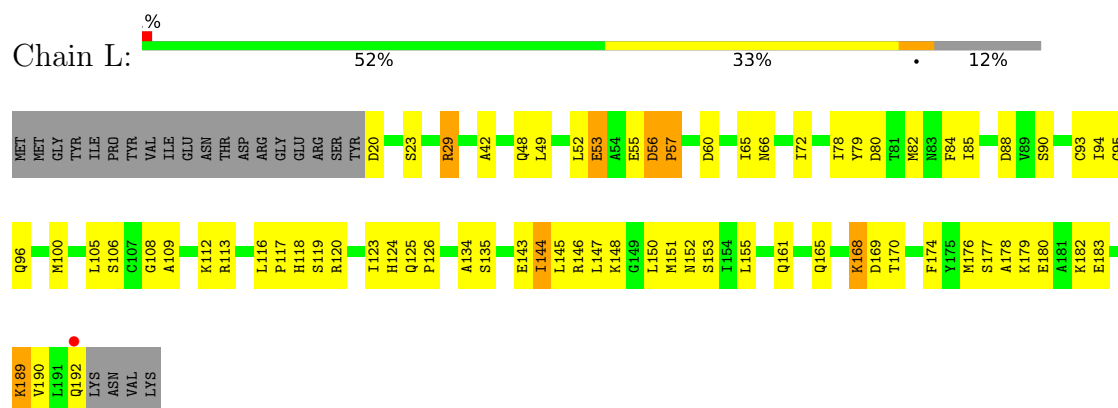


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

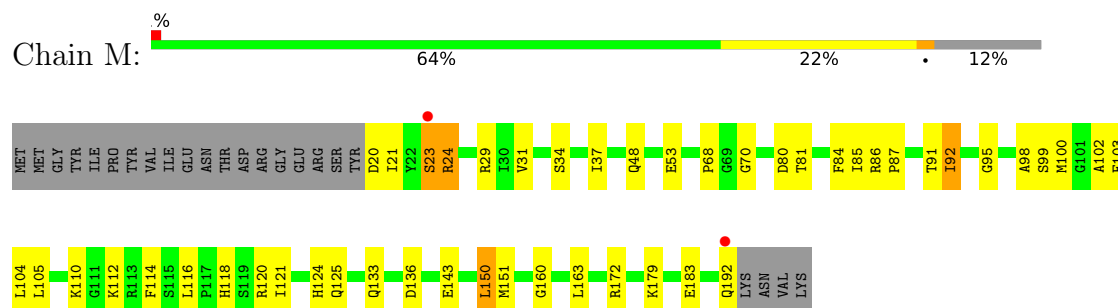




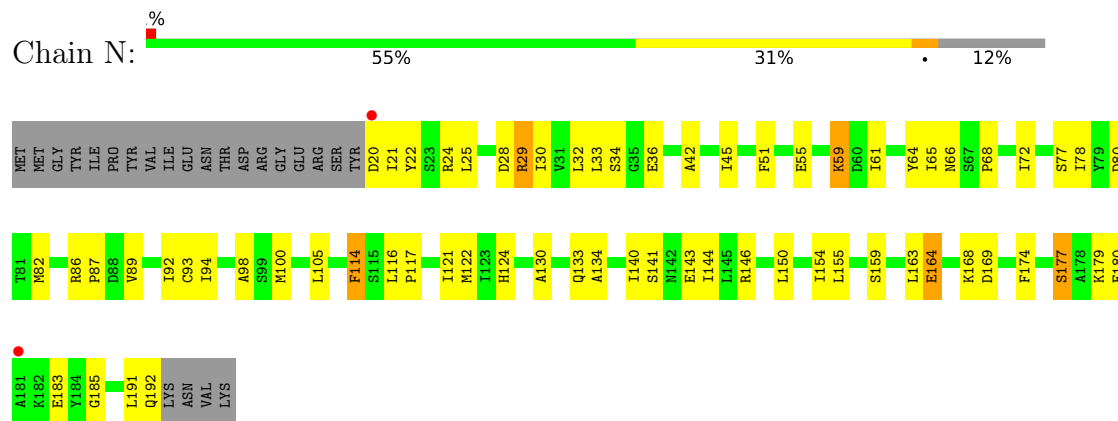
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.56Å 166.22Å 187.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.72 – 2.60 19.72 – 2.60	Depositor EDS
% Data completeness (in resolution range)	88.6 (19.72-2.60) 88.5 (19.72-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.59Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.231 , 0.299 0.232 , 0.301	Depositor DCC
R_{free} test set	7919 reflections (9.65%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 80.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18919	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.49	0/1331	1.04	5/1792 (0.3%)
1	B	0.47	0/1331	0.97	5/1792 (0.3%)
1	C	0.42	0/1331	0.99	6/1792 (0.3%)
1	D	0.44	0/1331	0.94	6/1792 (0.3%)
1	E	0.43	0/1331	0.92	3/1792 (0.2%)
1	F	0.46	0/1331	0.98	3/1792 (0.2%)
1	G	0.50	0/1331	0.97	7/1792 (0.4%)
1	H	0.49	0/1331	0.97	4/1792 (0.2%)
1	I	0.47	0/1331	0.99	6/1792 (0.3%)
1	J	0.45	0/1331	0.93	3/1792 (0.2%)
1	K	0.46	0/1331	0.94	1/1792 (0.1%)
1	L	0.46	0/1331	0.98	2/1792 (0.1%)
1	M	0.50	0/1331	0.95	2/1792 (0.1%)
1	N	0.48	0/1331	0.97	3/1792 (0.2%)
All	All	0.47	0/18634	0.97	56/25088 (0.2%)

There are no bond length outliers.

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	72	ILE	N-CA-C	8.22	118.25	110.53
1	L	152	ASN	N-CA-C	-8.10	102.53	111.36
1	A	65	ILE	N-CA-C	7.70	118.97	107.80
1	B	65	ILE	N-CA-C	7.50	118.61	108.11
1	B	182	LYS	N-CA-C	-6.86	103.88	111.36
1	E	65	ILE	N-CA-C	6.76	117.60	107.80
1	F	184	TYR	N-CA-C	-6.69	105.41	113.97
1	A	160	GLY	N-CA-C	-6.67	106.54	115.21
1	H	65	ILE	N-CA-C	6.59	117.34	108.11
1	D	117	PRO	N-CA-C	6.41	122.44	113.53
1	A	153	SER	N-CA-C	-6.36	106.15	114.04
1	D	65	ILE	N-CA-C	6.35	117.37	107.28
1	F	99	SER	CB-CA-C	-6.33	109.29	116.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	65	ILE	N-CA-C	6.16	116.73	108.11
1	G	68	PRO	N-CA-C	-5.92	106.39	114.80
1	E	118	HIS	N-CA-C	5.90	119.24	112.57
1	C	32	LEU	N-CA-C	5.89	118.35	107.99
1	J	118	HIS	N-CA-C	5.84	119.17	112.57
1	N	177	SER	N-CA-C	-5.80	103.05	110.53
1	C	148	LYS	N-CA-C	-5.80	104.96	111.28
1	L	65	ILE	N-CA-C	5.77	116.19	108.11
1	G	117	PRO	N-CA-C	5.72	121.38	113.65
1	J	65	ILE	N-CA-C	5.72	116.86	107.24
1	I	65	ILE	N-CA-C	5.69	116.06	107.75
1	N	65	ILE	N-CA-C	5.60	115.93	107.75
1	C	151	MET	N-CA-C	5.57	118.11	111.71
1	B	102	ALA	N-CA-C	-5.55	105.31	111.36
1	B	99	SER	CB-CA-C	-5.51	110.24	116.63
1	K	155	LEU	N-CA-C	-5.51	105.43	111.82
1	D	99	SER	CB-CA-C	-5.41	110.36	116.63
1	H	116	LEU	CA-C-N	5.40	125.05	119.05
1	H	116	LEU	C-N-CA	5.40	125.05	119.05
1	A	117	PRO	N-CA-C	5.36	120.89	113.65
1	I	56	ASP	CA-C-N	5.35	124.97	119.56
1	I	56	ASP	C-N-CA	5.35	124.97	119.56
1	A	154	ILE	N-CA-C	-5.33	105.19	111.00
1	D	172	ARG	N-CA-C	-5.30	101.35	109.41
1	H	117	PRO	N-CA-C	5.27	120.85	113.53
1	I	99	SER	CB-CA-C	-5.27	110.07	117.23
1	M	23	SER	N-CA-C	-5.25	105.73	111.82
1	C	145	LEU	N-CA-C	-5.22	105.71	111.71
1	E	54	ALA	N-CA-C	-5.18	106.22	112.54
1	I	116	LEU	N-CA-C	-5.15	102.78	110.20
1	F	177	SER	N-CA-C	-5.14	103.14	110.59
1	G	24	ARG	N-CA-C	-5.12	106.54	112.89
1	I	72	ILE	N-CA-C	5.10	115.32	110.42
1	N	114	PHE	N-CA-C	5.09	117.89	109.85
1	G	169	ASP	N-CA-C	5.09	118.75	112.54
1	J	148	LYS	N-CA-C	-5.07	105.67	111.14
1	G	177	SER	N-CA-C	-5.07	103.36	110.35
1	D	96	GLN	N-CA-C	5.04	116.17	108.42
1	D	168	LYS	N-CA-C	5.04	116.46	111.07
1	M	160	GLY	N-CA-C	-5.03	108.67	115.21
1	G	148	LYS	N-CA-C	-5.02	105.46	111.03
1	B	118	HIS	N-CA-C	5.01	119.08	112.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	182	LYS	N-CA-C	-5.01	105.51	110.97

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	1315	0	1338	89	0
1	B	1315	0	1338	112	0
1	C	1315	0	1338	84	0
1	D	1315	0	1338	76	0
1	E	1315	0	1338	71	0
1	F	1315	0	1338	49	0
1	G	1315	0	1338	50	0
1	H	1315	0	1338	60	0
1	I	1315	0	1338	56	0
1	J	1315	0	1338	50	0
1	K	1315	0	1338	74	0
1	L	1315	0	1338	73	0
1	M	1315	0	1338	48	0
1	N	1315	0	1338	61	0
2	A	51	0	0	2	0
2	B	41	0	0	9	0
2	C	28	0	0	1	0
2	D	28	0	0	6	0
2	E	27	0	0	5	0
2	F	33	0	0	0	0
2	G	43	0	0	6	0
2	H	38	0	0	2	0
2	I	40	0	0	9	0
2	J	27	0	0	0	0
2	K	31	0	0	3	0
2	L	27	0	0	3	0
2	M	47	0	0	1	0
2	N	48	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18919	0	18732	836	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 23.

