



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:17 AM UTC

PDB ID : 3KM2 / pdb_00003km2
Title : As-isolated TOMATO CHLOROPLAST SUPEROXIDE DISMUTASE
Authors : Galaleldeen, A.; Taylor, A.B.; Hart, P.J.
Deposited on : 2009-11-09
Resolution : 3.10 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

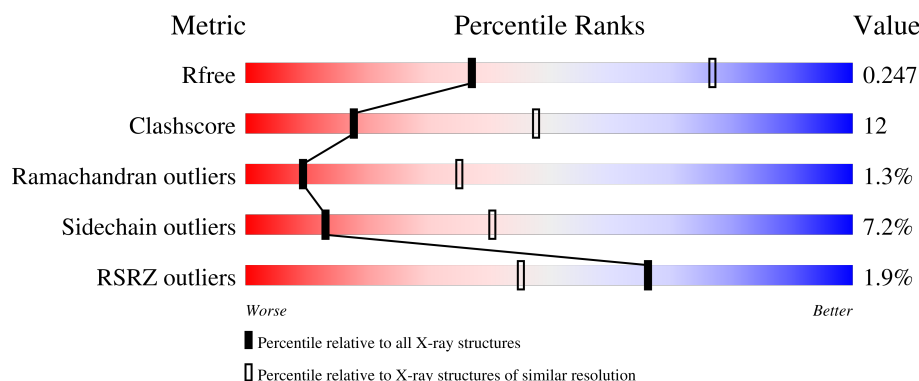
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



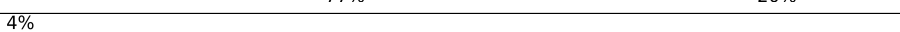
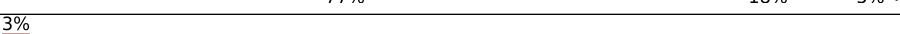
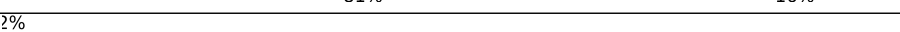
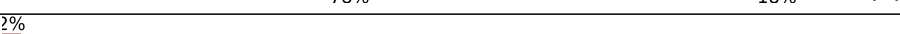
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	154	2% 81% 15% ..
1	B	154	% 81% 16% ..
1	C	154	% 77% 19% ..
1	D	154	2% 79% 16% 5% .
1	E	154	4% 81% 17% ..

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Mol	Chain	Length	Quality of chain
1	F	154	 81% 17% ..
1	G	154	 79% 18% ..
1	H	154	 77% 20% ...
1	I	154	 79% 18% ..
1	J	154	 77% 17% 5% .
1	K	154	 80% 18% ..
1	L	154	 77% 18% 5% .
1	M	154	 76% 19% ..
1	N	154	 78% 19% ..
1	O	154	 81% 16% ..
1	P	154	 81% 16% ..
1	Q	154	 79% 17% ..
1	R	154	 81% 16% ..
1	S	154	 79% 18% ..
1	T	154	 78% 18% ..
1	U	154	 80% 17% ..
1	V	154	 82% 16% ..
1	W	154	 75% 20% 5% .
1	X	154	 77% 18% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 26160 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 Superoxide dismutase [Cu-Zn], chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	B	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	C	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	D	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	E	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	F	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	G	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	H	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	I	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	J	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	K	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	L	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	M	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	N	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	O	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	P	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	R	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	S	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	T	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	U	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	V	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	W	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			
1	X	153	Total	C	N	O	S	0	0	0
			1089	667	199	220	3			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		
2	G	1	Total	Zn	0	0
			1	1		
2	H	1	Total	Zn	0	0
			1	1		
2	I	1	Total	Zn	0	0
			1	1		
2	J	1	Total	Zn	0	0
			1	1		
2	K	1	Total	Zn	0	0
			1	1		

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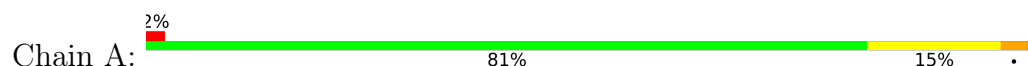
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	L	1	Total 1	Zn 1	0	0
2	M	1	Total 1	Zn 1	0	0
2	N	1	Total 1	Zn 1	0	0
2	O	1	Total 1	Zn 1	0	0
2	P	1	Total 1	Zn 1	0	0
2	Q	1	Total 1	Zn 1	0	0
2	R	1	Total 1	Zn 1	0	0
2	S	1	Total 1	Zn 1	0	0
2	T	1	Total 1	Zn 1	0	0
2	U	1	Total 1	Zn 1	0	0
2	V	1	Total 1	Zn 1	0	0
2	W	1	Total 1	Zn 1	0	0
2	X	1	Total 1	Zn 1	0	0

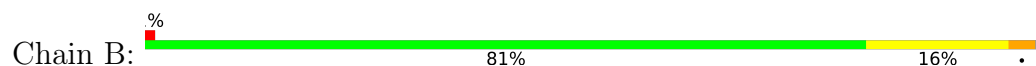
3 Residue-property plots [i](#)

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.

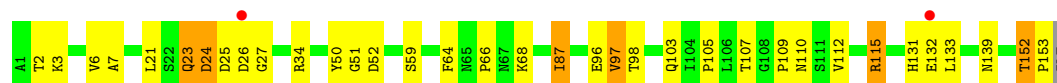
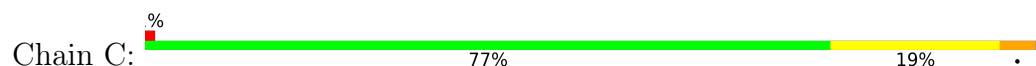
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



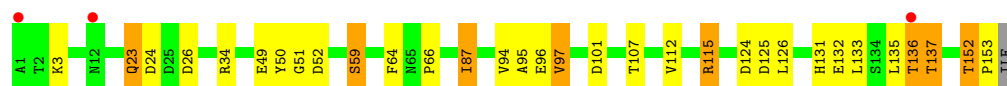
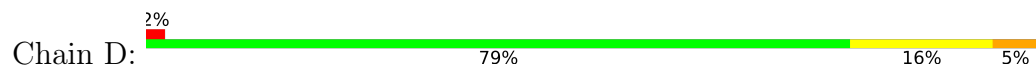
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



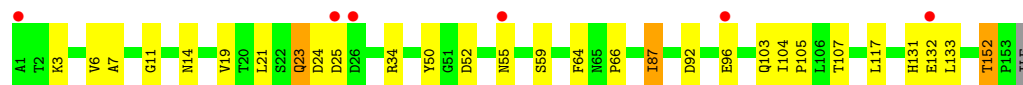
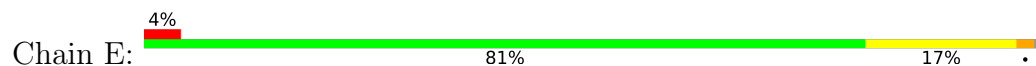
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

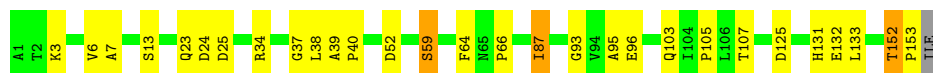


- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain F:  81% 17% ..



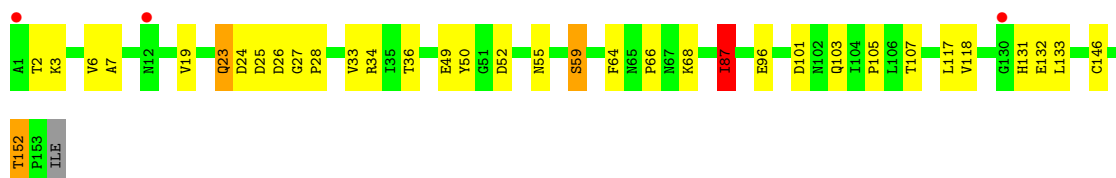
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain G:  79% 18% ..



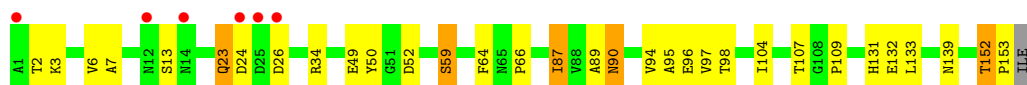
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain H:  77% 20% ..



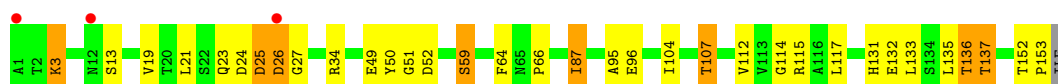
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain I:  79% 18% ..



- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain J:  77% 17% 5% .



- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain K:  80% 18% ..

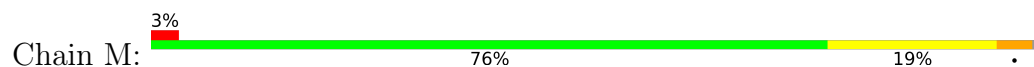


- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

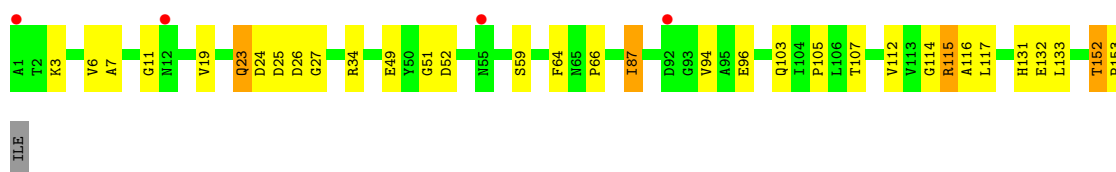
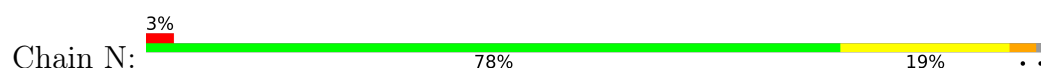
Chain L:  77% 18% 5% .



