



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:57 PM UTC

PDB ID : 4QFF / pdb_00004qff
Title : Structure of a 16 nm protein cage designed by fusing symmetric oligomeric domains, quadruple mutant, P212121 form
Authors : Lai, Y.-T.; Yeates, T.O.
Deposited on : 2014-05-20
Resolution : 7.81 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:

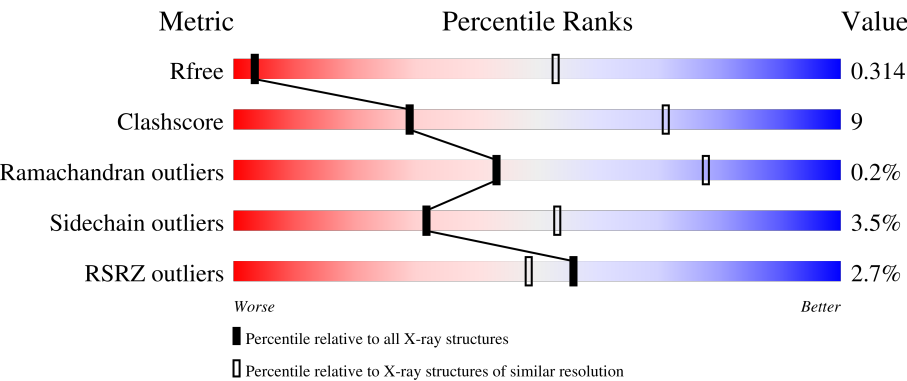
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 7.81 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	1168 (11.50-4.00)
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
Sidechain outliers	187428	1018 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)

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	456	
1	B	456	
1	C	456	
1	D	456	
1	E	456	

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Mol	Chain	Length	Quality of chain
1	F	456	4% 78% 17%
1	G	456	% 78% 17%
1	H	456	3% 77% 19%
1	I	456	% 77% 18%
1	J	456	2% 79% 16%
1	K	456	% 74% 21%
1	L	456	4% 79% 17%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 40512 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	B	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	C	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	D	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	E	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	F	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	G	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	H	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	I	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	J	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	K	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			
1	L	441	Total	C	N	O	S	0	0	0
			3376	2151	569	648	8			

There are 228 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	THR	GLN	engineered mutation	UNP P29715
A	51	ALA	TYR	engineered mutation	UNP P29715
A	118	ALA	LYS	engineered mutation	UNP P29715
A	278	ALA	-	linker	UNP P03485
A	279	GLN	-	linker	UNP P03485

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Chain	Residue	Modelled	Actual	Comment	Reference
A	280	GLU	-	linker	UNP P03485
A	281	ALA	-	linker	UNP P03485
A	282	GLN	-	linker	UNP P03485
A	283	LYS	-	linker	UNP P03485
A	284	GLN	-	linker	UNP P03485
A	285	LYS	-	linker	UNP P03485
A	448	LEU	-	expression tag	UNP P03485
A	449	GLU	-	expression tag	UNP P03485
A	450	HIS	-	expression tag	UNP P03485
A	451	HIS	-	expression tag	UNP P03485
A	452	HIS	-	expression tag	UNP P03485
A	453	HIS	-	expression tag	UNP P03485
A	454	HIS	-	expression tag	UNP P03485
A	455	HIS	-	expression tag	UNP P03485
B	24	THR	GLN	engineered mutation	UNP P29715
B	51	ALA	TYR	engineered mutation	UNP P29715
B	118	ALA	LYS	engineered mutation	UNP P29715
B	278	ALA	-	linker	UNP P03485
B	279	GLN	-	linker	UNP P03485
B	280	GLU	-	linker	UNP P03485
B	281	ALA	-	linker	UNP P03485
B	282	GLN	-	linker	UNP P03485
B	283	LYS	-	linker	UNP P03485
B	284	GLN	-	linker	UNP P03485
B	285	LYS	-	linker	UNP P03485
B	448	LEU	-	expression tag	UNP P03485
B	449	GLU	-	expression tag	UNP P03485
B	450	HIS	-	expression tag	UNP P03485
B	451	HIS	-	expression tag	UNP P03485
B	452	HIS	-	expression tag	UNP P03485
B	453	HIS	-	expression tag	UNP P03485
B	454	HIS	-	expression tag	UNP P03485
B	455	HIS	-	expression tag	UNP P03485
C	24	THR	GLN	engineered mutation	UNP P29715
C	51	ALA	TYR	engineered mutation	UNP P29715
C	118	ALA	LYS	engineered mutation	UNP P29715
C	278	ALA	-	linker	UNP P03485
C	279	GLN	-	linker	UNP P03485
C	280	GLU	-	linker	UNP P03485
C	281	ALA	-	linker	UNP P03485
C	282	GLN	-	linker	UNP P03485
C	283	LYS	-	linker	UNP P03485