All (836) 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:C:24:ARG:HE	1:C:27:LYS:HE3	1.30	0.93
1:N:87:PRO:HB2	2:N:242:HOH:O	1.69	0.92
1:F:90:SER:HB2	1:F:112:LYS:HB3	1.50	0.91
1:A:179:LYS:O	1:A:183:GLU:HG3	1.72	0.90
1:F:53:GLU:HG3	1:F:85:ILE:HB	1.55	0.88
1:E:135:SER:H	1:L:125:GLN:NE2	1.72	0.88
1:L:120:ARG:HD2	1:M:143:GLU:OE2	1.75	0.87
1:L:53:GLU:HG3	1:L:85:ILE:HB	1.57	0.87
1:N:33:LEU:HD13	1:N:45:ILE:HD11	1.56	0.85
1:D:116:LEU:HB3	1:D:117:PRO:HD2	1.59	0.84
1:C:24:ARG:HA	1:C:27:LYS:HE2	1.59	0.83
1:E:82:MET:HG2	1:E:89:VAL:HG11	1.60	0.83
1:M:120:ARG:HD2	1:N:143:GLU:OE2	1.78	0.83
1:E:32:LEU:HD12	1:E:64:TYR:HB2	1.60	0.83
1:F:177:SER:OG	1:F:180:GLU:HG3	1.79	0.81
1:J:53:GLU:HG3	1:J:85:ILE:HB	1.61	0.81
1:I:65:ILE:HG22	2:I:202:HOH:O	1.80	0.80
1:K:120:ARG:HH22	1:L:146:ARG:HG2	1.47	0.80
1:A:53:GLU:HG3	1:A:85:ILE:HB	1.64	0.80
1:E:135:SER:H	1:L:125:GLN:HE22	1.28	0.80
1:G:92:ILE:HG22	2:G:209:HOH:O	1.82	0.78
1:N:29:ARG:NH2	1:N:55:GLU:HB3	1.99	0.78
1:B:38:ASN:C	1:B:38:ASN:HD22	1.92	0.77
1:A:32:LEU:HD22	1:A:64:TYR:HB2	1.66	0.77
1:F:143:GLU:HA	1:F:146:ARG:NH1	1.99	0.77
1:G:116:LEU:HG	2:G:209:HOH:O	1.84	0.77
1:M:24:ARG:HD3	1:M:24:ARG:C	2.11	0.76
1:B:80:ASP:HB3	1:C:116:LEU:HD13	1.66	0.76
1:L:116:LEU:HD13	1:M:80:ASP:HB3	1.68	0.76
1:C:24:ARG:HE	1:C:27:LYS:CE	1.98	0.75
1:D:80:ASP:HB3	1:E:116:LEU:HD13	1.68	0.75
1:J:24:ARG:O	1:J:27:LYS:HB3	1.86	0.75
1:C:33:LEU:HD23	1:C:65:ILE:HG23	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:ASP:OD1	1:D:88:ASP:HB2	1.86	0.74
1:H:177:SER:OG	1:H:180:GLU:HG3	1.87	0.74
1:I:29:ARG:NH1	1:I:59:LYS:O	2.21	0.74
1:D:34:SER:HA	1:D:66:ASN:O	1.88	0.73
1:D:80:ASP:HB3	1:E:116:LEU:CD1	2.19	0.73
1:B:20:ASP:HB3	1:B:23:SER:HB2	1.71	0.73
1:G:32:LEU:HD23	1:G:64:TYR:HB2	1.70	0.73
1:N:169:ASP:HB3	1:N:174:PHE:CD2	2.24	0.73
1:A:51:PHE:HE1	1:B:24:ARG:HE	1.37	0.72
1:D:150:LEU:HD12	1:D:150:LEU:O	1.90	0.72
1:J:92:ILE:HD12	1:J:92:ILE:N	2.04	0.72
1:H:121:ILE:HG13	1:H:181:ALA:HB2	1.71	0.72
1:B:84:PHE:HB2	1:C:116:LEU:HD21	1.71	0.71
1:H:121:ILE:HG13	1:H:181:ALA:CB	2.21	0.71
1:B:38:ASN:ND2	1:B:41:VAL:H	1.89	0.70
1:J:82:MET:HG2	1:J:89:VAL:HG11	1.73	0.70
1:L:177:SER:HB2	2:L:213:HOH:O	1.91	0.70
1:H:29:ARG:NH2	1:H:52:LEU:O	2.25	0.70
1:F:143:GLU:HA	1:F:146:ARG:HH12	1.56	0.69
1:N:33:LEU:HD13	1:N:45:ILE:CD1	2.22	0.69
1:A:168:LYS:HB2	1:A:168:LYS:NZ	2.07	0.69
1:I:24:ARG:HA	1:I:27:LYS:HD3	1.73	0.69
1:K:117:PRO:HB3	1:K:192:GLN:NE2	2.07	0.69
1:L:177:SER:OG	1:L:180:GLU:HG3	1.92	0.69
1:G:24:ARG:O	1:G:24:ARG:HD3	1.92	0.69
1:K:21:ILE:HG23	1:K:22:TYR:N	2.07	0.69
1:B:190:VAL:C	1:B:192:GLN:H	2.00	0.69
1:C:24:ARG:O	1:C:27:LYS:HG2	1.93	0.69
1:L:123:ILE:HG13	1:L:170:THR:HG22	1.75	0.69
1:D:56:ASP:O	2:D:203:HOH:O	2.11	0.68
1:M:68:PRO:HA	1:M:98:ALA:HB3	1.75	0.68
1:N:32:LEU:HD23	1:N:64:TYR:HB2	1.76	0.68
1:A:125:GLN:HE21	1:H:134:ALA:HB3	1.58	0.68
1:A:176:MET:HE1	1:A:186:LEU:HD11	1.74	0.68
1:L:182:LYS:HE3	1:L:189:LYS:HA	1.76	0.68
1:D:140:ILE:O	1:D:144:ILE:HG22	1.92	0.68
1:M:92:ILE:HD12	1:M:92:ILE:N	2.09	0.68
1:D:59:LYS:O	2:D:203:HOH:O	2.11	0.68
1:K:177:SER:OG	1:K:180:GLU:HG3	1.93	0.68
1:D:87:PRO:HG3	2:D:203:HOH:O	1.93	0.67
1:D:130:ALA:HB2	1:D:140:ILE:HG21	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:ALA:HB1	1:E:122:MET:HE3	1.76	0.67
1:K:120:ARG:HD2	1:L:143:GLU:OE2	1.94	0.67
1:K:120:ARG:NH2	1:L:146:ARG:HG2	2.10	0.67
1:C:150:LEU:C	1:C:150:LEU:HD23	2.20	0.67
1:H:24:ARG:HD3	1:H:24:ARG:C	2.20	0.67
1:D:146:ARG:O	1:D:150:LEU:HB3	1.94	0.67
1:D:92:ILE:N	1:D:92:ILE:HD12	2.10	0.66
1:E:143:GLU:HA	1:E:146:ARG:HE	1.58	0.66
1:N:191:LEU:HG	2:N:234:HOH:O	1.96	0.66
1:B:82:MET:HE3	1:B:89:VAL:CG1	2.26	0.66
1:A:116:LEU:HD13	1:G:80:ASP:HB3	1.77	0.66
1:J:117:PRO:HG2	1:K:80:ASP:OD1	1.96	0.66
1:F:57:PRO:HB2	1:F:86:ARG:HD2	1.78	0.66
1:M:179:LYS:O	1:M:183:GLU:HG3	1.95	0.66
1:B:92:ILE:N	1:B:92:ILE:HD12	2.10	0.66
1:K:118:HIS:HD2	1:L:80:ASP:OD1	1.79	0.65
1:N:169:ASP:HB3	1:N:174:PHE:HD2	1.61	0.65
1:A:31:VAL:HG13	1:A:48:GLN:NE2	2.11	0.65
1:C:35:GLY:O	1:C:67:SER:HB2	1.97	0.65
1:D:24:ARG:O	1:D:24:ARG:HD3	1.96	0.65
1:A:80:ASP:OD1	1:B:118:HIS:HD2	1.80	0.65
1:H:24:ARG:HD3	1:H:24:ARG:O	1.96	0.65
1:E:126:PRO:HD2	1:E:148:LYS:HG3	1.79	0.64
1:A:182:LYS:HD3	1:A:182:LYS:C	2.22	0.64
1:A:24:ARG:O	1:A:24:ARG:HD3	1.97	0.64
1:B:125:GLN:NE2	1:I:134:ALA:HB3	2.13	0.64
1:K:130:ALA:HB2	1:K:140:ILE:HG21	1.78	0.64
1:M:116:LEU:HD13	1:N:80:ASP:HB3	1.79	0.64
1:G:90:SER:HB2	1:G:112:LYS:O	1.97	0.64
1:L:78:ILE:O	1:L:82:MET:HG3	1.98	0.63
1:A:118:HIS:HD2	1:G:80:ASP:OD1	1.81	0.63
1:I:32:LEU:HD23	1:I:64:TYR:HB2	1.80	0.63
1:N:29:ARG:HH21	1:N:55:GLU:HB3	1.62	0.63
1:B:25:LEU:HD22	1:B:30:ILE:HD12	1.79	0.63
1:A:31:VAL:HG22	1:A:48:GLN:NE2	2.13	0.63
1:D:24:ARG:HD3	1:D:24:ARG:C	2.24	0.63
1:E:134:ALA:HB3	1:L:125:GLN:HE21	1.63	0.63
1:A:72:ILE:HD11	1:A:126:PRO:HB3	1.81	0.63
1:C:29:ARG:HH21	1:C:56:ASP:HB3	1.64	0.63
1:A:133:GLN:HA	1:H:127:LEU:HD23	1.81	0.63
1:B:31:VAL:HG13	1:B:63:LEU:HA	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:116:LEU:HB3	1:I:117:PRO:HD2	1.81	0.63
1:F:135:SER:H	1:M:125:GLN:HE22	1.45	0.62
1:I:123:ILE:HG13	1:I:174:PHE:HB3	1.79	0.62
1:C:153:SER:O	1:C:157:GLN:HG3	1.99	0.62
1:D:165:GLN:HE21	1:D:165:GLN:HA	1.65	0.62
1:E:85:ILE:HD12	1:E:87:PRO:HG2	1.81	0.62
1:C:51:PHE:O	1:C:55:GLU:HG2	2.00	0.62
1:E:143:GLU:HA	1:E:146:ARG:NE	2.14	0.62
1:C:189:LYS:NZ	1:C:192:GLN:HE22	1.96	0.62
1:F:124:HIS:C	1:F:124:HIS:CD2	2.78	0.62
1:H:163:LEU:C	1:H:163:LEU:HD23	2.24	0.62
1:E:135:SER:N	1:L:125:GLN:HE22	1.98	0.62
1:B:177:SER:OG	1:B:180:GLU:HG3	2.00	0.62
1:C:159:SER:HA	1:C:185:GLY:O	2.00	0.62
1:B:126:PRO:HB2	1:B:144:ILE:HD11	1.82	0.61
1:H:20:ASP:HB3	1:H:23:SER:OG	2.00	0.61
1:N:164:GLU:HG2	1:N:168:LYS:HE2	1.82	0.61
1:A:84:PHE:CE1	1:B:191:LEU:HD13	2.34	0.61
1:C:60:ASP:OD1	1:C:88:ASP:HB2	2.00	0.61
1:E:189:LYS:HE3	1:E:191:LEU:CD2	2.30	0.61
1:A:24:ARG:HD3	1:A:24:ARG:C	2.25	0.61
1:D:93:CYS:HB2	1:D:105:LEU:HD22	1.81	0.61
1:E:92:ILE:HD12	1:E:92:ILE:N	2.16	0.61
1:E:80:ASP:HB3	1:F:116:LEU:HD13	1.82	0.61
1:I:120:ARG:CZ	2:I:219:HOH:O	2.48	0.61
1:N:179:LYS:O	1:N:183:GLU:HG3	2.00	0.61
1:A:163:LEU:HD23	1:A:163:LEU:O	2.01	0.61
1:C:42:ALA:HB1	1:C:78:ILE:HD11	1.83	0.61
1:B:82:MET:HE3	1:B:89:VAL:HG11	1.83	0.61
1:F:122:MET:HA	1:F:174:PHE:O	2.00	0.60
1:H:164:GLU:O	1:H:168:LYS:HG3	2.00	0.60
1:A:136:ASP:O	1:A:140:ILE:HD13	2.01	0.60
1:K:176:MET:HE1	1:K:186:LEU:HD12	1.83	0.60
1:C:24:ARG:NE	1:C:27:LYS:HE3	2.11	0.60
1:L:109:ALA:HB3	1:L:112:LYS:HB2	1.83	0.60
1:D:99:SER:HB3	1:D:124:HIS:NE2	2.17	0.60
1:E:126:PRO:HG2	1:L:134:ALA:HB2	1.82	0.60
1:M:120:ARG:HG3	1:N:146:ARG:NH2	2.15	0.60
1:A:146:ARG:HE	1:B:120:ARG:NH2	2.00	0.60
1:C:164:GLU:O	1:C:168:LYS:HG3	1.99	0.60
1:D:125:GLN:HE21	1:K:134:ALA:HB3	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:MET:HG2	1:A:89:VAL:HG11	1.84	0.60
1:C:80:ASP:HB3	1:D:116:LEU:HD13	1.84	0.60
1:G:29:ARG:NH1	1:G:59:LYS:O	2.35	0.60
1:A:21:ILE:HD11	1:G:51:PHE:CB	2.32	0.60
1:B:135:SER:O	1:B:139:ILE:HG12	2.02	0.60
1:I:116:LEU:CD1	1:J:80:ASP:HB3	2.32	0.60
1:C:164:GLU:H	1:C:164:GLU:CD	2.10	0.59
1:H:116:LEU:HB3	1:H:117:PRO:HD2	1.84	0.59
1:J:120:ARG:O	1:J:120:ARG:HG3	2.00	0.59
1:E:125:GLN:HE21	1:L:134:ALA:HB3	1.67	0.59
1:D:123:ILE:HG13	1:D:170:THR:HG22	1.84	0.59
1:I:44:SER:O	1:I:48:GLN:HG3	2.02	0.59
1:M:100:MET:HE1	1:M:103:PHE:CD2	2.37	0.59
1:F:74:SER:O	1:F:77:SER:HB3	2.02	0.59
1:F:32:LEU:CD2	1:F:64:TYR:HB2	2.32	0.59
1:A:91:THR:C	1:A:92:ILE:HD12	2.26	0.59
1:A:146:ARG:HG2	1:B:120:ARG:HH22	1.67	0.59
1:A:191:LEU:HD13	1:G:84:PHE:CE1	2.38	0.59
1:K:120:ARG:HH22	1:L:146:ARG:CG	2.14	0.59
1:N:130:ALA:HB2	1:N:140:ILE:HG21	1.84	0.59
1:E:154:ILE:HG22	1:E:158:ASN:HD21	1.68	0.59
1:G:124:HIS:HB2	2:N:212:HOH:O	2.02	0.59
1:I:116:LEU:HD13	1:J:80:ASP:HB3	1.85	0.59
1:C:31:VAL:HG13	1:C:48:GLN:OE1	2.02	0.59
1:D:150:LEU:O	1:D:154:ILE:HG13	2.03	0.59
1:I:124:HIS:C	1:I:124:HIS:CD2	2.81	0.58
1:E:154:ILE:HD11	1:F:118:HIS:CE1	2.38	0.58
1:B:25:LEU:HB3	1:B:30:ILE:HB	1.86	0.58
1:C:94:ILE:HG13	1:C:94:ILE:O	2.03	0.58
1:D:110:LYS:HD3	1:D:110:LYS:C	2.28	0.58
1:K:24:ARG:HD3	1:K:24:ARG:C	2.29	0.58
1:A:51:PHE:HE1	1:B:24:ARG:NE	2.02	0.58
1:F:169:ASP:HB3	1:F:174:PHE:CD2	2.38	0.58
1:A:157:GLN:O	1:A:157:GLN:HG2	2.03	0.58
1:D:125:GLN:NE2	1:K:135:SER:H	2.01	0.58
1:J:159:SER:HA	1:J:185:GLY:O	2.03	0.58
1:A:152:ASN:HB3	2:A:207:HOH:O	2.04	0.57
1:M:118:HIS:HD2	1:N:80:ASP:OD1	1.86	0.57
1:C:85:ILE:HB	1:C:87:PRO:HD2	1.86	0.57
1:H:135:SER:O	1:H:139:ILE:HG13	2.04	0.57
1:I:20:ASP:HB3	1:I:23:SER:OG	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:186:LEU:HG	2:E:209:HOH:O	2.03	0.57
1:B:62:GLY:O	1:B:64:TYR:HD1	1.87	0.57
1:E:144:ILE:HD13	1:L:134:ALA:HA	1.86	0.57
1:H:124:HIS:C	1:H:124:HIS:CD2	2.82	0.57
1:I:24:ARG:HD3	1:I:24:ARG:C	2.29	0.57
1:L:60:ASP:OD1	1:L:88:ASP:HB2	2.05	0.57
1:K:29:ARG:NH2	1:K:52:LEU:O	2.36	0.57
1:A:80:ASP:OD2	1:B:118:HIS:HB2	2.04	0.57
1:B:29:ARG:NH1	1:B:59:LYS:HB2	2.18	0.57