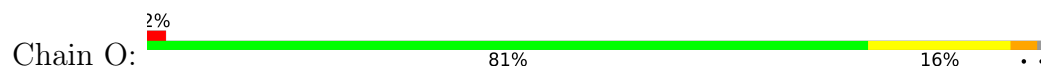
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



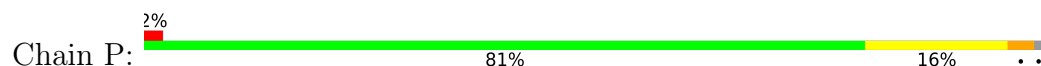
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



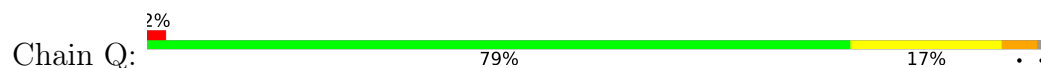
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



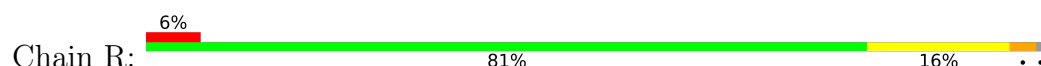
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

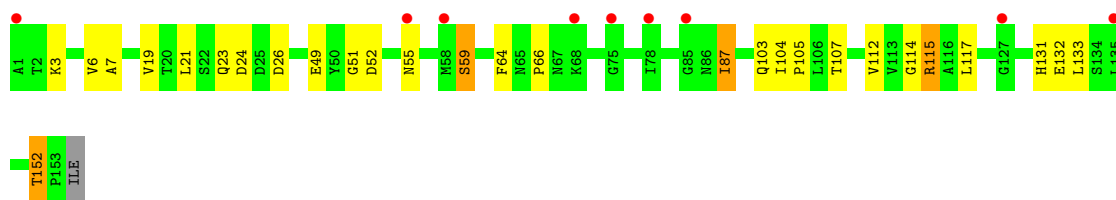


- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic



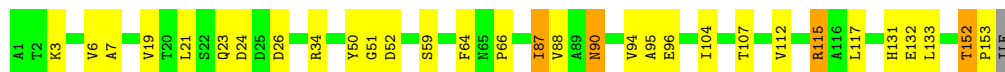
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic





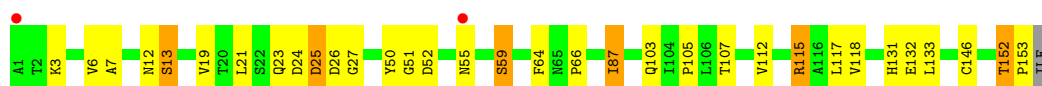
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain S: 79% 18% ..



- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain T: 78% 18% ..



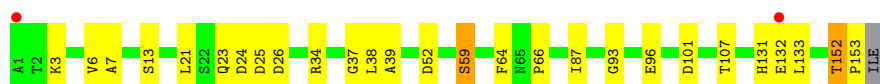
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain U: 80% 17% ..



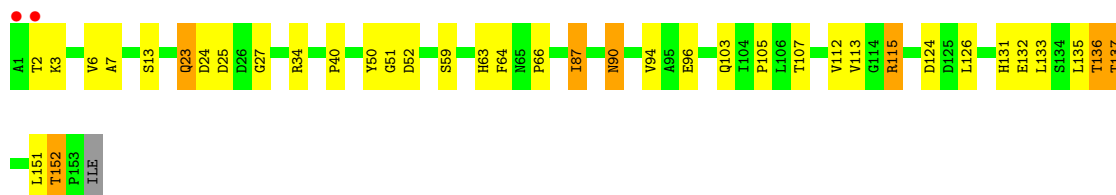
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain V: 82% 16% ..



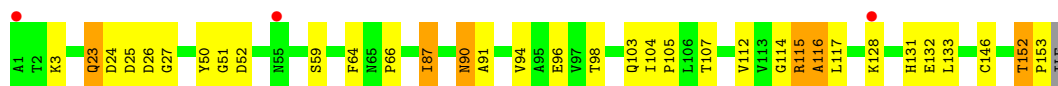
- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain W: 75% 20% 5% .



- Molecule 1: Superoxide dismutase [Cu-Zn], chloroplastic

Chain X: 77% 18% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	142.03Å 144.52Å 192.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.98 – 3.10 48.98 – 3.10	Depositor EDS
% Data completeness (in resolution range)	97.6 (48.98-3.10) 98.1 (48.98-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 3.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.4_4)	Depositor
R, R_{free}	0.220 , 0.252 0.215 , 0.247	Depositor DCC
R_{free} test set	3653 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	58.7	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.009 for k,h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	26160	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.19% 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

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

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	0.83	0/1106	1.02	4/1508 (0.3%)
1	B	0.82	0/1106	1.05	2/1508 (0.1%)
1	C	0.94	0/1106	1.00	0/1508
1	D	0.84	0/1106	0.99	1/1508 (0.1%)
1	E	0.88	0/1106	1.05	1/1508 (0.1%)
1	F	0.84	0/1106	0.99	0/1508
1	G	0.76	0/1106	1.00	1/1508 (0.1%)
1	H	0.84	0/1106	1.03	4/1508 (0.3%)
1	I	0.84	0/1106	1.03	1/1508 (0.1%)
1	J	0.81	0/1106	0.98	0/1508
1	K	0.80	0/1106	0.97	0/1508
1	L	0.78	0/1106	1.02	2/1508 (0.1%)
1	M	0.84	0/1106	1.02	0/1508
1	N	0.72	0/1106	0.96	1/1508 (0.1%)
1	O	0.69	0/1106	0.93	0/1508
1	P	0.78	0/1106	0.99	0/1508
1	Q	0.77	0/1106	1.00	0/1508
1	R	0.65	0/1106	0.91	0/1508
1	S	0.73	0/1106	0.96	1/1508 (0.1%)
1	T	0.73	0/1106	0.97	0/1508
1	U	0.76	0/1106	0.96	0/1508
1	V	0.78	0/1106	1.00	0/1508
1	W	0.73	0/1106	1.00	0/1508
1	X	0.74	0/1106	0.95	0/1508
All	All	0.79	0/26544	0.99	18/36192 (0.0%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	11	GLY	N-CA-C	6.47	119.92	110.80
1	L	138	GLY	N-CA-C	-5.50	107.52	115.27
1	I	49	GLU	N-CA-C	5.49	117.27	111.28
1	D	49	GLU	N-CA-C	5.44	117.21	111.28
1	B	28	PRO	CA-C-O	-5.42	115.14	122.08
1	H	49	GLU	N-CA-C	5.37	116.82	111.07
1	A	138	GLY	N-CA-C	-5.36	108.23	115.36
1	A	104	ILE	CA-C-N	5.34	125.32	120.03
1	A	104	ILE	C-N-CA	5.34	125.32	120.03
1	H	33	VAL	CB-CA-C	-5.31	102.77	110.63
1	N	11	GLY	N-CA-C	5.21	118.14	110.80
1	S	88	VAL	N-CA-C	5.15	115.51	107.99
1	H	101	ASP	N-CA-C	5.15	117.08	108.99
1	A	49	GLU	N-CA-C	5.14	116.88	111.28
1	L	49	GLU	N-CA-C	5.07	116.81	111.28
1	B	88	VAL	N-CA-C	5.06	115.38	107.99
1	H	87	ILE	N-CA-C	-5.06	101.03	108.11
1	G	49	GLU	N-CA-C	5.04	116.78	111.28

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	1089	0	1065	25	0
1	B	1089	0	1065	24	0
1	C	1089	0	1065	42	0
1	D	1089	0	1065	39	0
1	E	1089	0	1065	28	0
1	F	1089	0	1065	25	0
1	G	1089	0	1065	29	0
1	H	1089	0	1065	32	0
1	I	1089	0	1065	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1089	0	1065	37	0
1	K	1089	0	1065	27	0
1	L	1089	0	1065	45	0
1	M	1089	0	1065	35	0
1	N	1089	0	1065	30	0
1	O	1089	0	1065	27	0
1	P	1089	0	1065	25	0
1	Q	1089	0	1065	43	0
1	R	1089	0	1065	30	0
1	S	1089	0	1065	27	0
1	T	1089	0	1065	27	0
1	U	1089	0	1065	24	0
1	V	1089	0	1065	22	0
1	W	1089	0	1065	46	0
1	X	1089	0	1065	40	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
2	U	1	0	0	0	0
2	V	1	0	0	0	0
2	W	1	0	0	0	0
2	X	1	0	0	0	0
All	All	26160	0	25560	636	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 12.