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Chain	Residue	Modelled	Actual	Comment	Reference
C	284	GLN	-	linker	UNP P03485
C	285	LYS	-	linker	UNP P03485
C	448	LEU	-	expression tag	UNP P03485
C	449	GLU	-	expression tag	UNP P03485
C	450	HIS	-	expression tag	UNP P03485
C	451	HIS	-	expression tag	UNP P03485
C	452	HIS	-	expression tag	UNP P03485
C	453	HIS	-	expression tag	UNP P03485
C	454	HIS	-	expression tag	UNP P03485
C	455	HIS	-	expression tag	UNP P03485
D	24	THR	GLN	engineered mutation	UNP P29715
D	51	ALA	TYR	engineered mutation	UNP P29715
D	118	ALA	LYS	engineered mutation	UNP P29715
D	278	ALA	-	linker	UNP P03485
D	279	GLN	-	linker	UNP P03485
D	280	GLU	-	linker	UNP P03485
D	281	ALA	-	linker	UNP P03485
D	282	GLN	-	linker	UNP P03485
D	283	LYS	-	linker	UNP P03485
D	284	GLN	-	linker	UNP P03485
D	285	LYS	-	linker	UNP P03485
D	448	LEU	-	expression tag	UNP P03485
D	449	GLU	-	expression tag	UNP P03485
D	450	HIS	-	expression tag	UNP P03485
D	451	HIS	-	expression tag	UNP P03485
D	452	HIS	-	expression tag	UNP P03485
D	453	HIS	-	expression tag	UNP P03485
D	454	HIS	-	expression tag	UNP P03485
D	455	HIS	-	expression tag	UNP P03485
E	24	THR	GLN	engineered mutation	UNP P29715
E	51	ALA	TYR	engineered mutation	UNP P29715
E	118	ALA	LYS	engineered mutation	UNP P29715
E	278	ALA	-	linker	UNP P03485
E	279	GLN	-	linker	UNP P03485
E	280	GLU	-	linker	UNP P03485
E	281	ALA	-	linker	UNP P03485
E	282	GLN	-	linker	UNP P03485
E	283	LYS	-	linker	UNP P03485
E	284	GLN	-	linker	UNP P03485
E	285	LYS	-	linker	UNP P03485
E	448	LEU	-	expression tag	UNP P03485
E	449	GLU	-	expression tag	UNP P03485