1:B:133:GLN:OE1	1:C:172:ARG:NH2	2.37	0.57
1:G:177:SER:OG	1:G:180:GLU:HG3	2.05	0.57
1:H:165:GLN:HE21	1:H:165:GLN:HA	1.68	0.57
1:F:143:GLU:OE1	1:F:146:ARG:NH1	2.38	0.57
1:K:78:ILE:O	1:K:82:MET:HG3	2.05	0.57
1:B:75:GLY:HA3	1:B:100:MET:SD	2.45	0.57
1:C:86:ARG:N	1:C:87:PRO:CD	2.68	0.57
1:G:117:PRO:HD3	1:G:191:LEU:O	2.05	0.57
1:I:97:ALA:O	1:I:102:ALA:HB2	2.03	0.57
1:B:93:CYS:SG	2:B:225:HOH:O	2.58	0.57
1:E:124:HIS:CD2	1:E:124:HIS:C	2.83	0.57
1:L:42:ALA:HA	1:L:78:ILE:HD11	1.86	0.57
1:B:72:ILE:HD11	1:B:126:PRO:HB3	1.85	0.56
1:H:34:SER:HA	1:H:66:ASN:O	2.04	0.56
1:K:74:SER:O	1:K:77:SER:HB2	2.05	0.56
1:C:29:ARG:HD3	1:C:60:ASP:O	2.06	0.56
1:L:179:LYS:HE3	1:L:190:VAL:HG21	1.87	0.56
1:D:164:GLU:O	1:D:168:LYS:HG3	2.06	0.56
1:M:24:ARG:HD2	1:N:51:PHE:HD1	1.68	0.56
2:C:209:HOH:O	1:J:124:HIS:HB2	2.05	0.56
1:B:55:GLU:O	1:B:56:ASP:HB2	2.06	0.56
1:F:34:SER:HA	1:F:66:ASN:O	2.06	0.56
1:I:29:ARG:NH2	1:I:52:LEU:O	2.38	0.56
1:N:150:LEU:O	1:N:154:ILE:HG13	2.06	0.56
1:G:159:SER:HA	1:G:185:GLY:O	2.05	0.56
1:H:165:GLN:HA	1:H:165:GLN:NE2	2.20	0.56
1:D:71:VAL:HB	1:D:74:SER:OG	2.06	0.56
1:D:109:ALA:O	1:D:112:LYS:HB2	2.06	0.56
1:K:60:ASP:OD1	1:K:88:ASP:HB2	2.06	0.56
1:M:31:VAL:HG13	1:M:48:GLN:OE1	2.06	0.55
1:C:42:ALA:CB	1:C:78:ILE:HD11	2.35	0.55
1:B:119:SER:HB3	2:B:225:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:106:SER:O	1:D:158:ASN:ND2	2.40	0.55
1:J:130:ALA:HB2	1:J:140:ILE:HG21	1.89	0.55
1:C:42:ALA:CA	1:C:78:ILE:HD11	2.36	0.55
1:C:50:LEU:O	1:C:53:GLU:HB3	2.06	0.55
1:C:91:THR:C	1:C:92:ILE:HD12	2.31	0.55
1:I:114:PHE:HB3	1:I:191:LEU:HG	1.89	0.55
1:A:31:VAL:HG13	1:A:48:GLN:HE22	1.70	0.55
1:H:182:LYS:HE2	1:H:188:ASP:O	2.07	0.55
1:I:24:ARG:O	1:I:27:LYS:HB2	2.06	0.55
1:A:31:VAL:HG22	1:A:48:GLN:HE21	1.72	0.55
1:C:190:VAL:O	1:C:192:GLN:N	2.40	0.55
1:H:85:ILE:HB	1:H:87:PRO:HD2	1.89	0.55
1:M:91:THR:C	1:M:92:ILE:HD12	2.31	0.55
1:K:169:ASP:C	2:K:211:HOH:O	2.48	0.55
1:M:118:HIS:CD2	1:N:80:ASP:OD1	2.60	0.55
1:E:172:ARG:HH12	1:K:172:ARG:NH1	2.05	0.55
1:N:22:TYR:CE1	1:N:32:LEU:HD12	2.41	0.55
1:A:92:ILE:HD12	1:A:92:ILE:N	2.21	0.54
1:J:71:VAL:HB	1:J:74:SER:HB2	1.90	0.54
1:B:125:GLN:HE21	1:I:134:ALA:HB3	1.71	0.54
1:B:159:SER:HA	1:B:185:GLY:O	2.06	0.54
1:B:48:GLN:O	1:B:51:PHE:HB3	2.07	0.54
1:C:92:ILE:HD12	1:C:92:ILE:N	2.22	0.54
1:D:56:ASP:OD2	1:D:58:GLU:HB2	2.06	0.54
1:I:120:ARG:NE	2:I:219:HOH:O	2.40	0.54
1:J:22:TYR:CE1	1:J:32:LEU:HD12	2.42	0.54
1:L:55:GLU:O	1:L:56:ASP:HB2	2.06	0.54
1:D:109:ALA:HB3	1:D:112:LYS:HB2	1.90	0.54
1:B:56:ASP:CG	1:B:59:LYS:HG3	2.32	0.54
1:M:24:ARG:HD2	1:N:51:PHE:CD1	2.42	0.54
1:N:92:ILE:N	1:N:92:ILE:HD12	2.23	0.54
1:A:29:ARG:HD3	1:A:60:ASP:O	2.08	0.54
1:J:21:ILE:O	1:J:25:LEU:HG	2.08	0.54
1:M:150:LEU:C	1:M:150:LEU:HD23	2.32	0.54
1:E:151:MET:O	1:E:155:LEU:HB2	2.08	0.54
1:K:92:ILE:N	1:K:92:ILE:HD12	2.23	0.54
1:E:159:SER:HA	1:E:185:GLY:O	2.08	0.54
1:F:64:TYR:CZ	1:F:92:ILE:HD12	2.43	0.54
1:B:53:GLU:HG3	1:B:85:ILE:HB	1.89	0.53
1:K:111:GLY:H	1:K:188:ASP:CG	2.16	0.53
1:I:92:ILE:N	1:I:92:ILE:HD12	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:124:HIS:C	1:M:124:HIS:CD2	2.85	0.53
1:A:182:LYS:HD3	1:A:183:GLU:N	2.22	0.53
1:C:28:ASP:O	1:C:29:ARG:HB2	2.07	0.53
1:K:124:HIS:C	1:K:124:HIS:CD2	2.86	0.53
1:D:176:MET:HE1	1:D:186:LEU:HD11	1.91	0.53
1:B:63:LEU:HG	1:B:65:ILE:HD11	1.89	0.53
1:F:72:ILE:HA	1:F:100:MET:HE3	1.90	0.53
1:K:153:SER:HA	1:K:163:LEU:HD23	1.90	0.53
1:M:120:ARG:HG3	1:N:146:ARG:HH21	1.73	0.53
1:G:29:ARG:NH2	1:G:52:LEU:O	2.42	0.53
1:J:20:ASP:HB3	1:J:23:SER:HB2	1.91	0.53
1:K:42:ALA:O	1:K:46:VAL:HG23	2.08	0.53
1:L:96:GLN:OE1	1:L:120:ARG:NH2	2.42	0.53
1:A:146:ARG:HG2	1:B:120:ARG:NH2	2.24	0.53
1:E:142:ASN:O	1:E:146:ARG:HG3	2.09	0.53
1:G:22:TYR:CE1	1:G:32:LEU:HD12	2.44	0.53
1:K:122:MET:HA	1:K:174:PHE:O	2.09	0.53
1:G:147:LEU:O	1:G:151:MET:HG3	2.09	0.53
1:K:21:ILE:CG2	1:K:22:TYR:N	2.71	0.53
1:N:59:LYS:NZ	1:N:59:LYS:HB3	2.24	0.53
1:B:80:ASP:OD2	1:C:116:LEU:HB3	2.09	0.53
1:E:86:ARG:N	1:E:87:PRO:HD2	2.24	0.53
1:K:24:ARG:HD3	1:K:24:ARG:O	2.09	0.53
1:B:190:VAL:O	1:B:192:GLN:N	2.40	0.52
1:C:107:CYS:HA	1:C:158:ASN:ND2	2.24	0.52
1:I:164:GLU:CD	1:I:164:GLU:H	2.17	0.52
1:N:116:LEU:HB3	1:N:117:PRO:HD2	1.89	0.52
1:A:156:ALA:C	1:A:158:ASN:H	2.16	0.52
1:B:190:VAL:C	1:B:192:GLN:N	2.68	0.52
1:L:150:LEU:O	1:L:153:SER:HB3	2.08	0.52
1:B:63:LEU:N	2:B:234:HOH:O	2.41	0.52
1:F:90:SER:HB2	1:F:112:LYS:CB	2.32	0.52
1:L:168:LYS:NZ	1:L:168:LYS:HB2	2.24	0.52
1:N:159:SER:HA	1:N:185:GLY:O	2.08	0.52
1:N:34:SER:HA	1:N:66:ASN:O	2.09	0.52
1:C:91:THR:HG23	1:C:108:GLY:HA3	1.92	0.52
1:D:96:GLN:HG3	1:D:97:ALA:N	2.24	0.52
1:N:61:ILE:HG13	2:N:242:HOH:O	2.08	0.52
1:B:53:GLU:HG3	1:B:87:PRO:HD2	1.92	0.52
1:B:126:PRO:CB	1:B:144:ILE:HD11	2.39	0.52
1:C:150:LEU:C	1:C:150:LEU:CD2	2.82	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:114:PHE:HB3	1:F:191:LEU:HD13	1.92	0.52
1:M:124:HIS:HB2	2:M:214:HOH:O	2.09	0.52
1:M:150:LEU:HD23	1:M:151:MET:N	2.25	0.52
1:B:34:SER:HA	1:B:66:ASN:O	2.10	0.52
1:C:189:LYS:HZ2	1:C:192:GLN:HE22	1.58	0.52
1:D:72:ILE:O	1:D:100:MET:HE3	2.09	0.52
1:H:44:SER:O	1:H:48:GLN:HG3	2.10	0.52
1:J:22:TYR:HE1	1:J:32:LEU:HD12	1.75	0.52
1:C:94:ILE:HG22	1:C:116:LEU:HD12	1.92	0.52
1:H:57:PRO:HA	1:H:87:PRO:HG3	1.91	0.51
1:K:29:ARG:NH1	1:K:59:LYS:O	2.43	0.51
1:K:123:ILE:CD1	2:K:211:HOH:O	2.58	0.51
1:B:121:ILE:HD12	2:B:225:HOH:O	2.08	0.51
1:C:30:ILE:HG23	1:C:64:TYR:CD1	2.46	0.51
1:N:124:HIS:HB2	2:N:204:HOH:O	2.09	0.51
1:A:53:GLU:HG2	1:A:87:PRO:HD3	1.93	0.51
1:F:86:ARG:N	1:F:87:PRO:HD2	2.25	0.51
1:H:150:LEU:O	1:H:153:SER:HB3	2.11	0.51
1:K:120:ARG:HH12	1:L:146:ARG:HD2	1.75	0.51
1:L:189:LYS:NZ	1:L:189:LYS:HB3	2.25	0.51
1:C:21:ILE:HG23	1:C:22:TYR:N	2.24	0.51
1:E:125:GLN:NE2	1:L:135:SER:H	2.09	0.51
1:C:42:ALA:HA	1:C:78:ILE:HD11	1.92	0.51
1:G:90:SER:CB	1:G:112:LYS:HB3	2.40	0.51
1:N:164:GLU:O	1:N:168:LYS:HG3	2.09	0.51
1:B:21:ILE:O	1:B:24:ARG:HB2	2.10	0.51
1:I:32:LEU:CD2	1:I:64:TYR:HB2	2.41	0.51
1:B:147:LEU:HD11	1:C:120:ARG:NH1	2.25	0.51
1:D:38:ASN:OD1	1:D:41:VAL:HG23	2.11	0.51
1:K:20:ASP:HB3	1:K:23:SER:HG	1.74	0.51
1:B:176:MET:HB2	1:B:180:GLU:HB2	1.93	0.51
1:B:189:LYS:HG2	1:B:190:VAL:N	2.26	0.51
1:H:124:HIS:HB2	2:H:207:HOH:O	2.10	0.51
1:A:42:ALA:HA	1:A:78:ILE:HD11	1.91	0.51
1:A:125:GLN:NE2	1:H:134:ALA:HB3	2.25	0.51
1:D:91:THR:C	1:D:92:ILE:HD12	2.35	0.51
1:D:176:MET:HE1	1:D:186:LEU:CD1	2.41	0.51
1:I:176:MET:C	2:I:219:HOH:O	2.53	0.51
1:A:33:LEU:HD23	1:A:65:ILE:HG23	1.92	0.51
1:A:80:ASP:OD1	1:B:118:HIS:CD2	2.63	0.51
1:B:79:TYR:HE2	1:C:118:HIS:CE1	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:125:GLN:NE2	1:H:148:LYS:NZ	2.59	0.51
1:E:31:VAL:HG23	1:E:63:LEU:HD12	1.93	0.50
1:F:29:ARG:NH2	1:F:52:LEU:O	2.44	0.50
1:H:51:PHE:CB	1:N:21:ILE:HD11	2.42	0.50
1:L:106:SER:O	1:L:113:ARG:HD3	2.10	0.50
1:I:118:HIS:HD2	1:J:80:ASP:OD1	1.94	0.50
1:M:192:GLN:O	1:M:192:GLN:HG3	2.11	0.50
1:J:60:ASP:OD1	1:J:88:ASP:HB2	2.11	0.50
1:D:49:LEU:HD23	1:D:81:THR:HG22	1.92	0.50
1:D:144:ILE:HD13	1:K:137:ILE:HD12	1.93	0.50
1:F:29:ARG:NH2	1:F:56:ASP:O	2.44	0.50
1:A:150:LEU:C	1:A:150:LEU:HD23	2.36	0.50
1:A:72:ILE:CD1	1:A:126:PRO:HB3	2.42	0.50
1:B:122:MET:HA	2:B:220:HOH:O	2.11	0.50
1:B:150:LEU:HD11	1:C:118:HIS:HD2	1.76	0.50
1:F:52:LEU:HD23	1:F:61:ILE:HD13	1.93	0.50
1:H:36:GLU:OE2	1:H:68:PRO:HG2	2.12	0.50
1:H:94:ILE:HG22	1:H:116:LEU:CD1	2.41	0.50
1:K:21:ILE:HG23	1:K:22:TYR:H	1.74	0.50
1:K:55:GLU:OE1	1:K:55:GLU:HA	2.12	0.50
1:A:94:ILE:HG13	1:A:94:ILE:O	2.10	0.50
1:A:124:HIS:C	1:A:124:HIS:CD2	2.89	0.50
1:L:93:CYS:HB2	1:L:105:LEU:HD22	1.94	0.50
1:M:37:ILE:HB	1:M:70:GLY:HA3	1.92	0.50
1:A:177:SER:OG	1:A:180:GLU:HG3	2.12	0.50
1:K:96:GLN:HA	1:K:120:ARG:O	2.12	0.50
1:K:116:LEU:HB3	1:K:117:PRO:HD2	1.94	0.50
1:M:100:MET:CE	1:M:104:LEU:HG	2.42	0.50
1:J:53:GLU:HG2	1:J:87:PRO:HD3	1.93	0.50
1:K:20:ASP:HB3	1:K:23:SER:OG	2.12	0.50
1:N:114:PHE:HB3	2:N:234:HOH:O	2.12	0.50
1:A:168:LYS:HB2	1:A:168:LYS:HZ2	1.76	0.49
1:M:100:MET:HE3	1:M:104:LEU:HG	1.94	0.49
1:N:28:ASP:O	1:N:29:ARG:HB2	2.12	0.49
1:B:79:TYR:CD1	1:B:107:CYS:SG	3.05	0.49
1:C:182:LYS:HG3	1:C:188:ASP:O	2.12	0.49
1:E:120:ARG:C	1:E:121:ILE:HD12	2.37	0.49
1:L:124:HIS:C	1:L:124:HIS:CD2	2.90	0.49
1:E:159:SER:HB2	2:E:209:HOH:O	2.12	0.49
1:E:184:TYR:HD2	2:E:209:HOH:O	1.94	0.49
1:I:68:PRO:HA	1:I:98:ALA:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:MET:HA	1:A:174:PHE:O	2.13	0.49
1:B:38:ASN:HD21	1:B:41:VAL:H	1.57	0.49
1:B:92:ILE:CD1	2:B:234:HOH:O	2.59	0.49
1:L:93:CYS:SG	1:L:119:SER:HB3	2.52	0.49
1:C:124:HIS:C	1:C:124:HIS:CD2	2.90	0.49
1:H:143:GLU:OE2	1:H:146:ARG:NH1	2.46	0.49
1:J:95:GLY:HA3	1:K:77:SER:OG	2.12	0.49
1:L:48:GLN:O	1:L:52:LEU:HG	2.11	0.49
1:M:91:THR:OG1	1:M:105:LEU:HD12	2.13	0.49
1:M:20:ASP:HB3	1:M:23:SER:HB2	1.94	0.49
1:B:29:ARG:NH2	1:B:52:LEU:O	2.46	0.49
1:B:164:GLU:CD	1:B:164:GLU:H	2.21	0.49
1:F:32:LEU:HD23	1:F:64:TYR:HB2	1.94	0.49
1:H:120:ARG:HB3	2:I:226:HOH:O	2.11	0.49