All (636) 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:D:94:VAL:HG11	1:O:55:ASN:ND2	1.51	1.24
1:C:26:ASP:HB2	1:X:98:THR:HB	1.30	1.07
1:C:68:LYS:HE3	1:X:91:ALA:HB1	1.36	1.07
1:D:34:ARG:HG2	1:D:96:GLU:HG2	1.36	1.06
1:B:96:GLU:OE1	1:E:55:ASN:HB3	1.61	1.00
1:M:135:LEU:O	1:M:136:THR:HG23	1.63	0.99
1:L:135:LEU:O	1:L:136:THR:HG23	1.64	0.96
1:I:132:GLU:OE1	1:V:39:ALA:HB1	1.64	0.95
1:B:77:GLU:HA	1:B:77:GLU:OE1	1.63	0.95
1:H:28:PRO:HG2	1:X:128:LYS:HB2	1.50	0.92
1:C:26:ASP:CB	1:X:98:THR:HB	2.00	0.92
1:P:121:GLU:OE1	1:P:144:LEU:HD21	1.71	0.91
1:L:35:ILE:HG21	1:L:38:LEU:HD11	1.55	0.89
1:W:152:THR:CG2	1:X:52:ASP:OD2	2.21	0.88
1:W:152:THR:HG23	1:X:52:ASP:HB2	1.52	0.88
1:A:1:ALA:O	1:A:24:ASP:HA	1.73	0.88
1:Q:136:THR:O	1:Q:137:THR:HG22	1.74	0.87
1:W:136:THR:O	1:W:137:THR:HG22	1.74	0.87
1:H:55:ASN:HB3	1:I:96:GLU:OE1	1.75	0.86
1:Q:135:LEU:O	1:Q:136:THR:HG23	1.75	0.86
1:J:135:LEU:O	1:J:136:THR:HG23	1.74	0.85
1:D:136:THR:O	1:D:137:THR:HG22	1.78	0.83
1:X:51:GLY:HA2	1:X:115:ARG:O	1.79	0.81
1:D:34:ARG:HG2	1:D:96:GLU:CG	2.10	0.80
1:M:136:THR:O	1:M:137:THR:HG22	1.80	0.80
1:D:135:LEU:O	1:D:136:THR:CG2	2.30	0.80
1:D:136:THR:O	1:D:137:THR:CG2	2.30	0.80
1:W:136:THR:O	1:W:137:THR:CG2	2.30	0.80
1:L:136:THR:O	1:L:137:THR:CG2	2.30	0.80
1:J:136:THR:O	1:J:137:THR:CG2	2.30	0.79
1:Q:135:LEU:O	1:Q:136:THR:CG2	2.30	0.79
1:M:136:THR:O	1:M:137:THR:CG2	2.30	0.79
1:J:136:THR:O	1:J:137:THR:HG22	1.83	0.79
1:Q:136:THR:O	1:Q:137:THR:CG2	2.30	0.79
1:J:135:LEU:O	1:J:136:THR:CG2	2.30	0.79
1:B:77:GLU:OE1	1:B:77:GLU:CA	2.30	0.79
1:L:135:LEU:O	1:L:136:THR:CG2	2.30	0.79
1:M:135:LEU:O	1:M:136:THR:CG2	2.30	0.79
1:Q:112:VAL:HA	1:Q:115:ARG:HG3	1.66	0.78
1:Q:52:ASP:HB2	1:R:152:THR:HG23	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:135:LEU:O	1:D:136:THR:HG23	1.85	0.77
1:I:153:PRO:HG3	1:J:50:TYR:CZ	2.18	0.77
1:L:96:GLU:OE1	1:U:55:ASN:HB2	1.84	0.77
1:O:96:GLU:C	1:O:97:VAL:HG12	2.11	0.76
1:C:133:LEU:HD21	1:F:40:PRO:HG3	1.69	0.73
1:A:1:ALA:O	1:A:24:ASP:HB3	1.89	0.73
1:K:131:HIS:CD2	1:K:132:GLU:N	2.57	0.72
1:I:132:GLU:CD	1:V:39:ALA:HB1	2.15	0.72
1:A:131:HIS:CD2	1:A:132:GLU:N	2.57	0.71
1:C:68:LYS:HE3	1:X:91:ALA:CB	2.17	0.71
1:A:1:ALA:O	1:A:24:ASP:CA	2.39	0.71
1:I:50:TYR:CZ	1:J:153:PRO:HG3	2.26	0.70
1:P:121:GLU:OE1	1:P:144:LEU:HD11	1.90	0.70
1:X:51:GLY:CA	1:X:115:ARG:O	2.38	0.70
1:E:92:ASP:OD2	1:Q:143:ARG:NE	2.24	0.70
1:D:94:VAL:HG11	1:O:55:ASN:HD22	1.55	0.70
1:D:94:VAL:HG11	1:O:55:ASN:HD21	1.52	0.70
1:L:136:THR:O	1:L:137:THR:HG22	1.92	0.70
1:C:132:GLU:OE1	1:F:39:ALA:HB1	1.92	0.69
1:H:34:ARG:HG3	1:H:96:GLU:HG3	1.74	0.69
1:J:112:VAL:HA	1:J:115:ARG:HG3	1.72	0.69
1:Q:152:THR:HG23	1:R:52:ASP:HB2	1.73	0.69
1:W:136:THR:C	1:W:137:THR:CG2	2.65	0.69
1:K:112:VAL:HA	1:K:115:ARG:HG3	1.73	0.69
1:K:152:THR:HG23	1:L:52:ASP:HB2	1.74	0.69
1:L:136:THR:C	1:L:137:THR:HG23	2.17	0.69
1:J:136:THR:C	1:J:137:THR:HG23	2.18	0.69
1:G:112:VAL:HA	1:G:115:ARG:HG3	1.75	0.69
1:D:135:LEU:C	1:D:136:THR:HG23	2.18	0.68
1:K:131:HIS:HD2	1:K:132:GLU:N	1.91	0.68
1:Q:52:ASP:OD2	1:R:152:THR:CG2	2.41	0.68
1:Q:136:THR:C	1:Q:137:THR:CG2	2.65	0.68
1:W:152:THR:HG21	1:X:52:ASP:OD2	1.93	0.68
1:I:131:HIS:CD2	1:I:132:GLU:N	2.61	0.68
1:J:131:HIS:CD2	1:J:132:GLU:N	2.61	0.68
1:I:131:HIS:HE1	1:V:37:GLY:O	1.75	0.68
1:O:96:GLU:O	1:O:97:VAL:HG12	1.94	0.68
1:M:136:THR:C	1:M:137:THR:HG23	2.18	0.68
1:D:136:THR:C	1:D:137:THR:HG23	2.19	0.67
1:E:34:ARG:HG3	1:E:96:GLU:HG3	1.75	0.67
1:N:51:GLY:HA2	1:N:115:ARG:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:136:THR:C	1:M:137:THR:CG2	2.68	0.67
1:D:136:THR:C	1:D:137:THR:CG2	2.67	0.67
1:J:135:LEU:C	1:J:136:THR:HG23	2.20	0.67
1:C:131:HIS:CD2	1:C:132:GLU:N	2.63	0.67
1:Q:136:THR:C	1:Q:137:THR:HG23	2.19	0.67
1:L:35:ILE:CG2	1:L:38:LEU:HD11	2.24	0.67
1:W:136:THR:C	1:W:137:THR:HG23	2.20	0.67
1:Q:112:VAL:CA	1:Q:115:ARG:HG3	2.25	0.66
1:K:131:HIS:CD2	1:K:132:GLU:H	2.13	0.66
1:H:131:HIS:HD2	1:H:133:LEU:H	1.44	0.66
1:Q:135:LEU:C	1:Q:136:THR:HG23	2.19	0.66
1:T:55:ASN:CG	1:T:55:ASN:O	2.39	0.66
1:B:131:HIS:CD2	1:B:132:GLU:N	2.63	0.66
1:H:34:ARG:HH12	1:H:36:THR:CG2	2.09	0.66
1:J:136:THR:C	1:J:137:THR:CG2	2.69	0.66
1:G:131:HIS:CD2	1:G:132:GLU:N	2.64	0.66
1:M:78:ILE:HD11	1:P:70:THR:HG23	1.78	0.66
1:E:131:HIS:CD2	1:E:132:GLU:N	2.64	0.66
1:T:131:HIS:HD2	1:T:133:LEU:H	1.44	0.66
1:A:50:TYR:CZ	1:B:153:PRO:HG3	2.30	0.65
1:L:131:HIS:CD2	1:L:132:GLU:N	2.64	0.65
1:W:152:THR:HG23	1:X:52:ASP:CB	2.26	0.65
1:B:96:GLU:OE1	1:E:55:ASN:ND2	2.28	0.65
1:O:131:HIS:CD2	1:O:132:GLU:N	2.64	0.65
1:W:131:HIS:CD2	1:W:132:GLU:N	2.65	0.65
1:A:131:HIS:HD2	1:A:132:GLU:N	1.92	0.65
1:N:112:VAL:HA	1:N:115:ARG:HG3	1.78	0.65
1:I:131:HIS:HD2	1:I:132:GLU:N	1.95	0.65
1:R:112:VAL:HA	1:R:115:ARG:HG3	1.79	0.65
1:V:131:HIS:CD2	1:V:132:GLU:N	2.65	0.65
1:D:131:HIS:CD2	1:D:132:GLU:N	2.64	0.64
1:R:131:HIS:CD2	1:R:132:GLU:N	2.65	0.64
1:Q:152:THR:CG2	1:R:52:ASP:OD2	2.44	0.64
1:A:131:HIS:CD2	1:A:132:GLU:H	2.15	0.64
1:F:131:HIS:CD2	1:F:132:GLU:N	2.66	0.64
1:L:135:LEU:C	1:L:136:THR:HG23	2.23	0.64
1:P:34:ARG:HG3	1:P:96:GLU:HG3	1.80	0.64
1:G:131:HIS:HD2	1:G:132:GLU:N	1.96	0.63
1:L:9:LEU:HD22	1:L:35:ILE:HD11	1.79	0.63
1:M:135:LEU:C	1:M:136:THR:HG23	2.23	0.63
1:G:39:ALA:HB1	1:L:132:GLU:OE1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:131:HIS:HD2	1:J:132:GLU:N	1.95	0.63
1:M:152:THR:HG23	1:N:52:ASP:HB2	1.81	0.63
1:Q:131:HIS:CD2	1:Q:132:GLU:N	2.67	0.63
1:I:132:GLU:OE1	1:V:39:ALA:CB	2.45	0.63
1:O:131:HIS:HD2	1:O:132:GLU:N	1.97	0.62
1:U:131:HIS:CD2	1:U:132:GLU:N	2.67	0.62
1:F:131:HIS:HD2	1:F:133:LEU:H	1.47	0.62
1:P:131:HIS:CD2	1:P:132:GLU:N	2.68	0.62
1:K:55:ASN:CG	1:K:55:ASN:O	2.43	0.62
1:L:35:ILE:HG21	1:L:38:LEU:CD1	2.29	0.62
1:M:131:HIS:CD2	1:M:132:GLU:N	2.68	0.62
1:U:131:HIS:HD2	1:U:133:LEU:H	1.44	0.62
1:X:131:HIS:CD2	1:X:132:GLU:N	2.68	0.62
1:L:136:THR:C	1:L:137:THR:CG2	2.73	0.62
1:N:131:HIS:CD2	1:N:132:GLU:N	2.68	0.62
1:O:52:ASP:HB2	1:P:152:THR:HG23	1.81	0.62
1:O:96:GLU:C	1:O:97:VAL:CG1	2.73	0.62
1:U:64:PHE:CZ	1:U:66:PRO:HG3	2.35	0.62
1:M:34:ARG:HG3	1:M:96:GLU:HG3	1.82	0.62
1:G:96:GLU:C	1:G:97:VAL:HG12	2.25	0.61
1:N:131:HIS:HD2	1:N:133:LEU:H	1.48	0.61
1:H:131:HIS:CD2	1:H:132:GLU:N	2.68	0.61
1:Q:34:ARG:HG3	1:Q:96:GLU:HG3	1.82	0.61
1:E:131:HIS:HD2	1:E:132:GLU:N	1.98	0.61
1:I:131:HIS:CD2	1:I:132:GLU:H	2.19	0.61
1:L:131:HIS:HD2	1:L:132:GLU:N	1.98	0.61
1:D:131:HIS:HD2	1:D:132:GLU:N	1.97	0.61
1:H:131:HIS:CD2	1:H:133:LEU:H	2.18	0.61
1:I:133:LEU:HD11	1:V:93:GLY:HA3	1.81	0.61
1:W:112:VAL:HA	1:W:115:ARG:CG	2.31	0.61
1:W:131:HIS:HD2	1:W:132:GLU:N	1.98	0.61
1:L:136:THR:O	1:L:137:THR:HG23	1.99	0.61
1:U:131:HIS:CD2	1:U:133:LEU:H	2.18	0.61
1:V:131:HIS:HD2	1:V:132:GLU:N	1.99	0.61
1:B:131:HIS:HD2	1:B:132:GLU:N	1.98	0.61
1:L:35:ILE:CG2	1:L:38:LEU:CD1	2.79	0.61
1:V:131:HIS:HD2	1:V:133:LEU:H	1.48	0.61
1:W:34:ARG:HG3	1:W:96:GLU:HG3	1.82	0.61
1:H:55:ASN:ND2	1:I:96:GLU:OE1	2.30	0.60
1:B:96:GLU:OE1	1:E:55:ASN:CB	2.43	0.60
1:C:152:THR:HG23	1:D:52:ASP:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:34:ARG:HG3	1:N:96:GLU:HG3	1.84	0.60
1:F:131:HIS:CD2	1:F:133:LEU:H	2.18	0.60
1:F:131:HIS:HD2	1:F:132:GLU:N	2.00	0.60
1:W:90:ASN:HD21	1:W:94:VAL:HB	1.67	0.60
1:T:131:HIS:CD2	1:T:133:LEU:H	2.19	0.60
1:Q:112:VAL:HA	1:Q:115:ARG:CG	2.32	0.60
1:R:131:HIS:HD2	1:R:132:GLU:N	2.00	0.60
1:A:1:ALA:O	1:A:24:ASP:CB	2.50	0.59
1:I:131:HIS:CE1	1:V:37:GLY:O	2.54	0.59
1:V:34:ARG:HG3	1:V:96:GLU:HG3	1.85	0.59
1:C:109:PRO:HD2	1:X:96:GLU:HB3	1.83	0.59
1:I:90:ASN:HD21	1:I:94:VAL:HB	1.67	0.59
1:O:131:HIS:CD2	1:O:132:GLU:H	2.20	0.59
1:U:34:ARG:HG3	1:U:96:GLU:HG3	1.85	0.59
1:I:64:PHE:CZ	1:I:66:PRO:HG3	2.38	0.59
1:I:34:ARG:HG3	1:I:96:GLU:HG3	1.84	0.59
1:M:152:THR:CG2	1:N:52:ASP:OD2	2.51	0.59
1:W:135:LEU:O	1:W:136:THR:HG23	2.02	0.59
1:X:131:HIS:HD2	1:X:133:LEU:H	1.49	0.59
1:K:131:HIS:CD2	1:K:133:LEU:H	2.21	0.59
1:C:131:HIS:HD2	1:C:132:GLU:N	1.99	0.59
1:O:52:ASP:OD2	1:P:152:THR:CG2	2.51	0.59
1:G:93:GLY:HA3	1:L:133:LEU:HD11	1.84	0.58
1:S:131:HIS:CD2	1:S:132:GLU:N	2.71	0.58
1:J:34:ARG:NH1	1:J:96:GLU:OE2	2.36	0.58
1:Q:131:HIS:HD2	1:Q:132:GLU:N	2.01	0.58
1:J:131:HIS:CD2	1:J:132:GLU:H	2.21	0.58
1:X:112:VAL:HA	1:X:115:ARG:HG3	1.84	0.58
1:B:131:HIS:CD2	1:B:132:GLU:H	2.22	0.58
1:T:131:HIS:CD2	1:T:132:GLU:N	2.71	0.58
1:V:131:HIS:CD2	1:V:133:LEU:H	2.20	0.58
1:W:112:VAL:HA	1:W:115:ARG:HG3	1.86	0.58
1:C:52:ASP:HB2	1:D:152:THR:HG23	1.85	0.58
1:E:131:HIS:HD2	1:E:133:LEU:H	1.50	0.58
1:H:34:ARG:HH12	1:H:36:THR:HG23	1.69	0.58
1:M:52:ASP:HB2	1:N:152:THR:HG23	1.86	0.58
1:L:96:GLU:O	1:U:58:MET:HE2	2.04	0.57
1:M:131:HIS:HD2	1:M:132:GLU:N	2.02	0.57
1:W:131:HIS:CD2	1:W:132:GLU:H	2.21	0.57
1:F:34:ARG:HG3	1:F:96:GLU:HG3	1.85	0.57
1:E:131:HIS:CD2	1:E:133:LEU:H	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:152:THR:HG21	1:R:52:ASP:OD2	2.05	0.57
1:A:153:PRO:HG3	1:B:50:TYR:CZ	2.40	0.57
1:C:34:ARG:HG3	1:C:96:GLU:HG3	1.87	0.57
1:I:52:ASP:O	1:I:59:SER:HB2	2.05	0.57
1:M:50:TYR:CZ	1:N:153:PRO:HG3	2.40	0.57
1:S:51:GLY:HA2	1:S:115:ARG:O	2.05	0.57
1:X:90:ASN:HD21	1:X:94:VAL:HB	1.69	0.57
1:X:131:HIS:CD2	1:X:133:LEU:H	2.23	0.57
1:W:131:HIS:HD2	1:W:133:LEU:H	1.52	0.56
1:L:131:HIS:CD2	1:L:132:GLU:H	2.22	0.56
1:R:131:HIS:HD2	1:R:133:LEU:H	1.53	0.56
1:A:131:HIS:CD2	1:A:133:LEU:H	2.23	0.56
1:D:131:HIS:CD2	1:D:132:GLU:H	2.23	0.56
1:G:40:PRO:HG3	1:L:133:LEU:HD21	1.87	0.56
1:I:152:THR:HG23	1:J:52:ASP:HB2	1.87	0.56
1:J:131:HIS:HD2	1:J:133:LEU:H	1.53	0.56