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Chain	Residue	Modelled	Actual	Comment	Reference
E	450	HIS	-	expression tag	UNP P03485
E	451	HIS	-	expression tag	UNP P03485
E	452	HIS	-	expression tag	UNP P03485
E	453	HIS	-	expression tag	UNP P03485
E	454	HIS	-	expression tag	UNP P03485
E	455	HIS	-	expression tag	UNP P03485
F	24	THR	GLN	engineered mutation	UNP P29715
F	51	ALA	TYR	engineered mutation	UNP P29715
F	118	ALA	LYS	engineered mutation	UNP P29715
F	278	ALA	-	linker	UNP P03485
F	279	GLN	-	linker	UNP P03485
F	280	GLU	-	linker	UNP P03485
F	281	ALA	-	linker	UNP P03485
F	282	GLN	-	linker	UNP P03485
F	283	LYS	-	linker	UNP P03485
F	284	GLN	-	linker	UNP P03485
F	285	LYS	-	linker	UNP P03485
F	448	LEU	-	expression tag	UNP P03485
F	449	GLU	-	expression tag	UNP P03485
F	450	HIS	-	expression tag	UNP P03485
F	451	HIS	-	expression tag	UNP P03485
F	452	HIS	-	expression tag	UNP P03485
F	453	HIS	-	expression tag	UNP P03485
F	454	HIS	-	expression tag	UNP P03485
F	455	HIS	-	expression tag	UNP P03485
G	24	THR	GLN	engineered mutation	UNP P29715
G	51	ALA	TYR	engineered mutation	UNP P29715
G	118	ALA	LYS	engineered mutation	UNP P29715
G	278	ALA	-	linker	UNP P03485
G	279	GLN	-	linker	UNP P03485
G	280	GLU	-	linker	UNP P03485
G	281	ALA	-	linker	UNP P03485
G	282	GLN	-	linker	UNP P03485
G	283	LYS	-	linker	UNP P03485
G	284	GLN	-	linker	UNP P03485
G	285	LYS	-	linker	UNP P03485
G	448	LEU	-	expression tag	UNP P03485
G	449	GLU	-	expression tag	UNP P03485
G	450	HIS	-	expression tag	UNP P03485
G	451	HIS	-	expression tag	UNP P03485
G	452	HIS	-	expression tag	UNP P03485
G	453	HIS	-	expression tag	UNP P03485

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Chain	Residue	Modelled	Actual	Comment	Reference
G	454	HIS	-	expression tag	UNP P03485
G	455	HIS	-	expression tag	UNP P03485
H	24	THR	GLN	engineered mutation	UNP P29715
H	51	ALA	TYR	engineered mutation	UNP P29715
H	118	ALA	LYS	engineered mutation	UNP P29715
H	278	ALA	-	linker	UNP P03485
H	279	GLN	-	linker	UNP P03485
H	280	GLU	-	linker	UNP P03485
H	281	ALA	-	linker	UNP P03485
H	282	GLN	-	linker	UNP P03485
H	283	LYS	-	linker	UNP P03485
H	284	GLN	-	linker	UNP P03485
H	285	LYS	-	linker	UNP P03485
H	448	LEU	-	expression tag	UNP P03485
H	449	GLU	-	expression tag	UNP P03485
H	450	HIS	-	expression tag	UNP P03485
H	451	HIS	-	expression tag	UNP P03485
H	452	HIS	-	expression tag	UNP P03485
H	453	HIS	-	expression tag	UNP P03485
H	454	HIS	-	expression tag	UNP P03485
H	455	HIS	-	expression tag	UNP P03485
I	24	THR	GLN	engineered mutation	UNP P29715
I	51	ALA	TYR	engineered mutation	UNP P29715
I	118	ALA	LYS	engineered mutation	UNP P29715
I	278	ALA	-	linker	UNP P03485
I	279	GLN	-	linker	UNP P03485
I	280	GLU	-	linker	UNP P03485
I	281	ALA	-	linker	UNP P03485
I	282	GLN	-	linker	UNP P03485
I	283	LYS	-	linker	UNP P03485
I	284	GLN	-	linker	UNP P03485
I	285	LYS	-	linker	UNP P03485
I	448	LEU	-	expression tag	UNP P03485
I	449	GLU	-	expression tag	UNP P03485
I	450	HIS	-	expression tag	UNP P03485
I	451	HIS	-	expression tag	UNP P03485
I	452	HIS	-	expression tag	UNP P03485
I	453	HIS	-	expression tag	UNP P03485
I	454	HIS	-	expression tag	UNP P03485
I	455	HIS	-	expression tag	UNP P03485
J	24	THR	GLN	engineered mutation	UNP P29715
J	51	ALA	TYR	engineered mutation	UNP P29715