1:D:151:MET:HB2	2:D:224:HOH:O	2.13	0.49
1:C:29:ARG:HH11	1:C:61:ILE:HG12	1.78	0.49
1:C:182:LYS:O	1:C:183:GLU:C	2.56	0.49
1:D:36:GLU:HB3	2:D:213:HOH:O	2.12	0.49
1:I:152:ASN:O	1:I:166:ILE:HG21	2.13	0.49
1:I:30:ILE:HG23	1:I:64:TYR:CE1	2.48	0.48
1:D:143:GLU:HG2	1:E:175:TYR:CE2	2.49	0.48
1:G:163:LEU:HD13	1:G:163:LEU:O	2.12	0.48
1:K:44:SER:O	1:K:48:GLN:HG3	2.13	0.48
1:K:148:LYS:HG2	1:K:152:ASN:HD21	1.79	0.48
1:A:56:ASP:CG	1:A:59:LYS:HG3	2.38	0.48
1:A:120:ARG:HH22	1:G:146:ARG:CD	2.26	0.48
1:B:124:HIS:C	1:B:124:HIS:CD2	2.91	0.48
1:B:127:LEU:HD23	1:I:133:GLN:HA	1.94	0.48
1:D:150:LEU:HD12	1:D:150:LEU:C	2.38	0.48
1:I:24:ARG:NH1	1:I:28:ASP:OD1	2.46	0.48
1:M:24:ARG:HD3	1:M:24:ARG:O	2.12	0.48
1:A:29:ARG:NH1	1:A:59:LYS:HB2	2.28	0.48
1:A:82:MET:C	1:A:83:ASN:HD22	2.21	0.48
1:B:182:LYS:HE2	1:B:183:GLU:N	2.28	0.48
1:G:174:PHE:CD2	1:G:176:MET:HE2	2.49	0.48
1:L:53:GLU:O	1:L:57:PRO:HG3	2.14	0.48
1:C:121:ILE:HG13	1:C:181:ALA:HB2	1.95	0.48
1:D:80:ASP:HB3	1:E:116:LEU:HD12	1.96	0.48
2:D:207:HOH:O	1:K:124:HIS:HB2	2.13	0.48
1:H:79:TYR:O	1:H:82:MET:HB2	2.13	0.48
1:K:163:LEU:HD13	1:K:163:LEU:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:ASP:OD1	1:C:22:TYR:N	2.42	0.48
1:D:116:LEU:HB3	1:D:117:PRO:CD	2.38	0.48
1:F:52:LEU:HD23	1:F:61:ILE:CD1	2.44	0.48
1:F:176:MET:HE1	1:F:186:LEU:HD11	1.95	0.48
1:H:42:ALA:O	1:H:46:VAL:HG23	2.14	0.48
1:A:56:ASP:OD1	1:A:58:GLU:HB3	2.14	0.48
1:B:62:GLY:O	1:B:64:TYR:CD1	2.65	0.48
1:C:114:PHE:HA	1:C:189:LYS:O	2.14	0.48
1:J:124:HIS:C	1:J:124:HIS:CD2	2.92	0.48
1:A:116:LEU:CD1	1:G:80:ASP:HB3	2.43	0.48
1:F:116:LEU:HB3	1:F:117:PRO:HD2	1.95	0.48
1:B:25:LEU:C	1:B:27:LYS:N	2.71	0.48
1:B:120:ARG:C	2:B:225:HOH:O	2.56	0.48
1:C:163:LEU:O	1:C:163:LEU:HD23	2.13	0.48
1:E:176:MET:HB3	1:E:180:GLU:HB2	1.95	0.48
1:A:114:PHE:CD1	1:A:189:LYS:HB3	2.49	0.48
1:I:159:SER:HA	1:I:185:GLY:O	2.14	0.48
1:B:28:ASP:O	1:B:29:ARG:HB2	2.13	0.47
1:E:57:PRO:HB2	1:E:86:ARG:CZ	2.44	0.47
1:G:124:HIS:C	1:G:124:HIS:CD2	2.92	0.47
1:K:94:ILE:HG13	1:K:94:ILE:O	2.13	0.47
1:N:82:MET:HG2	1:N:89:VAL:HG11	1.96	0.47
1:B:78:ILE:O	1:B:82:MET:HG3	2.15	0.47
1:D:55:GLU:O	1:D:56:ASP:HB2	2.14	0.47
1:E:150:LEU:C	1:E:150:LEU:HD23	2.39	0.47
1:F:153:SER:HA	1:F:163:LEU:CD2	2.44	0.47
1:J:98:ALA:HB1	1:J:122:MET:HE3	1.96	0.47
1:L:20:ASP:O	1:L:23:SER:N	2.43	0.47
1:D:29:ARG:NH2	1:D:52:LEU:O	2.48	0.47
1:I:24:ARG:HD3	1:I:24:ARG:O	2.14	0.47
1:B:80:ASP:CB	1:C:116:LEU:HD13	2.42	0.47
1:B:74:SER:O	1:B:77:SER:HB2	2.14	0.47
1:E:31:VAL:HG23	1:E:63:LEU:CD1	2.44	0.47
1:H:179:LYS:O	1:H:183:GLU:HG3	2.13	0.47
1:N:122:MET:HA	1:N:174:PHE:O	2.14	0.47
1:A:146:ARG:CG	1:B:120:ARG:HH22	2.27	0.47
1:F:28:ASP:O	1:F:29:ARG:HB2	2.15	0.47
1:H:21:ILE:HG23	1:H:22:TYR:N	2.29	0.47
1:I:86:ARG:HG2	1:I:86:ARG:HH11	1.80	0.47
1:L:55:GLU:O	1:L:55:GLU:HG3	2.14	0.47
1:M:110:LYS:HD2	1:M:110:LYS:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:HIS:HB2	2:H:219:HOH:O	2.15	0.47
1:J:64:TYR:CD2	1:J:92:ILE:HB	2.50	0.47
1:J:192:GLN:HG3	1:J:192:GLN:O	2.14	0.47
1:K:21:ILE:CG2	1:K:22:TYR:H	2.28	0.47
1:F:80:ASP:HB3	1:G:116:LEU:HD13	1.96	0.47
1:I:179:LYS:O	1:I:183:GLU:HG3	2.15	0.47
1:K:120:ARG:HH22	1:L:146:ARG:CD	2.28	0.47
1:K:190:VAL:O	1:K:192:GLN:N	2.47	0.47
1:N:72:ILE:HA	1:N:100:MET:HE3	1.97	0.47
1:B:86:ARG:N	1:B:87:PRO:HD2	2.30	0.47
1:C:73:THR:HB	1:D:96:GLN:HB3	1.95	0.47
1:F:169:ASP:HB3	1:F:174:PHE:HD2	1.80	0.47
1:G:116:LEU:HB3	1:G:117:PRO:HD2	1.96	0.47
1:H:92:ILE:HD12	1:H:92:ILE:N	2.30	0.47
1:J:108:GLY:HA3	1:J:113:ARG:HG2	1.97	0.47
1:K:33:LEU:C	1:K:33:LEU:HD23	2.39	0.47
1:L:117:PRO:HD3	1:L:192:GLN:CB	2.45	0.47
1:L:178:ALA:HB2	2:L:219:HOH:O	2.15	0.47
1:E:176:MET:HE1	1:E:186:LEU:HD12	1.97	0.47
1:G:90:SER:HB3	1:G:112:LYS:HB3	1.97	0.47
1:H:163:LEU:HD23	1:H:163:LEU:O	2.15	0.47
1:L:176:MET:HB2	1:L:180:GLU:HB2	1.96	0.47
1:M:86:ARG:N	1:M:87:PRO:CD	2.78	0.47
1:B:169:ASP:O	1:B:174:PHE:HB2	2.15	0.46
1:D:126:PRO:HD2	1:D:148:LYS:HG3	1.98	0.46
1:E:71:VAL:O	1:E:74:SER:HB2	2.14	0.46
2:G:200:HOH:O	1:N:133:GLN:HG2	2.14	0.46
1:J:175:TYR:CD2	1:K:143:GLU:HG2	2.51	0.46
1:K:176:MET:HE1	1:K:186:LEU:CD1	2.46	0.46
1:A:125:GLN:NE2	1:H:135:SER:H	2.13	0.46
1:D:91:THR:HG21	1:D:104:LEU:O	2.15	0.46
1:E:74:SER:O	1:E:77:SER:HB3	2.16	0.46
1:I:74:SER:O	1:I:77:SER:HB3	2.15	0.46
1:I:79:TYR:O	1:I:82:MET:HB2	2.15	0.46
1:J:64:TYR:C	1:J:65:ILE:HG13	2.40	0.46
1:B:44:SER:O	1:B:48:GLN:HG3	2.16	0.46
1:C:42:ALA:O	1:C:46:VAL:HG23	2.16	0.46
1:E:82:MET:HA	1:E:89:VAL:HG21	1.98	0.46
1:G:55:GLU:O	1:G:56:ASP:HB2	2.14	0.46
1:N:22:TYR:CD1	1:N:32:LEU:HD12	2.51	0.46
1:D:103:PHE:HD1	1:D:155:LEU:HD13	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:44:SER:O	1:E:48:GLN:HG3	2.15	0.46
1:E:84:PHE:CE1	1:F:191:LEU:HD23	2.51	0.46
1:G:145:LEU:HD23	1:N:134:ALA:HB1	1.97	0.46
1:L:72:ILE:O	1:L:100:MET:HE3	2.15	0.46
1:N:124:HIS:C	1:N:124:HIS:CD2	2.92	0.46
1:A:146:ARG:HE	1:B:120:ARG:HH22	1.62	0.46
1:E:60:ASP:OD1	1:E:88:ASP:HB2	2.15	0.46
1:J:71:VAL:HB	1:J:74:SER:CB	2.46	0.46
1:K:191:LEU:HD13	1:L:84:PHE:CE1	2.50	0.46
1:B:182:LYS:HD2	1:B:182:LYS:C	2.40	0.46
1:J:72:ILE:HA	1:J:100:MET:HE3	1.97	0.46
1:K:86:ARG:N	1:K:87:PRO:CD	2.78	0.46
1:C:52:LEU:O	1:C:55:GLU:HB2	2.16	0.46
1:C:53:GLU:C	1:C:55:GLU:N	2.74	0.46
1:E:135:SER:N	1:L:125:GLN:NE2	2.52	0.46
1:H:24:ARG:C	1:H:24:ARG:CD	2.88	0.46
1:B:141:SER:O	1:B:144:ILE:HG22	2.16	0.46
1:D:91:THR:HB	1:D:105:LEU:HD12	1.98	0.46
1:E:58:GLU:O	1:E:59:LYS:O	2.34	0.46
1:F:146:ARG:HB2	1:F:146:ARG:CZ	2.45	0.46
1:G:92:ILE:N	1:G:92:ILE:HD12	2.31	0.46
1:K:141:SER:O	1:K:144:ILE:HG22	2.16	0.46
1:L:147:LEU:O	1:L:151:MET:HG3	2.16	0.46
1:N:86:ARG:N	1:N:87:PRO:HD2	2.31	0.46
2:G:220:HOH:O	1:M:172:ARG:HG3	2.15	0.46
1:I:97:ALA:HB2	2:I:202:HOH:O	2.15	0.46
1:I:177:SER:HA	2:I:219:HOH:O	2.16	0.46
1:L:144:ILE:HG22	1:L:145:LEU:N	2.31	0.46
1:M:20:ASP:HB3	1:M:23:SER:CB	2.46	0.45
1:C:47:ALA:O	1:D:21:ILE:HD11	2.16	0.45
1:D:24:ARG:CZ	1:D:27:LYS:HD3	2.46	0.45
1:H:118:HIS:HD2	1:I:80:ASP:OD2	1.99	0.45
1:H:190:VAL:HG12	1:H:192:GLN:HB3	1.97	0.45
1:J:93:CYS:HB2	1:J:105:LEU:HD22	1.98	0.45
1:A:103:PHE:HD1	1:A:155:LEU:CD1	2.29	0.45
1:C:23:SER:O	1:C:26:LEU:HB3	2.16	0.45
1:C:189:LYS:HE3	1:C:191:LEU:HD23	1.98	0.45
1:G:161:GLN:OE1	1:G:165:GLN:HG2	2.16	0.45
1:M:95:GLY:CA	1:N:77:SER:HB3	2.46	0.45
1:H:86:ARG:N	1:H:87:PRO:CD	2.79	0.45
1:I:20:ASP:OD2	1:I:22:TYR:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:110:LYS:HG2	2:I:230:HOH:O	2.16	0.45
1:B:135:SER:CB	1:C:172:ARG:HE	2.29	0.45
1:F:93:CYS:HB2	1:F:105:LEU:HD22	1.98	0.45
1:G:29:ARG:NH2	1:G:52:LEU:HB3	2.32	0.45
1:H:64:TYR:CD1	1:H:64:TYR:N	2.84	0.45
1:A:103:PHE:HD1	1:A:155:LEU:HD11	1.81	0.45
1:B:108:GLY:O	1:B:109:ALA:C	2.59	0.45
1:E:176:MET:HE1	1:E:186:LEU:CD1	2.46	0.45
1:L:29:ARG:NH2	1:L:52:LEU:O	2.34	0.45
1:L:90:SER:HB3	1:L:112:LYS:HB3	1.98	0.45
1:M:116:LEU:CD1	1:N:80:ASP:HB3	2.44	0.45
1:B:72:ILE:CD1	1:B:126:PRO:HB3	2.46	0.45
1:E:84:PHE:CZ	1:F:191:LEU:HD23	2.52	0.45
1:E:98:ALA:O	1:E:99:SER:C	2.60	0.45
1:F:20:ASP:HB3	1:F:23:SER:OG	2.16	0.45
1:F:94:ILE:O	1:F:94:ILE:HG13	2.17	0.45
1:H:80:ASP:HB3	1:N:116:LEU:CD1	2.46	0.45
1:M:100:MET:HE1	1:M:103:PHE:HD2	1.80	0.45
1:B:93:CYS:HB2	1:B:105:LEU:HD22	1.99	0.45
1:E:42:ALA:O	1:E:46:VAL:HG23	2.16	0.45
1:F:32:LEU:HD22	1:F:64:TYR:HB2	1.98	0.45
1:F:85:ILE:HD12	1:F:87:PRO:HG2	1.98	0.45
1:B:97:ALA:O	1:B:102:ALA:HB2	2.16	0.45
1:B:150:LEU:O	1:B:153:SER:HB3	2.16	0.45
1:E:125:GLN:HE22	1:L:135:SER:H	1.65	0.45
1:G:163:LEU:HD12	1:G:164:GLU:OE2	2.17	0.45
1:L:95:GLY:O	1:L:119:SER:HA	2.16	0.45
1:F:135:SER:H	1:M:125:GLN:NE2	2.13	0.45
1:G:22:TYR:CD1	1:G:32:LEU:HD12	2.52	0.45
1:J:51:PHE:O	1:J:54:ALA:HB3	2.17	0.45
1:L:72:ILE:HG21	1:L:147:LEU:HD13	1.99	0.45
1:D:20:ASP:O	1:D:23:SER:N	2.50	0.44
1:D:123:ILE:CG1	1:D:170:THR:HG22	2.46	0.44
1:H:126:PRO:HD2	1:H:148:LYS:HG3	1.99	0.44
1:I:122:MET:HA	1:I:174:PHE:O	2.17	0.44
1:A:53:GLU:OE2	1:A:86:ARG:NH2	2.50	0.44
1:A:56:ASP:C	1:A:58:GLU:H	2.25	0.44
1:A:150:LEU:O	1:A:154:ILE:HG13	2.17	0.44
1:A:163:LEU:HD23	1:A:163:LEU:C	2.42	0.44
1:B:27:LYS:C	1:B:29:ARG:H	2.23	0.44
1:C:33:LEU:HD23	1:C:65:ILE:HG12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:174:PHE:CD2	1:J:176:MET:HE2	2.52	0.44
1:L:126:PRO:HG2	1:L:148:LYS:HA	1.98	0.44
1:N:61:ILE:N	2:N:242:HOH:O	2.50	0.44
1:B:111:GLY:N	1:B:188:ASP:OD2	2.50	0.44
1:C:179:LYS:O	1:C:183:GLU:HG3	2.17	0.44
1:F:166:ILE:HD13	1:F:166:ILE:HA	1.89	0.44
1:A:140:ILE:N	1:A:140:ILE:HD12	2.32	0.44
1:I:93:CYS:SG	1:I:97:ALA:HB2	2.58	0.44
1:J:146:ARG:O	1:J:150:LEU:HD13	2.17	0.44
1:A:114:PHE:HD1	1:A:189:LYS:HB3	1.81	0.44
1:B:38:ASN:C	1:B:38:ASN:ND2	2.65	0.44
1:D:163:LEU:H	1:D:163:LEU:CD1	2.30	0.44
1:F:93:CYS:SG	1:F:119:SER:HB3	2.57	0.44
1:C:163:LEU:HD23	1:C:163:LEU:C	2.42	0.44
1:D:105:LEU:HD11	1:D:114:PHE:O	2.17	0.44
1:D:122:MET:HA	1:D:174:PHE:O	2.17	0.44
1:I:182:LYS:HA	1:I:187:ILE:HG13	1.99	0.44
1:L:94:ILE:O	1:L:94:ILE:HG13	2.17	0.44
1:M:112:LYS:HA	1:M:114:PHE:CZ	2.53	0.44
1:A:182:LYS:HA	1:A:187:ILE:HG13	1.98	0.44