1:Q:131:HIS:CD2	1:Q:132:GLU:H	2.24	0.56
1:G:64:PHE:CZ	1:G:66:PRO:HG3	2.40	0.56
1:J:131:HIS:CD2	1:J:133:LEU:H	2.23	0.56
1:N:131:HIS:CD2	1:N:133:LEU:H	2.22	0.56
1:B:34:ARG:HG3	1:B:96:GLU:HG3	1.88	0.56
1:E:152:THR:CG2	1:F:52:ASP:OD2	2.54	0.56
1:H:34:ARG:HG2	1:H:34:ARG:HH11	1.71	0.56
1:G:112:VAL:CA	1:G:115:ARG:HG3	2.35	0.56
1:O:34:ARG:HG3	1:O:96:GLU:HG3	1.88	0.56
1:R:131:HIS:CD2	1:R:133:LEU:H	2.23	0.56
1:L:131:HIS:CD2	1:L:133:LEU:H	2.24	0.56
1:T:112:VAL:HA	1:T:115:ARG:HG3	1.88	0.56
1:W:131:HIS:CD2	1:W:133:LEU:H	2.23	0.56
1:S:34:ARG:HG3	1:S:96:GLU:HG3	1.86	0.56
1:S:131:HIS:HD2	1:S:132:GLU:N	2.04	0.56
1:G:131:HIS:CD2	1:G:132:GLU:H	2.23	0.56
1:K:51:GLY:HA3	1:K:114:GLY:O	2.06	0.56
1:K:131:HIS:HD2	1:K:133:LEU:H	1.52	0.56
1:L:96:GLU:OE1	1:U:55:ASN:CB	2.51	0.56
1:O:64:PHE:CZ	1:O:66:PRO:HG3	2.41	0.56
1:C:131:HIS:CD2	1:C:132:GLU:H	2.23	0.55
1:C:131:HIS:CD2	1:C:133:LEU:H	2.24	0.55
1:P:131:HIS:HD2	1:P:132:GLU:N	2.02	0.55
1:R:131:HIS:CD2	1:R:132:GLU:H	2.24	0.55
1:A:131:HIS:HD2	1:A:133:LEU:H	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:135:LEU:O	1:D:136:THR:HG22	2.06	0.55
1:I:139:ASN:HD21	1:V:37:GLY:HA2	1.71	0.55
1:K:90:ASN:HD21	1:R:55:ASN:CG	2.14	0.55
1:U:131:HIS:HD2	1:U:132:GLU:N	2.04	0.55
1:R:51:GLY:HA3	1:R:114:GLY:O	2.06	0.55
1:D:34:ARG:NE	1:D:96:GLU:OE2	2.40	0.55
1:I:109:PRO:HD3	1:N:96:GLU:O	2.05	0.55
1:B:131:HIS:CD2	1:B:133:LEU:H	2.25	0.54
1:L:131:HIS:HD2	1:L:133:LEU:H	1.55	0.54
1:F:6:VAL:HG22	1:F:7:ALA:N	2.21	0.54
1:C:112:VAL:HA	1:C:115:ARG:HG3	1.89	0.54
1:T:112:VAL:HA	1:T:115:ARG:CG	2.38	0.54
1:W:152:THR:CG2	1:X:52:ASP:HB2	2.31	0.54
1:H:131:HIS:HD2	1:H:132:GLU:N	2.04	0.54
1:J:107:THR:HB	1:N:34:ARG:NH1	2.22	0.54
1:D:135:LEU:C	1:D:136:THR:CG2	2.79	0.54
1:E:52:ASP:HB2	1:F:152:THR:HG23	1.90	0.54
1:K:52:ASP:HB2	1:L:152:THR:HG23	1.89	0.54
1:N:131:HIS:HD2	1:N:132:GLU:N	2.06	0.54
1:D:96:GLU:C	1:D:97:VAL:HG12	2.32	0.54
1:T:52:ASP:O	1:T:59:SER:HB2	2.08	0.54
1:D:51:GLY:HA2	1:D:115:ARG:O	2.07	0.54
1:S:112:VAL:HA	1:S:115:ARG:CG	2.38	0.54
1:W:64:PHE:CZ	1:W:66:PRO:HG3	2.43	0.54
1:B:131:HIS:HD2	1:B:133:LEU:H	1.56	0.54
1:K:34:ARG:HG3	1:K:96:GLU:HG3	1.89	0.53
1:G:131:HIS:CD2	1:G:133:LEU:H	2.26	0.53
1:N:51:GLY:CA	1:N:115:ARG:O	2.56	0.53
1:N:112:VAL:CA	1:N:115:ARG:HG3	2.39	0.53
1:R:49:GLU:O	1:R:115:ARG:HD3	2.07	0.53
1:P:121:GLU:OE1	1:P:144:LEU:CD2	2.50	0.53
1:C:51:GLY:HA2	1:C:115:ARG:O	2.08	0.53
1:O:131:HIS:HD2	1:O:133:LEU:H	1.56	0.53
1:V:64:PHE:CZ	1:V:66:PRO:HG3	2.43	0.53
1:A:21:LEU:N	1:A:21:LEU:HD12	2.24	0.53
1:E:34:ARG:NH2	1:Q:121:GLU:OE1	2.42	0.53
1:O:131:HIS:CD2	1:O:133:LEU:H	2.26	0.53
1:R:64:PHE:CZ	1:R:66:PRO:HG3	2.43	0.53
1:F:52:ASP:O	1:F:59:SER:HB2	2.09	0.53
1:G:34:ARG:HG3	1:G:96:GLU:HG3	1.90	0.53
1:J:51:GLY:HA3	1:J:114:GLY:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:112:VAL:CA	1:J:115:ARG:HG3	2.39	0.53
1:X:131:HIS:HD2	1:X:132:GLU:N	2.06	0.53
1:K:49:GLU:O	1:K:115:ARG:HD3	2.09	0.53
1:Q:52:ASP:OD2	1:R:152:THR:HG21	2.09	0.53
1:T:25:ASP:C	1:T:27:GLY:H	2.15	0.53
1:W:51:GLY:HA2	1:W:115:ARG:O	2.09	0.53
1:A:64:PHE:CZ	1:A:66:PRO:HG3	2.44	0.52
1:T:51:GLY:HA2	1:T:115:ARG:O	2.10	0.52
1:T:64:PHE:CZ	1:T:66:PRO:HG3	2.44	0.52
1:G:131:HIS:HD2	1:G:133:LEU:H	1.58	0.52
1:J:34:ARG:HD3	1:J:96:GLU:CG	2.39	0.52
1:M:131:HIS:HD2	1:M:133:LEU:H	1.57	0.52
1:E:64:PHE:CZ	1:E:66:PRO:HG3	2.45	0.52
1:G:51:GLY:HA2	1:G:115:ARG:O	2.10	0.52
1:Q:51:GLY:HA2	1:Q:115:ARG:O	2.10	0.52
1:X:115:ARG:O	1:X:116:ALA:HB2	2.09	0.52
1:H:64:PHE:CZ	1:H:66:PRO:HG3	2.45	0.52
1:C:131:HIS:HD2	1:C:133:LEU:H	1.56	0.52
1:D:131:HIS:CD2	1:D:133:LEU:H	2.28	0.52
1:E:131:HIS:CD2	1:E:132:GLU:H	2.26	0.52
1:G:153:PRO:HG3	1:H:50:TYR:CE2	2.44	0.52
1:K:152:THR:CG2	1:L:52:ASP:HB2	2.40	0.52
1:W:135:LEU:O	1:W:136:THR:CG2	2.58	0.52
1:J:49:GLU:O	1:J:115:ARG:HD3	2.09	0.52
1:Q:52:ASP:HB2	1:R:152:THR:CG2	2.37	0.52
1:P:131:HIS:CD2	1:P:132:GLU:H	2.26	0.51
1:F:64:PHE:CZ	1:F:66:PRO:HG3	2.45	0.51
1:S:131:HIS:HD2	1:S:133:LEU:H	1.59	0.51
1:M:131:HIS:CD2	1:M:132:GLU:H	2.28	0.51
1:D:64:PHE:CZ	1:D:66:PRO:HG3	2.45	0.51
1:E:52:ASP:OD2	1:F:152:THR:CG2	2.58	0.51
1:G:152:THR:HG23	1:H:52:ASP:HB2	1.92	0.51
1:P:131:HIS:HD2	1:P:133:LEU:H	1.59	0.51
1:X:64:PHE:CZ	1:X:66:PRO:HG3	2.46	0.51
1:M:131:HIS:CD2	1:M:133:LEU:H	2.29	0.51
1:C:64:PHE:CZ	1:C:66:PRO:HG3	2.46	0.51
1:A:52:ASP:HB2	1:B:152:THR:HG23	1.93	0.50
1:C:133:LEU:HD21	1:F:40:PRO:CG	2.38	0.50
1:C:152:THR:CG2	1:D:52:ASP:OD2	2.60	0.50
1:I:133:LEU:HD11	1:V:38:LEU:O	2.12	0.50
1:M:118:VAL:HG22	1:M:146:CYS:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:131:HIS:CD2	1:F:132:GLU:H	2.28	0.50
1:Q:131:HIS:HD2	1:Q:133:LEU:H	1.59	0.50
1:T:131:HIS:HD2	1:T:132:GLU:N	2.09	0.50
1:L:97:VAL:HG22	1:L:98:THR:N	2.27	0.50
1:W:152:THR:CG2	1:X:52:ASP:CG	2.84	0.50
1:H:131:HIS:CD2	1:H:132:GLU:H	2.30	0.50
1:P:131:HIS:CD2	1:P:133:LEU:H	2.29	0.50
1:V:131:HIS:CD2	1:V:132:GLU:H	2.28	0.50
1:B:64:PHE:CZ	1:B:66:PRO:HG3	2.46	0.50
1:J:64:PHE:CZ	1:J:66:PRO:HG3	2.46	0.50
1:N:131:HIS:CD2	1:N:132:GLU:H	2.29	0.50
1:S:131:HIS:CD2	1:S:133:LEU:H	2.29	0.50
1:W:112:VAL:C	1:W:115:ARG:HG2	2.37	0.50
1:D:112:VAL:HA	1:D:115:ARG:CG	2.42	0.49
1:Q:135:LEU:C	1:Q:136:THR:CG2	2.84	0.49
1:S:112:VAL:HA	1:S:115:ARG:HG2	1.94	0.49
1:I:109:PRO:CD	1:N:96:GLU:O	2.60	0.49
1:M:21:LEU:HD12	1:M:21:LEU:N	2.27	0.49
1:P:64:PHE:CZ	1:P:66:PRO:HG3	2.48	0.49
1:Q:131:HIS:CD2	1:Q:133:LEU:H	2.30	0.49
1:S:112:VAL:C	1:S:115:ARG:HG2	2.37	0.49
1:S:112:VAL:O	1:S:115:ARG:HG2	2.13	0.49
1:C:109:PRO:HD2	1:X:96:GLU:CB	2.43	0.49
1:J:136:THR:O	1:J:137:THR:HG23	2.08	0.49
1:M:64:PHE:CZ	1:M:66:PRO:HG3	2.48	0.49
1:S:64:PHE:CZ	1:S:66:PRO:HG3	2.47	0.49
1:I:131:HIS:CD2	1:I:133:LEU:H	2.31	0.49
1:U:112:VAL:HA	1:U:115:ARG:HG3	1.94	0.49
1:H:6:VAL:HG22	1:H:7:ALA:N	2.28	0.49
1:J:87:ILE:HG23	1:J:95:ALA:HB1	1.94	0.49
1:K:90:ASN:ND2	1:R:55:ASN:HD21	2.10	0.49
1:K:112:VAL:CA	1:K:115:ARG:HG3	2.42	0.49
1:C:112:VAL:HA	1:C:115:ARG:CG	2.43	0.49
1:A:104:ILE:HG13	1:A:104:ILE:O	2.13	0.48
1:G:52:ASP:OD2	1:H:152:THR:CG2	2.61	0.48
1:S:90:ASN:HD21	1:S:94:VAL:HB	1.77	0.48
1:W:113:VAL:CG1	1:X:114:GLY:HA3	2.43	0.48
1:W:135:LEU:C	1:W:136:THR:HG23	2.37	0.48
1:C:6:VAL:HG22	1:C:7:ALA:N	2.28	0.48
1:F:87:ILE:HD12	1:F:87:ILE:HA	1.62	0.48
1:S:131:HIS:CD2	1:S:132:GLU:H	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:64:PHE:CZ	1:N:66:PRO:HG3	2.49	0.48
1:O:152:THR:HG23	1:P:52:ASP:HB2	1.94	0.48
1:S:6:VAL:HG22	1:S:7:ALA:N	2.29	0.48
1:X:131:HIS:CD2	1:X:132:GLU:H	2.31	0.48
1:R:104:ILE:O	1:R:104:ILE:HG13	2.13	0.48
1:S:52:ASP:HB2	1:T:152:THR:HG23	1.95	0.48
1:C:50:TYR:CZ	1:D:153:PRO:HG3	2.49	0.48
1:H:34:ARG:HG2	1:H:34:ARG:NH1	2.28	0.48
1:L:64:PHE:CZ	1:L:66:PRO:HG3	2.48	0.48
1:G:37:GLY:O	1:L:131:HIS:HE1	1.97	0.48
1:H:19:VAL:HG11	1:H:117:LEU:HD13	1.94	0.48
1:E:21:LEU:HD12	1:E:21:LEU:N	2.29	0.48
1:J:3:LYS:NZ	1:N:94:VAL:HG21	2.29	0.48
1:D:131:HIS:HD2	1:D:133:LEU:H	1.61	0.47
1:K:90:ASN:ND2	1:R:55:ASN:OD1	2.33	0.47
1:L:9:LEU:CD2	1:L:35:ILE:HD11	2.44	0.47
1:S:50:TYR:CZ	1:T:153:PRO:HG3	2.49	0.47
1:U:50:TYR:CZ	1:V:153:PRO:HG3	2.49	0.47
1:U:52:ASP:HB2	1:V:152:THR:HG23	1.95	0.47
1:L:35:ILE:HG22	1:L:38:LEU:CD1	2.45	0.47
1:T:103:GLN:C	1:T:105:PRO:HD3	2.40	0.47
1:W:113:VAL:HG12	1:X:114:GLY:HA3	1.96	0.47
1:E:34:ARG:HG3	1:E:96:GLU:CG	2.41	0.47
1:A:34:ARG:HG3	1:A:96:GLU:HG3	1.97	0.47
1:W:23:GLN:NE2	1:W:27:GLY:O	2.47	0.47
1:Q:52:ASP:O	1:Q:59:SER:HB2	2.15	0.47
1:Q:52:ASP:CB	1:R:152:THR:HG23	2.42	0.47
1:R:52:ASP:O	1:R:59:SER:HB2	2.15	0.47
1:T:19:VAL:HG11	1:T:117:LEU:HD13	1.97	0.47
1:N:34:ARG:HG3	1:N:96:GLU:CG	2.44	0.47
1:S:87:ILE:HD12	1:S:87:ILE:HA	1.73	0.47
1:W:63:HIS:CE1	1:W:137:THR:HA	2.50	0.47
1:K:153:PRO:HG3	1:L:50:TYR:CZ	2.50	0.47
1:E:14:ASN:HB2	1:Q:131:HIS:CE1	2.49	0.47
1:K:50:TYR:CZ	1:L:153:PRO:HG3	2.50	0.47
1:X:25:ASP:C	1:X:27:GLY:H	2.23	0.47
1:H:103:GLN:C	1:H:105:PRO:HD3	2.41	0.46
1:U:103:GLN:C	1:U:105:PRO:HD3	2.40	0.46
1:C:97:VAL:CG2	1:C:98:THR:N	2.78	0.46
1:H:52:ASP:O	1:H:59:SER:HB2	2.15	0.46
1:I:90:ASN:ND2	1:I:94:VAL:HB	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:52:ASP:O	1:M:59:SER:HB2	2.15	0.46
1:Q:21:LEU:HD12	1:Q:21:LEU:N	2.29	0.46
1:S:153:PRO:HG3	1:T:50:TYR:CZ	2.50	0.46
1:C:23:GLN:HE21	1:C:23:GLN:HB2	1.45	0.46
1:H:34:ARG:NH1	1:H:36:THR:CG2	2.76	0.46
1:J:87:ILE:HD12	1:J:87:ILE:HA	1.64	0.46
1:S:51:GLY:CA	1:S:115:ARG:O	2.63	0.46
1:U:131:HIS:CD2	1:U:132:GLU:H	2.31	0.46
1:W:112:VAL:CA	1:W:115:ARG:HG3	2.45	0.46
1:C:105:PRO:HD2	1:C:110:ASN:O	2.16	0.46
1:E:50:TYR:CE2	1:F:153:PRO:HG3	2.49	0.46
1:H:34:ARG:NH1	1:H:36:THR:HG23	2.29	0.46
1:T:112:VAL:CA	1:T:115:ARG:HG3	2.46	0.46
1:I:153:PRO:HG3	1:J:50:TYR:CE2	2.51	0.46
1:X:112:VAL:CA	1:X:115:ARG:HG3	2.45	0.46
1:B:21:LEU:N	1:B:21:LEU:HD12	2.30	0.46
1:C:26:ASP:CG	1:C:26:ASP:O	2.58	0.46
1:H:87:ILE:HA	1:H:87:ILE:HD12	1.65	0.46
1:M:50:TYR:CE2	1:N:153:PRO:HG3	2.51	0.46
1:A:152:THR:HG23	1:B:52:ASP:HB2	1.97	0.46
1:P:34:ARG:HG3	1:P:96:GLU:CG	2.44	0.46
1:H:68:LYS:NZ	1:I:2:THR:OG1	2.49	0.46
1:M:87:ILE:HA	1:M:87:ILE:HD12	1.67	0.46
1:W:112:VAL:HA	1:W:115:ARG:HG2	1.98	0.46
1:B:23:GLN:NE2	1:B:27:GLY:O	2.49	0.45
1:H:55:ASN:CB	1:I:96:GLU:OE1	2.55	0.45
1:W:23:GLN:HE21	1:W:23:GLN:HB2	1.50	0.45
1:D:51:GLY:CA	1:D:115:ARG:O	2.64	0.45
1:G:23:GLN:HE21	1:G:23:GLN:HB2	1.60	0.45
1:L:25:ASP:C	1:L:27:GLY:H	2.24	0.45
1:M:34:ARG:HG3	1:M:96:GLU:CG	2.46	0.45
1:U:6:VAL:HG22	1:U:7:ALA:N	2.30	0.45
1:W:87:ILE:HD12	1:W:87:ILE:HA	1.65	0.45
1:X:87:ILE:HD12	1:X:87:ILE:HA	1.73	0.45
1:A:87:ILE:HD12	1:A:87:ILE:HA	1.63	0.45