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Chain	Residue	Modelled	Actual	Comment	Reference
J	118	ALA	LYS	engineered mutation	UNP P29715
J	278	ALA	-	linker	UNP P03485
J	279	GLN	-	linker	UNP P03485
J	280	GLU	-	linker	UNP P03485
J	281	ALA	-	linker	UNP P03485
J	282	GLN	-	linker	UNP P03485
J	283	LYS	-	linker	UNP P03485
J	284	GLN	-	linker	UNP P03485
J	285	LYS	-	linker	UNP P03485
J	448	LEU	-	expression tag	UNP P03485
J	449	GLU	-	expression tag	UNP P03485
J	450	HIS	-	expression tag	UNP P03485
J	451	HIS	-	expression tag	UNP P03485
J	452	HIS	-	expression tag	UNP P03485
J	453	HIS	-	expression tag	UNP P03485
J	454	HIS	-	expression tag	UNP P03485
J	455	HIS	-	expression tag	UNP P03485
K	24	THR	GLN	engineered mutation	UNP P29715
K	51	ALA	TYR	engineered mutation	UNP P29715
K	118	ALA	LYS	engineered mutation	UNP P29715
K	278	ALA	-	linker	UNP P03485
K	279	GLN	-	linker	UNP P03485
K	280	GLU	-	linker	UNP P03485
K	281	ALA	-	linker	UNP P03485
K	282	GLN	-	linker	UNP P03485
K	283	LYS	-	linker	UNP P03485
K	284	GLN	-	linker	UNP P03485
K	285	LYS	-	linker	UNP P03485
K	448	LEU	-	expression tag	UNP P03485
K	449	GLU	-	expression tag	UNP P03485
K	450	HIS	-	expression tag	UNP P03485
K	451	HIS	-	expression tag	UNP P03485
K	452	HIS	-	expression tag	UNP P03485
K	453	HIS	-	expression tag	UNP P03485
K	454	HIS	-	expression tag	UNP P03485
K	455	HIS	-	expression tag	UNP P03485
L	24	THR	GLN	engineered mutation	UNP P29715
L	51	ALA	TYR	engineered mutation	UNP P29715
L	118	ALA	LYS	engineered mutation	UNP P29715
L	278	ALA	-	linker	UNP P03485
L	279	GLN	-	linker	UNP P03485
L	280	GLU	-	linker	UNP P03485

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Chain	Residue	Modelled	Actual	Comment	Reference
L	281	ALA	-	linker	UNP P03485
L	282	GLN	-	linker	UNP P03485
L	283	LYS	-	linker	UNP P03485
L	284	GLN	-	linker	UNP P03485
L	285	LYS	-	linker	UNP P03485
L	448	LEU	-	expression tag	UNP P03485
L	449	GLU	-	expression tag	UNP P03485
L	450	HIS	-	expression tag	UNP P03485
L	451	HIS	-	expression tag	UNP P03485
L	452	HIS	-	expression tag	UNP P03485
L	453	HIS	-	expression tag	UNP P03485
L	454	HIS	-	expression tag	UNP P03485
L	455	HIS	-	expression tag	UNP P03485