1:B:81:THR:O	1:B:85:ILE:HG12	2.17	0.44
1:B:92:ILE:HD12	2:B:234:HOH:O	2.17	0.44
1:B:136:ASP:O	1:B:140:ILE:HG13	2.18	0.44
1:C:93:CYS:HB2	1:C:105:LEU:HD22	1.99	0.44
1:H:66:ASN:HA	1:H:96:GLN:O	2.17	0.44
1:C:151:MET:O	1:C:155:LEU:HB2	2.18	0.44
1:F:112:LYS:HA	1:F:114:PHE:CZ	2.52	0.44
1:F:190:VAL:O	1:F:192:GLN:N	2.51	0.44
1:G:121:ILE:O	1:G:176:MET:N	2.47	0.44
1:K:144:ILE:HA	1:K:147:LEU:HD12	1.99	0.44
1:M:143:GLU:HA	1:M:143:GLU:OE1	2.18	0.44
1:B:103:PHE:HD1	1:B:155:LEU:CD2	2.31	0.44
1:C:121:ILE:HG13	1:C:181:ALA:CB	2.47	0.44
1:J:86:ARG:N	1:J:87:PRO:CD	2.81	0.44
1:M:53:GLU:OE1	1:M:85:ILE:HG22	2.17	0.44
1:M:99:SER:O	1:M:102:ALA:N	2.51	0.44
1:N:32:LEU:CD2	1:N:64:TYR:HB2	2.45	0.44
1:A:21:ILE:HD11	1:G:51:PHE:HB2	2.00	0.43
1:A:80:ASP:HB3	1:B:116:LEU:CD1	2.48	0.43
1:B:120:ARG:N	2:B:225:HOH:O	2.51	0.43
1:G:44:SER:O	1:G:48:GLN:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:116:LEU:HD13	1:I:80:ASP:HB3	1.98	0.43
1:J:57:PRO:HA	1:J:87:PRO:HG3	1.98	0.43
1:L:49:LEU:HB3	1:L:85:ILE:HD13	1.98	0.43
1:N:93:CYS:HB2	1:N:105:LEU:HD22	2.01	0.43
1:A:120:ARG:C	1:A:121:ILE:HD12	2.42	0.43
1:C:30:ILE:HG22	1:C:32:LEU:HD12	2.00	0.43
1:E:109:ALA:O	1:E:110:LYS:C	2.61	0.43
1:E:154:ILE:O	1:E:158:ASN:ND2	2.51	0.43
1:E:169:ASP:O	1:E:174:PHE:HB2	2.18	0.43
1:G:192:GLN:HA	2:G:223:HOH:O	2.17	0.43
1:L:66:ASN:HA	1:L:96:GLN:O	2.18	0.43
1:F:92:ILE:HA	1:F:114:PHE:O	2.18	0.43
1:J:141:SER:O	1:J:144:ILE:HG22	2.17	0.43
1:K:176:MET:HA	1:K:180:GLU:OE1	2.19	0.43
1:D:72:ILE:HG21	1:D:147:LEU:HD13	2.01	0.43
1:L:118:HIS:HD2	1:M:80:ASP:OD1	2.00	0.43
1:L:179:LYS:HE3	1:L:179:LYS:HA	2.00	0.43
1:N:155:LEU:HD12	1:N:155:LEU:HA	1.88	0.43
1:E:140:ILE:HG13	2:E:218:HOH:O	2.18	0.43
1:G:163:LEU:HD13	1:G:163:LEU:C	2.43	0.43
1:H:20:ASP:OD2	1:H:23:SER:HB3	2.18	0.43
1:K:20:ASP:HB3	1:K:23:SER:CB	2.48	0.43
1:M:81:THR:HA	1:M:84:PHE:HB3	2.00	0.43
1:A:169:ASP:OD2	1:A:184:TYR:OH	2.21	0.43
1:B:24:ARG:O	1:B:27:LYS:HB2	2.19	0.43
1:H:52:LEU:HD13	1:H:61:ILE:HD12	2.00	0.43
1:J:118:HIS:N	1:K:80:ASP:OD2	2.40	0.43
1:K:123:ILE:HD12	2:K:211:HOH:O	2.18	0.43
1:N:94:ILE:HG22	1:N:116:LEU:HG	2.00	0.43
1:A:118:HIS:CD2	1:G:79:TYR:CE2	3.06	0.43
1:B:179:LYS:O	1:B:182:LYS:HE2	2.19	0.43
1:C:127:LEU:HD23	1:J:133:GLN:HA	2.00	0.43
1:F:80:ASP:OD1	1:G:118:HIS:HD2	2.01	0.43
1:G:20:ASP:HB3	1:G:23:SER:HB2	2.00	0.43
1:B:126:PRO:HB2	1:B:144:ILE:CD1	2.49	0.43
1:H:66:ASN:C	1:H:66:ASN:HD22	2.25	0.43
1:L:29:ARG:HA	1:L:52:LEU:HD13	1.99	0.43
1:L:90:SER:CB	1:L:112:LYS:HB3	2.49	0.43
1:N:68:PRO:HA	1:N:98:ALA:HB3	2.00	0.43
1:G:64:TYR:CE1	1:G:92:ILE:HD13	2.54	0.43
1:G:189:LYS:HG2	1:G:190:VAL:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:141:SER:O	1:J:144:ILE:CG2	2.67	0.43
1:K:170:THR:O	1:K:171:ASP:C	2.62	0.43
1:N:25:LEU:HB3	1:N:30:ILE:HB	2.00	0.43
1:N:141:SER:O	1:N:144:ILE:HG22	2.19	0.43
1:C:29:ARG:NH2	1:C:56:ASP:HB3	2.33	0.42
1:D:52:LEU:HD13	1:D:61:ILE:HG12	2.01	0.42
1:E:172:ARG:NH1	1:K:172:ARG:HH12	2.16	0.42
1:A:98:ALA:HB1	1:A:122:MET:HE3	2.01	0.42
1:D:144:ILE:HG12	1:K:134:ALA:HB2	2.02	0.42
1:I:24:ARG:HH12	1:J:54:ALA:HB1	1.84	0.42
1:I:117:PRO:HG2	1:I:118:HIS:CD2	2.54	0.42
1:J:82:MET:HA	1:J:89:VAL:HG21	2.00	0.42
1:N:20:ASP:OD2	1:N:20:ASP:C	2.61	0.42
1:E:177:SER:HG	1:E:180:GLU:HG3	1.85	0.42
1:H:190:VAL:O	1:H:192:GLN:N	2.53	0.42
1:I:141:SER:O	1:I:144:ILE:HG22	2.19	0.42
1:L:106:SER:HA	1:L:113:ARG:HD2	2.01	0.42
1:A:94:ILE:O	1:A:94:ILE:CG1	2.66	0.42
1:B:122:MET:HA	1:B:174:PHE:O	2.19	0.42
1:C:24:ARG:CA	1:C:27:LYS:HE2	2.41	0.42
1:E:82:MET:HE2	2:E:213:HOH:O	2.19	0.42
1:I:30:ILE:HG23	1:I:64:TYR:CD1	2.55	0.42
1:I:27:LYS:C	1:I:29:ARG:H	2.27	0.42
1:L:116:LEU:HB3	1:L:117:PRO:HD2	2.01	0.42
1:A:38:ASN:OD1	1:A:38:ASN:C	2.62	0.42
1:A:168:LYS:HB2	1:A:168:LYS:HZ3	1.80	0.42
1:B:25:LEU:C	1:B:27:LYS:H	2.28	0.42
1:C:53:GLU:C	1:C:55:GLU:H	2.27	0.42
1:E:42:ALA:HA	1:E:78:ILE:HD11	2.02	0.42
1:G:90:SER:HB2	1:G:112:LYS:HB3	2.02	0.42
1:I:147:LEU:HD21	2:I:226:HOH:O	2.20	0.42
1:K:85:ILE:HB	1:K:87:PRO:HD2	2.02	0.42
1:K:114:PHE:CD1	1:K:189:LYS:HB3	2.54	0.42
1:A:143:GLU:OE1	1:A:143:GLU:HA	2.19	0.42
1:C:66:ASN:HB2	1:C:94:ILE:HG13	2.02	0.42
1:D:51:PHE:O	1:D:54:ALA:HB3	2.19	0.42
1:E:71:VAL:HB	1:E:74:SER:OG	2.20	0.42
1:L:90:SER:HB2	1:L:112:LYS:O	2.19	0.42
1:B:22:TYR:C	1:B:24:ARG:H	2.28	0.42
1:D:166:ILE:O	1:D:167:ALA:C	2.63	0.42
1:J:145:LEU:HD23	1:J:145:LEU:HA	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:121:ILE:HD12	1:K:181:ALA:HB3	2.02	0.42
1:L:124:HIS:HB2	2:L:204:HOH:O	2.20	0.42
1:L:189:LYS:HB3	1:L:189:LYS:HZ3	1.85	0.42
1:M:133:GLN:HB2	1:M:136:ASP:OD2	2.19	0.42
1:C:30:ILE:HG22	1:C:32:LEU:CD1	2.50	0.42
1:C:48:GLN:O	1:C:52:LEU:HG	2.20	0.42
1:D:107:CYS:HA	1:D:158:ASN:HD21	1.85	0.42
1:K:148:LYS:O	1:K:152:ASN:ND2	2.53	0.42
1:K:163:LEU:HD13	1:K:163:LEU:C	2.44	0.42
1:A:145:LEU:O	1:A:148:LYS:HB3	2.20	0.42
1:B:84:PHE:CE1	1:C:191:LEU:HD13	2.54	0.42
1:C:105:LEU:CD2	1:C:121:ILE:HD12	2.50	0.42
1:G:36:GLU:HA	1:G:69:GLY:O	2.20	0.42
1:H:133:GLN:O	1:H:134:ALA:C	2.61	0.42
1:K:173:ASP:HB3	1:K:175:TYR:CE1	2.54	0.42
1:M:21:ILE:O	1:M:24:ARG:HB3	2.19	0.42
1:M:29:ARG:HG2	1:M:29:ARG:HH11	1.84	0.42
1:B:103:PHE:HD1	1:B:155:LEU:HD21	1.85	0.41
1:C:30:ILE:HG23	1:C:64:TYR:CE1	2.56	0.41
1:G:172:ARG:O	1:G:173:ASP:C	2.62	0.41
1:H:154:ILE:HG22	1:H:158:ASN:ND2	2.35	0.41
1:J:96:GLN:HG2	1:J:97:ALA:N	2.33	0.41
1:J:116:LEU:HD13	1:K:80:ASP:HB3	2.01	0.41
1:L:161:GLN:NE2	1:L:165:GLN:HG2	2.35	0.41
1:N:121:ILE:N	1:N:121:ILE:HD12	2.35	0.41
1:A:99:SER:OG	1:A:124:HIS:CE1	2.73	0.41
1:A:146:ARG:CD	1:B:120:ARG:HH22	2.33	0.41
1:A:146:ARG:NE	1:B:120:ARG:HH22	2.17	0.41
1:B:176:MET:HE3	1:B:186:LEU:HD23	2.02	0.41
1:H:51:PHE:HB2	1:N:21:ILE:HD11	2.01	0.41
1:K:130:ALA:HB2	1:K:140:ILE:CG2	2.47	0.41
1:N:42:ALA:HA	1:N:78:ILE:HD11	2.02	0.41
1:B:80:ASP:HB3	1:C:116:LEU:HD22	2.02	0.41
1:D:163:LEU:H	1:D:163:LEU:HD12	1.85	0.41
1:E:20:ASP:HB3	1:E:23:SER:OG	2.20	0.41
1:J:156:ALA:HB1	1:J:161:GLN:O	2.20	0.41
1:A:20:ASP:HB3	1:A:23:SER:OG	2.20	0.41
1:B:80:ASP:O	1:C:116:LEU:HD22	2.20	0.41
1:G:126:PRO:HD2	1:G:148:LYS:HG3	2.03	0.41
1:H:80:ASP:HB3	1:N:116:LEU:HD12	2.02	0.41
1:J:130:ALA:HB2	1:J:140:ILE:CG2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:169:ASP:O	1:L:174:PHE:HB2	2.20	0.41
1:A:192:GLN:HE21	1:A:192:GLN:HB2	1.54	0.41
1:D:174:PHE:HD2	1:D:176:MET:HE2	1.85	0.41
1:J:79:TYR:CD1	1:J:107:CYS:SG	3.11	0.41
1:F:52:LEU:HB3	1:F:61:ILE:HD11	2.03	0.41
1:J:176:MET:HB2	1:J:180:GLU:HB2	2.02	0.41
1:M:53:GLU:OE2	1:M:85:ILE:HA	2.21	0.41
1:B:22:TYR:C	1:B:24:ARG:N	2.77	0.41
1:B:28:ASP:O	1:B:29:ARG:CB	2.69	0.41
1:B:84:PHE:HB2	1:C:116:LEU:CD2	2.47	0.41
1:D:177:SER:OG	1:D:180:GLU:HG3	2.20	0.41
1:E:48:GLN:O	1:E:52:LEU:HG	2.21	0.41
1:H:37:ILE:O	1:H:70:GLY:HA3	2.20	0.41
1:I:182:LYS:NZ	1:I:189:LYS:HA	2.36	0.41
1:K:118:HIS:CD2	1:L:79:TYR:CE2	3.08	0.41
1:D:38:ASN:CG	1:D:41:VAL:HG23	2.46	0.41
1:E:38:ASN:H	1:E:41:VAL:HB	1.85	0.41
1:F:57:PRO:CB	1:F:86:ARG:HD2	2.49	0.41
1:G:32:LEU:CD2	1:G:64:TYR:HB2	2.44	0.41
1:H:31:VAL:O	1:H:63:LEU:HD12	2.20	0.41
1:H:68:PRO:HA	1:H:98:ALA:HB3	2.02	0.41
1:I:106:SER:C	1:I:158:ASN:HD22	2.29	0.41
1:K:68:PRO:HA	1:K:98:ALA:HB3	2.02	0.41
1:L:106:SER:C	1:L:108:GLY:H	2.29	0.41
1:A:52:LEU:O	1:A:55:GLU:HB2	2.21	0.41
1:A:152:ASN:ND2	2:A:217:HOH:O	2.52	0.41
1:B:114:PHE:HA	1:B:189:LYS:O	2.20	0.41
1:B:186:LEU:HD12	1:B:186:LEU:HA	1.77	0.41
1:C:45:ILE:HB	1:C:78:ILE:HD12	2.02	0.41
1:D:94:ILE:O	1:D:94:ILE:HG13	2.20	0.41
1:D:106:SER:HA	1:D:113:ARG:HD2	2.02	0.41
1:E:41:VAL:O	1:E:45:ILE:HG12	2.21	0.41
1:E:125:GLN:HE22	1:L:135:SER:N	2.18	0.41
1:E:143:GLU:HB2	1:E:146:ARG:NH1	2.35	0.41
1:G:104:LEU:HD23	1:G:104:LEU:HA	1.93	0.41
1:H:163:LEU:C	1:H:163:LEU:CD2	2.93	0.41
1:H:176:MET:HE1	1:H:186:LEU:CD1	2.51	0.41
1:K:148:LYS:HG2	1:K:152:ASN:ND2	2.36	0.41
1:L:53:GLU:HG3	1:L:85:ILE:CB	2.40	0.41
1:L:124:HIS:C	1:L:170:THR:HB	2.46	0.41
1:N:191:LEU:N	2:N:234:HOH:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:21:ILE:HG23	1:E:22:TYR:N	2.36	0.41
2:G:220:HOH:O	1:M:172:ARG:CG	2.69	0.41
1:D:28:ASP:O	1:D:29:ARG:CB	2.69	0.40
1:I:59:LYS:O	1:I:87:PRO:HB3	2.21	0.40
1:J:116:LEU:HB3	1:J:117:PRO:HD2	2.02	0.40
1:N:177:SER:OG	1:N:180:GLU:HG3	2.21	0.40
1:B:93:CYS:SG	1:B:119:SER:HB3	2.61	0.40
1:C:97:ALA:O	1:C:102:ALA:HB2	2.22	0.40
1:D:161:GLN:HG3	1:D:184:TYR:CE2	2.56	0.40
1:E:80:ASP:O	1:E:84:PHE:HB2	2.21	0.40
1:A:56:ASP:OD2	1:A:59:LYS:HE3	2.20	0.40
1:B:145:LEU:HD11	1:I:138:GLU:CD	2.46	0.40
1:D:142:ASN:O	1:D:146:ARG:HD3	2.20	0.40
1:G:125:GLN:HE21	1:N:134:ALA:HB3	1.87	0.40
1:I:143:GLU:OE1	1:I:143:GLU:HA	2.22	0.40
1:J:100:MET:CE	1:J:151:MET:HE1	2.51	0.40
1:K:102:ALA:O	1:K:105:LEU:HB3	2.22	0.40
1:B:30:ILE:HG22	1:B:31:VAL:N	2.36	0.40
1:D:84:PHE:CE1	1:E:191:LEU:HD13	2.56	0.40
1:D:93:CYS:HB2	1:D:105:LEU:CD2	2.51	0.40
1:K:27:LYS:C	1:K:29:ARG:H	2.27	0.40
1:A:125:GLN:HE22	1:H:135:SER:H	1.69	0.40
1:D:99:SER:HB3	1:D:124:HIS:CE1	2.56	0.40
1:N:143:GLU:HA	1:N:143:GLU:OE1	2.22	0.40