1:G:153:PRO:HG3	1:H:50:TYR:CZ	2.51	0.45
1:R:112:VAL:CA	1:R:115:ARG:HG3	2.45	0.45
1:E:23:GLN:HE21	1:E:23:GLN:HB2	1.59	0.45
1:I:97:VAL:HG22	1:I:98:THR:N	2.31	0.45
1:R:103:GLN:C	1:R:105:PRO:HD3	2.42	0.45
1:D:87:ILE:HD12	1:D:87:ILE:HA	1.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:87:ILE:HD12	1:T:87:ILE:HA	1.69	0.45
1:C:153:PRO:HG3	1:D:50:TYR:CZ	2.52	0.45
1:W:124:ASP:O	1:W:126:LEU:HD13	2.15	0.45
1:O:104:ILE:HG13	1:O:104:ILE:O	2.17	0.45
1:W:152:THR:HG22	1:X:52:ASP:OD2	2.10	0.45
1:T:131:HIS:CD2	1:T:132:GLU:H	2.34	0.45
1:W:112:VAL:CA	1:W:115:ARG:CG	2.95	0.45
1:N:87:ILE:HA	1:N:87:ILE:HD12	1.70	0.45
1:O:87:ILE:HA	1:O:87:ILE:HD12	1.69	0.45
1:W:50:TYR:CZ	1:X:153:PRO:HG3	2.52	0.45
1:W:151:LEU:O	1:X:50:TYR:HB3	2.17	0.45
1:J:104:ILE:O	1:J:104:ILE:HG13	2.17	0.44
1:M:6:VAL:HG22	1:M:7:ALA:N	2.33	0.44
1:N:25:ASP:C	1:N:27:GLY:H	2.25	0.44
1:A:1:ALA:N	1:A:25:ASP:OD1	2.42	0.44
1:C:131:HIS:HE1	1:F:37:GLY:O	2.00	0.44
1:C:133:LEU:HD11	1:F:93:GLY:HA3	2.00	0.44
1:E:34:ARG:NH2	1:Q:121:GLU:CD	2.75	0.44
1:P:121:GLU:OE1	1:P:144:LEU:CD1	2.63	0.44
1:A:23:GLN:HE21	1:A:23:GLN:HB2	1.60	0.44
1:H:25:ASP:C	1:H:27:GLY:H	2.25	0.44
1:L:21:LEU:HD12	1:L:21:LEU:N	2.33	0.44
1:G:112:VAL:HA	1:G:115:ARG:CG	2.45	0.44
1:L:87:ILE:HD12	1:L:87:ILE:HA	1.66	0.44
1:M:70:THR:HG23	1:P:78:ILE:HD12	1.99	0.44
1:Q:51:GLY:CA	1:Q:115:ARG:O	2.66	0.44
1:R:21:LEU:N	1:R:21:LEU:HD12	2.32	0.44
1:U:19:VAL:HG11	1:U:117:LEU:HD13	2.00	0.44
1:B:104:ILE:O	1:B:104:ILE:HG13	2.16	0.44
1:E:19:VAL:HG11	1:E:117:LEU:HD13	2.00	0.44
1:J:26:ASP:CG	1:J:26:ASP:O	2.60	0.44
1:M:103:GLN:C	1:M:105:PRO:HD3	2.42	0.44
1:U:25:ASP:C	1:U:27:GLY:H	2.25	0.44
1:U:104:ILE:HG13	1:U:104:ILE:O	2.17	0.44
1:V:6:VAL:HG22	1:V:7:ALA:N	2.33	0.44
1:X:23:GLN:HE21	1:X:23:GLN:HB2	1.65	0.44
1:E:104:ILE:O	1:E:104:ILE:HG13	2.17	0.44
1:F:103:GLN:C	1:F:105:PRO:HD3	2.43	0.44
1:G:80:HIS:HB2	1:G:83:ASP:OD1	2.18	0.44
1:H:118:VAL:HG22	1:H:146:CYS:HB3	1.99	0.44
1:G:55:ASN:O	1:G:55:ASN:CG	2.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:97:VAL:HG22	1:M:98:THR:N	2.32	0.44
1:I:87:ILE:HD12	1:I:87:ILE:HA	1.75	0.43
1:M:125:ASP:OD1	1:M:125:ASP:C	2.60	0.43
1:Q:152:THR:CG2	1:R:52:ASP:HB2	2.44	0.43
1:G:21:LEU:N	1:G:21:LEU:HD12	2.33	0.43
1:K:87:ILE:HD12	1:K:87:ILE:HA	1.59	0.43
1:O:103:GLN:C	1:O:105:PRO:HD3	2.43	0.43
1:P:26:ASP:CG	1:P:26:ASP:O	2.61	0.43
1:U:23:GLN:HE21	1:U:23:GLN:HB2	1.65	0.43
1:K:90:ASN:ND2	1:R:55:ASN:ND2	2.66	0.43
1:Q:87:ILE:HA	1:Q:87:ILE:HD12	1.63	0.43
1:D:112:VAL:HA	1:D:115:ARG:HG3	1.99	0.43
1:I:6:VAL:HG22	1:I:7:ALA:N	2.33	0.43
1:A:25:ASP:C	1:A:27:GLY:H	2.27	0.43
1:B:25:ASP:C	1:B:27:GLY:H	2.27	0.43
1:H:55:ASN:HB2	1:I:34:ARG:HH12	1.82	0.43
1:J:34:ARG:HD3	1:J:96:GLU:CD	2.43	0.43
1:L:103:GLN:C	1:L:105:PRO:HD3	2.44	0.43
1:O:23:GLN:HE21	1:O:23:GLN:HB2	1.61	0.43
1:S:112:VAL:CA	1:S:115:ARG:HG2	2.48	0.43
1:W:152:THR:CG2	1:X:52:ASP:CB	2.95	0.43
1:F:87:ILE:HG23	1:F:95:ALA:HB1	1.99	0.43
1:O:52:ASP:OD2	1:P:152:THR:HG21	2.19	0.43
1:P:103:GLN:C	1:P:105:PRO:HD3	2.43	0.43
1:T:12:ASN:O	1:T:13:SER:HB3	2.18	0.43
1:W:40:PRO:HB3	1:W:90:ASN:O	2.19	0.43
1:C:51:GLY:CA	1:C:115:ARG:O	2.66	0.43
1:Q:135:LEU:O	1:Q:136:THR:HG22	2.17	0.43
1:V:21:LEU:HD12	1:V:21:LEU:N	2.34	0.43
1:K:152:THR:CG2	1:L:52:ASP:OD2	2.66	0.43
1:N:6:VAL:HG22	1:N:7:ALA:N	2.33	0.43
1:Q:34:ARG:HG3	1:Q:96:GLU:CG	2.46	0.43
1:T:6:VAL:HG22	1:T:7:ALA:N	2.33	0.43
1:I:152:THR:CG2	1:J:52:ASP:HB2	2.48	0.43
1:L:52:ASP:O	1:L:59:SER:HB2	2.19	0.43
1:P:87:ILE:HD12	1:P:87:ILE:HA	1.65	0.43
1:S:87:ILE:HG23	1:S:95:ALA:HB1	2.01	0.43
1:U:52:ASP:O	1:U:59:SER:HB2	2.18	0.43
1:V:52:ASP:O	1:V:59:SER:HB2	2.18	0.43
1:G:96:GLU:C	1:G:97:VAL:CG1	2.91	0.43
1:W:103:GLN:C	1:W:105:PRO:HD3	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:34:ARG:HG3	1:I:96:GLU:CG	2.47	0.42
1:N:23:GLN:HE21	1:N:23:GLN:HB2	1.60	0.42
1:N:103:GLN:C	1:N:105:PRO:HD3	2.44	0.42
1:S:152:THR:HG23	1:T:52:ASP:HB2	2.00	0.42
1:S:21:LEU:N	1:S:21:LEU:HD12	2.34	0.42
1:T:51:GLY:CA	1:T:115:ARG:O	2.67	0.42
1:C:21:LEU:HD12	1:C:21:LEU:N	2.34	0.42
1:F:125:ASP:C	1:F:125:ASP:OD1	2.62	0.42
1:O:25:ASP:C	1:O:27:GLY:H	2.27	0.42
1:P:25:ASP:C	1:P:27:GLY:H	2.28	0.42
1:Q:103:GLN:C	1:Q:105:PRO:HD3	2.44	0.42
1:X:103:GLN:C	1:X:105:PRO:HD3	2.44	0.42
1:E:87:ILE:HD12	1:E:87:ILE:HA	1.69	0.42
1:H:23:GLN:NE2	1:H:27:GLY:O	2.51	0.42
1:E:103:GLN:C	1:E:105:PRO:HD3	2.44	0.42
1:O:6:VAL:HG22	1:O:7:ALA:N	2.35	0.42
1:T:25:ASP:C	1:T:27:GLY:N	2.77	0.42
1:I:87:ILE:HG23	1:I:95:ALA:HB1	2.01	0.42
1:I:131:HIS:HD2	1:I:133:LEU:H	1.66	0.42
1:L:23:GLN:HE21	1:L:23:GLN:HB2	1.69	0.42
1:O:87:ILE:HG23	1:O:95:ALA:HB1	2.01	0.42
1:I:89:ALA:O	1:I:90:ASN:O	2.37	0.42
1:L:104:ILE:O	1:L:104:ILE:HG13	2.20	0.42
1:U:112:VAL:HA	1:U:115:ARG:CG	2.49	0.42
1:C:103:GLN:C	1:C:105:PRO:HD3	2.44	0.42
1:I:133:LEU:CD1	1:V:93:GLY:HA3	2.46	0.42
1:K:25:ASP:C	1:K:27:GLY:H	2.28	0.42
1:P:124:ASP:O	1:P:126:LEU:HD13	2.20	0.42
1:T:21:LEU:HD12	1:T:21:LEU:N	2.35	0.42
1:W:6:VAL:HG22	1:W:7:ALA:N	2.34	0.42
1:G:49:GLU:O	1:G:115:ARG:HD3	2.19	0.42
1:G:97:VAL:HG23	1:G:98:THR:N	2.35	0.42
1:J:52:ASP:O	1:J:59:SER:HB2	2.20	0.42
1:X:104:ILE:HG13	1:X:104:ILE:O	2.20	0.42
1:X:117:LEU:O	1:X:146:CYS:HA	2.20	0.42
1:C:112:VAL:CA	1:C:115:ARG:HG3	2.49	0.41
1:O:80:HIS:HB2	1:O:83:ASP:OD1	2.21	0.41
1:R:87:ILE:HD12	1:R:87:ILE:HA	1.69	0.41
1:B:52:ASP:O	1:B:59:SER:HB2	2.21	0.41
1:K:153:PRO:HB2	1:Q:1:ALA:N	2.36	0.41
1:W:52:ASP:HB2	1:X:152:THR:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:ASP:O	1:D:59:SER:HB2	2.19	0.41
1:H:23:GLN:HE21	1:H:23:GLN:HB2	1.67	0.41
1:N:115:ARG:O	1:N:116:ALA:HB2	2.19	0.41
1:P:52:ASP:O	1:P:59:SER:HB2	2.20	0.41
1:R:19:VAL:HG11	1:R:117:LEU:HD13	2.01	0.41
1:W:112:VAL:O	1:W:115:ARG:HG2	2.20	0.41
1:D:94:VAL:CG1	1:O:55:ASN:ND2	2.46	0.41
1:E:14:ASN:HB2	1:Q:131:HIS:ND1	2.35	0.41
1:G:93:GLY:CA	1:L:133:LEU:HD11	2.49	0.41
1:I:104:ILE:HG13	1:I:104:ILE:O	2.21	0.41
1:M:23:GLN:HE21	1:M:23:GLN:HB2	1.49	0.41
1:Q:25:ASP:C	1:Q:27:GLY:H	2.28	0.41
1:U:112:VAL:CA	1:U:115:ARG:HG3	2.51	0.41
1:W:152:THR:HG23	1:X:52:ASP:CG	2.44	0.41
1:A:125:ASP:C	1:A:125:ASP:OD1	2.64	0.41
1:C:153:PRO:HG3	1:D:50:TYR:CE2	2.55	0.41
1:G:103:GLN:C	1:G:105:PRO:HD3	2.45	0.41
1:J:21:LEU:HD12	1:J:21:LEU:N	2.36	0.41
1:K:34:ARG:HG3	1:K:96:GLU:CG	2.50	0.41
1:U:34:ARG:HG3	1:U:96:GLU:CG	2.50	0.41
1:A:52:ASP:HB2	1:B:152:THR:CG2	2.50	0.41
1:D:23:GLN:HE21	1:D:23:GLN:HB2	1.52	0.41
1:M:144:LEU:HD23	1:M:144:LEU:HA	1.84	0.41
1:S:104:ILE:O	1:S:104:ILE:HG13	2.21	0.41
1:W:51:GLY:CA	1:W:115:ARG:O	2.69	0.41
1:A:26:ASP:O	1:A:26:ASP:CG	2.63	0.41
1:I:23:GLN:HE21	1:I:23:GLN:HB2	1.54	0.41
1:J:25:ASP:C	1:J:27:GLY:H	2.29	0.41
1:P:118:VAL:HG22	1:P:146:CYS:HB3	2.02	0.41
1:Q:87:ILE:HG23	1:Q:95:ALA:HB1	2.02	0.41
1:K:118:VAL:HG22	1:K:146:CYS:HB3	2.03	0.41
1:L:87:ILE:HG23	1:L:95:ALA:HB1	2.02	0.41
1:M:113:VAL:HG12	1:N:114:GLY:HA3	2.02	0.41
1:N:19:VAL:HG11	1:N:117:LEU:HD13	2.02	0.41
1:C:2:THR:OG1	1:C:24:ASP:OD1	2.37	0.41
1:C:133:LEU:HG	1:F:40:PRO:HD3	2.03	0.41
1:C:139:ASN:HD21	1:F:37:GLY:HA2	1.85	0.41
1:K:21:LEU:HD12	1:K:21:LEU:N	2.36	0.41
1:M:117:LEU:O	1:M:146:CYS:HA	2.20	0.41
1:N:49:GLU:O	1:N:115:ARG:HD3	2.21	0.41
1:S:112:VAL:CA	1:S:115:ARG:CG	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:VAL:HG22	1:A:146:CYS:HB3	2.03	0.41
1:S:19:VAL:HG11	1:S:117:LEU:HD13	2.03	0.41
1:C:133:LEU:HD11	1:F:38:LEU:O	2.21	0.40
1:D:125:ASP:C	1:D:125:ASP:OD1	2.65	0.40
1:E:6:VAL:HG22	1:E:7:ALA:N	2.36	0.40
1:J:19:VAL:HG11	1:J:117:LEU:HD13	2.03	0.40
1:T:118:VAL:HG22	1:T:146:CYS:HB3	2.04	0.40
1:R:6:VAL:HG22	1:R:7:ALA:N	2.36	0.40
1:C:87:ILE:HD12	1:C:87:ILE:HA	1.65	0.40
1:D:87:ILE:HG23	1:D:95:ALA:HB1	2.03	0.40
1:D:124:ASP:O	1:D:126:LEU:HD13	2.21	0.40
1:J:135:LEU:O	1:J:136:THR:HG22	2.18	0.40
1:L:135:LEU:C	1:L:136:THR:CG2	2.89	0.40
1:M:55:ASN:O	1:M:55:ASN:CG	2.64	0.40
1:S:50:TYR:CE2	1:T:153:PRO:HG3	2.56	0.40
1:X:112:VAL:HA	1:X:115:ARG:CG	2.49	0.40
1:B:34:ARG:HH12	1:E:55:ASN:HB2	1.85	0.40
1:B:118:VAL:HG22	1:B:146:CYS:HB3	2.04	0.40
1:C:25:ASP:C	1:C:27:GLY:H	2.29	0.40
1:O:26:ASP:O	1:O:26:ASP:CG	2.64	0.40
1:Q:117:LEU:O	1:Q:146:CYS:HA	2.22	0.40
1:U:152:THR:CG2	1:V:52:ASP:OD2	2.70	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	151/154 (98%)	143 (95%)	8 (5%)	0	100	100
1	B	151/154 (98%)	144 (95%)	6 (4%)	1 (1%)	18	49
1	C	151/154 (98%)	142 (94%)	8 (5%)	1 (1%)	18	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	151/154 (98%)	138 (91%)	10 (7%)	3 (2%)	6	25
1	E	151/154 (98%)	141 (93%)	9 (6%)	1 (1%)	18	49
1	F	151/154 (98%)	144 (95%)	5 (3%)	2 (1%)	9	35
1	G	151/154 (98%)	142 (94%)	8 (5%)	1 (1%)	18	49
1	H	151/154 (98%)	143 (95%)	8 (5%)	0	100	100
1	I	151/154 (98%)	144 (95%)	5 (3%)	2 (1%)	9	35
1	J	151/154 (98%)	140 (93%)	8 (5%)	3 (2%)	6	25
1	K	151/154 (98%)	141 (93%)	8 (5%)	2 (1%)	9	35
1	L	151/154 (98%)	140 (93%)	9 (6%)	2 (1%)	9	35
1	M	151/154 (98%)	139 (92%)	10 (7%)	2 (1%)	9	35
1	N	151/154 (98%)	141 (93%)	9 (6%)	1 (1%)	18	49
1	O	151/154 (98%)	142 (94%)	8 (5%)	1 (1%)	18	49
1	P	151/154 (98%)	142 (94%)	7 (5%)	2 (1%)	9	35
1	Q	151/154 (98%)	140 (93%)	7 (5%)	4 (3%)	4	21
1	R	151/154 (98%)	141 (93%)	9 (6%)	1 (1%)	18	49
1	S	151/154 (98%)	142 (94%)	7 (5%)	2 (1%)	9	35
1	T	151/154 (98%)	140 (93%)	9 (6%)	2 (1%)	9	35
1	U	151/154 (98%)	144 (95%)	5 (3%)	2 (1%)	9	35
1	V	151/154 (98%)	144 (95%)	5 (3%)	2 (1%)	9	35
1	W	151/154 (98%)	140 (93%)	5 (3%)	6 (4%)	2	13
1	X	151/154 (98%)	141 (93%)	7 (5%)	3 (2%)	6	25
All	All	3624/3696 (98%)	3398 (94%)	180 (5%)	46 (1%)	9	35

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	115	ARG
1	I	90	ASN
1	K	115	ARG
1	P	13	SER
1	S	90	ASN
1	S	115	ARG
1	T	13	SER
1	W	90	ASN
1	X	90	ASN

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Mol	Chain	Res	Type
1	B	13	SER
1	C	115	ARG
1	J	13	SER
1	J	136	THR
1	L	136	THR
1	M	136	THR
1	Q	136	THR
1	R	115	ARG
1	T	115	ARG
1	U	115	ARG
1	W	115	ARG
1	D	136	THR
1	D	137	THR
1	F	13	SER
1	G	115	ARG
1	J	137	THR
1	L	137	THR
1	M	137	THR
1	Q	13	SER
1	Q	115	ARG
1	Q	137	THR
1	W	13	SER
1	W	137	THR
1	X	116	ALA
1	I	13	SER
1	K	13	SER
1	N	115	ARG
1	P	25	ASP
1	U	13	SER
1	V	13	SER
1	X	115	ARG
1	E	25	ASP
1	F	25	ASP
1	W	25	ASP
1	W	136	THR
1	V	25	ASP
1	O	27	GLY

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	116/117 (99%)	109 (94%)	7 (6%)	17	47
1	B	116/117 (99%)	105 (90%)	11 (10%)	8	30
1	C	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	D	116/117 (99%)	106 (91%)	10 (9%)	10	34
1	E	116/117 (99%)	109 (94%)	7 (6%)	17	47
1	F	116/117 (99%)	109 (94%)	7 (6%)	17	47
1	G	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	H	116/117 (99%)	107 (92%)	9 (8%)	11	38
1	I	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	J	116/117 (99%)	107 (92%)	9 (8%)	11	38
1	K	116/117 (99%)	107 (92%)	9 (8%)	11	38
1	L	116/117 (99%)	106 (91%)	10 (9%)	10	34
1	M	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	N	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	O	116/117 (99%)	107 (92%)	9 (8%)	11	38
1	P	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	Q	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	R	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	S	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	T	116/117 (99%)	107 (92%)	9 (8%)	11	38
1	U	116/117 (99%)	109 (94%)	7 (6%)	17	47
1	V	116/117 (99%)	107 (92%)	9 (8%)	11	38
1	W	116/117 (99%)	108 (93%)	8 (7%)	14	41
1	X	116/117 (99%)	108 (93%)	8 (7%)	14	41
All	All	2784/2808 (99%)	2583 (93%)	201 (7%)	13	40