There are no symmetry-related clashes.

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	171/196 (87%)	155 (91%)	13 (8%)	3 (2%)	6 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	171/196 (87%)	150 (88%)	17 (10%)	4 (2%)	5	9
1	C	171/196 (87%)	150 (88%)	18 (10%)	3 (2%)	6	14
1	D	171/196 (87%)	155 (91%)	13 (8%)	3 (2%)	6	14
1	E	171/196 (87%)	160 (94%)	9 (5%)	2 (1%)	10	23
1	F	171/196 (87%)	162 (95%)	8 (5%)	1 (1%)	21	42
1	G	171/196 (87%)	161 (94%)	8 (5%)	2 (1%)	10	23
1	H	171/196 (87%)	164 (96%)	6 (4%)	1 (1%)	21	42
1	I	171/196 (87%)	162 (95%)	8 (5%)	1 (1%)	21	42
1	J	171/196 (87%)	163 (95%)	7 (4%)	1 (1%)	21	42
1	K	171/196 (87%)	161 (94%)	10 (6%)	0	100	100
1	L	171/196 (87%)	158 (92%)	11 (6%)	2 (1%)	10	23
1	M	171/196 (87%)	167 (98%)	4 (2%)	0	100	100
1	N	171/196 (87%)	164 (96%)	7 (4%)	0	100	100
All	All	2394/2744 (87%)	2232 (93%)	139 (6%)	23 (1%)	12	28

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	59	LYS
1	C	191	LEU
1	E	59	LYS
1	E	191	LEU
1	F	191	LEU
1	C	158	ASN
1	A	191	LEU
1	I	158	ASN
1	L	56	ASP
1	B	56	ASP
1	B	191	LEU
1	G	29	ARG
1	A	157	GLN
1	B	63	LEU
1	D	29	ARG
1	G	56	ASP
1	H	191	LEU
1	C	57	PRO
1	J	191	LEU

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Mol	Chain	Res	Type
1	B	31	VAL
1	D	21	ILE
1	D	56	ASP
1	L	57	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	145/166 (87%)	138 (95%)	7 (5%)	23	47
1	B	145/166 (87%)	135 (93%)	10 (7%)	14	32
1	C	145/166 (87%)	141 (97%)	4 (3%)	38	66
1	D	145/166 (87%)	137 (94%)	8 (6%)	19	41
1	E	145/166 (87%)	144 (99%)	1 (1%)	76	89
1	F	145/166 (87%)	139 (96%)	6 (4%)	27	54
1	G	145/166 (87%)	143 (99%)	2 (1%)	59	81
1	H	145/166 (87%)	140 (97%)	5 (3%)	32	60
1	I	145/166 (87%)	142 (98%)	3 (2%)	47	73
1	J	145/166 (87%)	140 (97%)	5 (3%)	32	60
1	K	145/166 (87%)	142 (98%)	3 (2%)	47	73
1	L	145/166 (87%)	138 (95%)	7 (5%)	23	47
1	M	145/166 (87%)	139 (96%)	6 (4%)	27	54
1	N	145/166 (87%)	138 (95%)	7 (5%)	23	47
All	All	2030/2324 (87%)	1956 (96%)	74 (4%)	31	58