All (201) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS

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Mol	Chain	Res	Type
1	A	23	GLN
1	A	24	ASP
1	A	59	SER
1	A	87	ILE
1	A	107	THR
1	A	152	THR
1	B	2	THR
1	B	3	LYS
1	B	23	GLN
1	B	24	ASP
1	B	25	ASP
1	B	59	SER
1	B	77	GLU
1	B	78	ILE
1	B	87	ILE
1	B	107	THR
1	B	152	THR
1	C	3	LYS
1	C	23	GLN
1	C	24	ASP
1	C	59	SER
1	C	87	ILE
1	C	97	VAL
1	C	107	THR
1	C	152	THR
1	D	3	LYS
1	D	23	GLN
1	D	24	ASP
1	D	26	ASP
1	D	59	SER
1	D	87	ILE
1	D	97	VAL
1	D	101	ASP
1	D	107	THR
1	D	152	THR
1	E	3	LYS
1	E	23	GLN
1	E	24	ASP
1	E	59	SER
1	E	87	ILE
1	E	107	THR
1	E	152	THR

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Mol	Chain	Res	Type
1	F	3	LYS
1	F	23	GLN
1	F	24	ASP
1	F	59	SER
1	F	87	ILE
1	F	107	THR
1	F	152	THR
1	G	3	LYS
1	G	23	GLN
1	G	24	ASP
1	G	59	SER
1	G	87	ILE
1	G	97	VAL
1	G	107	THR
1	G	152	THR
1	H	2	THR
1	H	3	LYS
1	H	23	GLN
1	H	24	ASP
1	H	26	ASP
1	H	59	SER
1	H	87	ILE
1	H	107	THR
1	H	152	THR
1	I	3	LYS
1	I	23	GLN
1	I	24	ASP
1	I	26	ASP
1	I	59	SER
1	I	87	ILE
1	I	107	THR
1	I	152	THR
1	J	3	LYS
1	J	23	GLN
1	J	24	ASP
1	J	25	ASP
1	J	26	ASP
1	J	59	SER
1	J	87	ILE
1	J	107	THR
1	J	152	THR
1	K	2	THR