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LEU
1	A	41	VAL
1	A	88	ASP

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Mol	Chain	Res	Type
1	A	150	LEU
1	A	168	LYS
1	A	172	ARG
1	A	192	GLN
1	B	32	LEU
1	B	33	LEU
1	B	38	ASN
1	B	53	GLU
1	B	92	ILE
1	B	110	LYS
1	B	146	ARG
1	B	168	LYS
1	B	182	LYS
1	B	186	LEU
1	C	24	ARG
1	C	121	ILE
1	C	146	ARG
1	C	150	LEU
1	D	24	ARG
1	D	58	GLU
1	D	92	ILE
1	D	96	GLN
1	D	131	GLN
1	D	144	ILE
1	D	150	LEU
1	D	165	GLN
1	E	32	LEU
1	F	24	ARG
1	F	52	LEU
1	F	53	GLU
1	F	90	SER
1	F	112	LYS
1	F	163	LEU
1	G	25	LEU
1	G	34	SER
1	H	29	ARG
1	H	88	ASP
1	H	121	ILE
1	H	131	GLN
1	H	157	GLN
1	I	58	GLU
1	I	110	LYS

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Mol	Chain	Res	Type
1	I	155	LEU
1	J	27	LYS
1	J	53	GLU
1	J	63	LEU
1	J	92	ILE
1	J	155	LEU
1	K	32	LEU
1	K	88	ASP
1	K	155	LEU
1	L	29	ARG
1	L	53	GLU
1	L	144	ILE
1	L	155	LEU
1	L	168	LYS
1	L	183	GLU
1	L	189	LYS
1	M	24	ARG
1	M	34	SER
1	M	92	ILE
1	M	121	ILE
1	M	150	LEU
1	M	163	LEU
1	N	24	ARG
1	N	29	ARG
1	N	36	GLU
1	N	59	LYS
1	N	163	LEU
1	N	164	GLU
1	N	192	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	66	ASN
1	A	83	ASN
1	A	118	HIS
1	A	124	HIS
1	A	125	GLN
1	A	152	ASN
1	A	192	GLN
1	B	38	ASN

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Mol	Chain	Res	Type
1	B	118	HIS
1	B	125	GLN
1	B	131	GLN
1	B	165	GLN
1	B	192	GLN
1	C	125	GLN
1	C	165	GLN
1	C	192	GLN
1	D	118	HIS
1	D	125	GLN
1	D	131	GLN
1	D	158	ASN
1	D	165	GLN
1	E	83	ASN
1	E	96	GLN
1	E	124	HIS
1	E	125	GLN
1	E	158	ASN
1	E	165	GLN
1	F	118	HIS
1	F	124	HIS
1	F	125	GLN
1	F	131	GLN
1	F	165	GLN
1	G	118	HIS
1	G	124	HIS
1	G	125	GLN
1	H	66	ASN
1	H	124	HIS
1	H	125	GLN
1	H	165	GLN
1	H	192	GLN
1	I	118	HIS
1	I	125	GLN
1	I	152	ASN
1	I	165	GLN
1	J	125	GLN
1	J	152	ASN
1	K	118	HIS
1	K	124	HIS
1	K	125	GLN
1	K	152	ASN

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Mol	Chain	Res	Type
1	K	192	GLN
1	L	118	HIS
1	L	125	GLN
1	L	161	GLN
1	L	165	GLN
1	M	118	HIS
1	M	125	GLN
1	M	165	GLN
1	N	118	HIS
1	N	125	GLN
1	N	165	GLN

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 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	173/196 (88%)	0.28	6 (3%) 47 41	22, 39, 60, 63	0
1	B	173/196 (88%)	0.18	3 (1%) 69 64	23, 38, 59, 69	0
1	C	173/196 (88%)	0.44	7 (4%) 42 37	26, 45, 62, 78	0
1	D	173/196 (88%)	0.36	2 (1%) 76 73	31, 44, 64, 75	0
1	E	173/196 (88%)	0.24	6 (3%) 47 41	23, 41, 56, 71	0
1	F	173/196 (88%)	0.01	3 (1%) 69 64	19, 37, 59, 67	0
1	G	173/196 (88%)	-0.06	1 (0%) 85 83	16, 31, 54, 61	0
1	H	173/196 (88%)	-0.10	3 (1%) 69 64	17, 31, 48, 61	0
1	I	173/196 (88%)	-0.09	1 (0%) 85 83	22, 34, 50, 71	0
1	J	173/196 (88%)	0.11	4 (2%) 61 55	26, 37, 53, 61	0
1	K	173/196 (88%)	0.13	3 (1%) 69 64	26, 39, 53, 60	0
1	L	173/196 (88%)	0.03	1 (0%) 85 83	19, 36, 56, 64	0
1	M	173/196 (88%)	-0.18	2 (1%) 76 73	19, 30, 50, 62	0
1	N	173/196 (88%)	-0.08	2 (1%) 76 73	21, 35, 49, 68	0
All	All	2422/2744 (88%)	0.09	44 (1%) 67 63	16, 37, 57, 78	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	54	ALA	3.4
1	N	20	ASP	3.3
1	C	192	GLN	3.2
1	E	54	ALA	3.0
1	J	192	GLN	3.0
1	D	160	GLY	2.8
1	E	157	GLN	2.6
1	F	192	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	J	183	GLU	2.6
1	A	74	SER	2.6
1	B	57	PRO	2.6
1	A	54	ALA	2.5
1	A	181	ALA	2.5
1	J	54	ALA	2.5
1	M	192	GLN	2.4
1	K	181	ALA	2.4
1	H	54	ALA	2.4
1	J	20	ASP	2.3
1	E	183	GLU	2.3
1	B	54	ALA	2.3
1	C	156	ALA	2.3
1	F	54	ALA	2.3
1	D	58	GLU	2.3
1	C	160	GLY	2.3
1	E	89	VAL	2.3
1	A	23	SER	2.2
1	L	192	GLN	2.2
1	I	54	ALA	2.2
1	K	58	GLU	2.2
1	N	181	ALA	2.2
1	B	58	GLU	2.2
1	A	51	PHE	2.2
1	E	156	ALA	2.1
1	H	20	ASP	2.1
1	C	159	SER	2.1
1	H	86	ARG	2.1
1	C	27	LYS	2.1
1	A	20	ASP	2.1
1	E	56	ASP	2.1
1	C	178	ALA	2.1
1	C	105	LEU	2.1
1	F	58	GLU	2.0
1	K	20	ASP	2.0
1	M	23	SER	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 [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.