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Mol	Chain	Res	Type
1	K	3	LYS
1	K	23	GLN
1	K	24	ASP
1	K	26	ASP
1	K	59	SER
1	K	87	ILE
1	K	107	THR
1	K	152	THR
1	L	3	LYS
1	L	23	GLN
1	L	24	ASP
1	L	26	ASP
1	L	34	ARG
1	L	35	ILE
1	L	59	SER
1	L	87	ILE
1	L	107	THR
1	L	152	THR
1	M	2	THR
1	M	3	LYS
1	M	23	GLN
1	M	24	ASP
1	M	59	SER
1	M	87	ILE
1	M	107	THR
1	M	152	THR
1	N	3	LYS
1	N	23	GLN
1	N	24	ASP
1	N	26	ASP
1	N	59	SER
1	N	87	ILE
1	N	107	THR
1	N	152	THR
1	O	2	THR
1	O	3	LYS
1	O	23	GLN
1	O	24	ASP
1	O	59	SER
1	O	87	ILE
1	O	97	VAL
1	O	107	THR

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Mol	Chain	Res	Type
1	O	152	THR
1	P	3	LYS
1	P	23	GLN
1	P	24	ASP
1	P	26	ASP
1	P	59	SER
1	P	87	ILE
1	P	107	THR
1	P	152	THR
1	Q	2	THR
1	Q	3	LYS
1	Q	23	GLN
1	Q	24	ASP
1	Q	59	SER
1	Q	87	ILE
1	Q	107	THR
1	Q	152	THR
1	R	3	LYS
1	R	23	GLN
1	R	24	ASP
1	R	26	ASP
1	R	59	SER
1	R	87	ILE
1	R	107	THR
1	R	152	THR
1	S	3	LYS
1	S	23	GLN
1	S	24	ASP
1	S	26	ASP
1	S	59	SER
1	S	87	ILE
1	S	107	THR
1	S	152	THR
1	T	3	LYS
1	T	23	GLN
1	T	24	ASP
1	T	25	ASP
1	T	26	ASP
1	T	59	SER
1	T	87	ILE
1	T	107	THR
1	T	152	THR

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Mol	Chain	Res	Type
1	U	23	GLN
1	U	24	ASP
1	U	26	ASP
1	U	59	SER
1	U	87	ILE
1	U	107	THR
1	U	152	THR
1	V	3	LYS
1	V	23	GLN
1	V	24	ASP
1	V	26	ASP
1	V	59	SER
1	V	87	ILE
1	V	101	ASP
1	V	107	THR
1	V	152	THR
1	W	2	THR
1	W	3	LYS
1	W	23	GLN
1	W	24	ASP
1	W	59	SER
1	W	87	ILE
1	W	107	THR
1	W	152	THR
1	X	3	LYS
1	X	23	GLN
1	X	24	ASP
1	X	26	ASP
1	X	59	SER
1	X	87	ILE
1	X	107	THR
1	X	152	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	131	HIS
1	A	139	ASN
1	B	23	GLN
1	B	131	HIS
1	B	139	ASN

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Mol	Chain	Res	Type
1	C	23	GLN
1	C	131	HIS
1	C	139	ASN
1	D	23	GLN
1	D	131	HIS
1	D	139	ASN
1	E	14	ASN
1	E	23	GLN
1	E	131	HIS
1	E	139	ASN
1	F	23	GLN
1	F	131	HIS
1	F	139	ASN
1	G	23	GLN
1	G	131	HIS
1	G	139	ASN
1	H	23	GLN
1	H	131	HIS
1	H	139	ASN
1	I	23	GLN
1	I	131	HIS
1	I	139	ASN
1	J	23	GLN
1	J	131	HIS
1	J	139	ASN
1	K	23	GLN
1	K	131	HIS
1	K	139	ASN
1	L	23	GLN
1	L	131	HIS
1	L	139	ASN
1	M	23	GLN
1	M	131	HIS
1	M	139	ASN
1	N	23	GLN
1	N	131	HIS
1	N	139	ASN
1	O	23	GLN
1	O	131	HIS
1	O	139	ASN
1	P	23	GLN
1	P	131	HIS

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Mol	Chain	Res	Type
1	P	139	ASN
1	Q	131	HIS
1	Q	139	ASN
1	R	23	GLN
1	R	131	HIS
1	R	139	ASN
1	S	131	HIS
1	S	139	ASN
1	T	23	GLN
1	T	80	HIS
1	T	131	HIS
1	T	139	ASN
1	U	23	GLN
1	U	131	HIS
1	U	139	ASN
1	V	23	GLN
1	V	131	HIS
1	V	139	ASN
1	W	23	GLN
1	W	131	HIS
1	W	139	ASN
1	X	23	GLN
1	X	131	HIS
1	X	139	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 24 ligands modelled in this entry, 24 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	153/154 (99%)	-0.03	3 (1%) 65 44	36, 55, 86, 139	0
1	B	153/154 (99%)	-0.09	1 (0%) 84 68	36, 54, 85, 140	0
1	C	153/154 (99%)	-0.04	2 (1%) 75 56	36, 54, 85, 142	0
1	D	153/154 (99%)	-0.07	3 (1%) 65 44	38, 55, 86, 144	0
1	E	153/154 (99%)	0.05	6 (3%) 43 24	36, 54, 85, 149	0
1	F	153/154 (99%)	-0.10	0 100 100	37, 54, 87, 146	0
1	G	153/154 (99%)	-0.20	2 (1%) 75 56	35, 55, 87, 146	0
1	H	153/154 (99%)	-0.09	3 (1%) 65 44	36, 55, 86, 144	0
1	I	153/154 (99%)	-0.02	6 (3%) 43 24	36, 54, 85, 144	0
1	J	153/154 (99%)	-0.04	3 (1%) 65 44	37, 55, 85, 144	0
1	K	153/154 (99%)	-0.11	2 (1%) 75 56	37, 55, 87, 146	0
1	L	153/154 (99%)	-0.02	2 (1%) 75 56	36, 55, 86, 147	0
1	M	153/154 (99%)	-0.00	4 (2%) 57 36	37, 55, 99, 154	0
1	N	153/154 (99%)	0.06	4 (2%) 57 36	37, 57, 91, 145	0
1	O	153/154 (99%)	0.14	3 (1%) 65 44	38, 59, 99, 144	0
1	P	153/154 (99%)	-0.04	3 (1%) 65 44	37, 54, 86, 145	0
1	Q	153/154 (99%)	0.06	3 (1%) 65 44	36, 55, 87, 146	0
1	R	153/154 (99%)	0.51	9 (5%) 28 15	39, 63, 116, 146	0
1	S	153/154 (99%)	0.13	0 100 100	37, 57, 91, 158	0
1	T	153/154 (99%)	-0.01	2 (1%) 75 56	38, 55, 88, 143	0
1	U	153/154 (99%)	-0.01	3 (1%) 65 44	38, 55, 88, 151	0
1	V	153/154 (99%)	-0.11	2 (1%) 75 56	38, 55, 88, 142	0
1	W	153/154 (99%)	0.04	2 (1%) 75 56	36, 55, 87, 146	0
1	X	153/154 (99%)	0.10	3 (1%) 65 44	36, 56, 88, 147	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3672/3696 (99%)	0.00	71 (1%) 66 45	35, 56, 97, 158	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	55	ASN	4.5
1	N	55	ASN	4.5
1	D	12	ASN	4.0
1	P	1	ALA	4.0
1	T	1	ALA	3.9
1	C	26	ASP	3.7
1	E	55	ASN	3.7
1	H	12	ASN	3.6
1	W	1	ALA	3.5
1	Q	1	ALA	3.4
1	K	1	ALA	3.3
1	D	1	ALA	3.2
1	T	55	ASN	3.1
1	I	25	ASP	3.1
1	O	1	ALA	3.1
1	R	78	ILE	3.1
1	Q	131	HIS	3.0
1	N	12	ASN	2.9
1	E	25	ASP	2.8
1	M	1	ALA	2.8
1	D	136	THR	2.8
1	C	132	GLU	2.8
1	R	135	LEU	2.8
1	R	1	ALA	2.8
1	I	1	ALA	2.8
1	M	130	GLY	2.8
1	I	14	ASN	2.7
1	I	26	ASP	2.7
1	E	96	GLU	2.7
1	J	1	ALA	2.7
1	O	51	GLY	2.6
1	P	121	GLU	2.6
1	L	1	ALA	2.6
1	N	1	ALA	2.6
1	P	132	GLU	2.6
1	B	1	ALA	2.5
1	I	12	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	R	75	GLY	2.4
1	E	1	ALA	2.4
1	X	1	ALA	2.4
1	O	58	MET	2.4
1	H	130	GLY	2.4
1	A	96	GLU	2.4
1	E	132	GLU	2.4
1	R	68	LYS	2.3
1	V	1	ALA	2.3
1	Q	136	THR	2.3
1	R	85	GLY	2.3
1	W	2	THR	2.3
1	X	55	ASN	2.3
1	G	1	ALA	2.3
1	R	58	MET	2.3
1	U	77	GLU	2.2
1	U	55	ASN	2.2
1	U	12	ASN	2.2
1	E	26	ASP	2.2
1	J	26	ASP	2.2
1	R	127	GLY	2.1
1	G	14	ASN	2.1
1	H	1	ALA	2.1
1	J	12	ASN	2.1
1	A	34	ARG	2.1
1	I	24	ASP	2.1
1	X	128	LYS	2.0
1	N	92	ASP	2.0
1	V	132	GLU	2.0
1	A	131	HIS	2.0
1	M	131	HIS	2.0
1	L	136	THR	2.0
1	M	136	THR	2.0
1	K	26	ASP	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	O	155	1/1	0.97	0.04	86,86,86,86	0
2	ZN	L	155	1/1	0.98	0.08	102,102,102,102	0
2	ZN	R	155	1/1	0.98	0.07	95,95,95,95	0
2	ZN	V	155	1/1	0.98	0.14	132,132,132,132	0
2	ZN	F	155	1/1	0.99	0.13	34,34,34,34	0
2	ZN	G	155	1/1	0.99	0.03	66,66,66,66	0
2	ZN	H	155	1/1	0.99	0.11	33,33,33,33	0
2	ZN	I	155	1/1	0.99	0.02	58,58,58,58	0
2	ZN	J	155	1/1	0.99	0.03	79,79,79,79	0
2	ZN	K	155	1/1	0.99	0.04	61,61,61,61	0
2	ZN	B	155	1/1	0.99	0.13	31,31,31,31	0
2	ZN	M	155	1/1	0.99	0.06	86,86,86,86	0
2	ZN	N	155	1/1	0.99	0.04	75,75,75,75	0
2	ZN	C	155	1/1	0.99	0.14	36,36,36,36	0
2	ZN	P	155	1/1	0.99	0.03	83,83,83,83	0
2	ZN	Q	155	1/1	0.99	0.06	95,95,95,95	0
2	ZN	D	155	1/1	0.99	0.07	88,88,88,88	0
2	ZN	S	155	1/1	0.99	0.05	102,102,102,102	0
2	ZN	T	155	1/1	0.99	0.03	82,82,82,82	0
2	ZN	U	155	1/1	0.99	0.05	82,82,82,82	0
2	ZN	E	155	1/1	0.99	0.09	30,30,30,30	0
2	ZN	W	155	1/1	0.99	0.03	67,67,67,67	0
2	ZN	A	155	1/1	1.00	0.14	32,32,32,32	0
2	ZN	X	155	1/1	1.00	0.02	69,69,69,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.