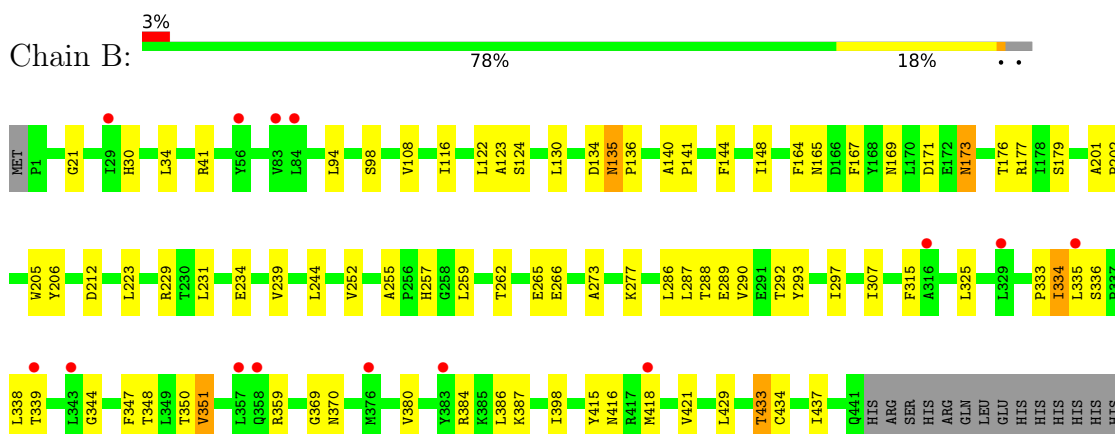
3 Residue-property plots

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.

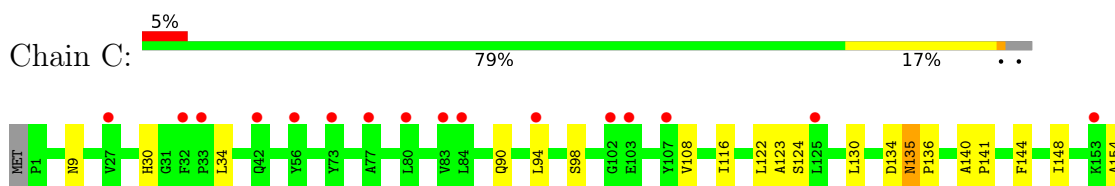
- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera

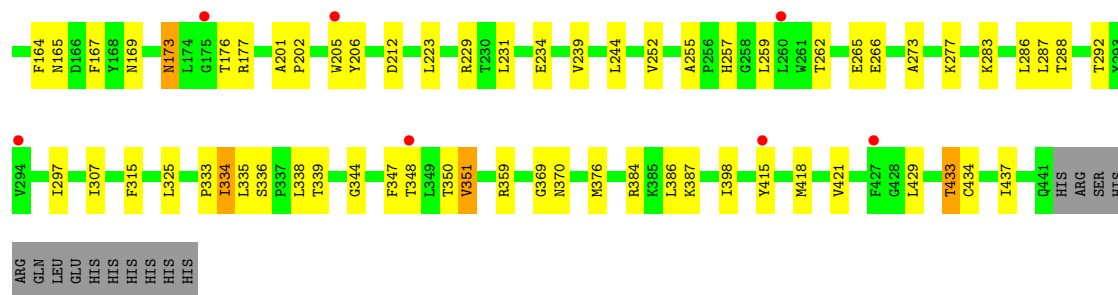


- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera

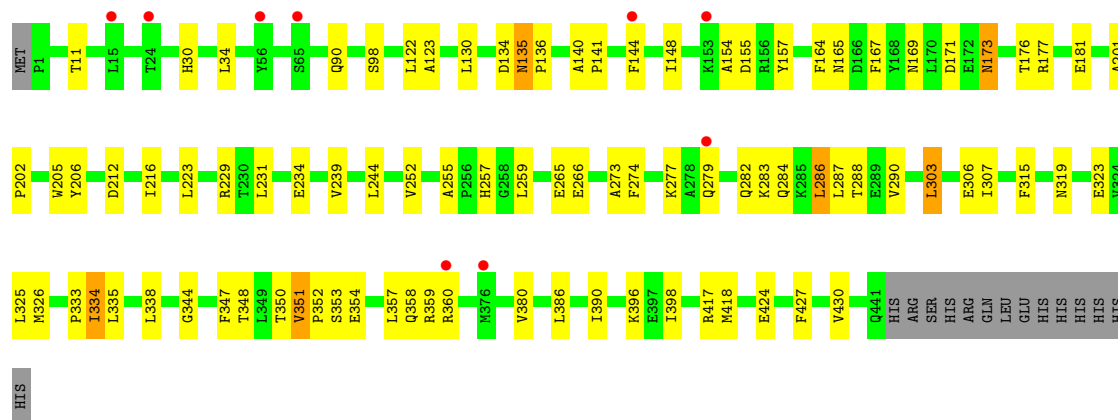
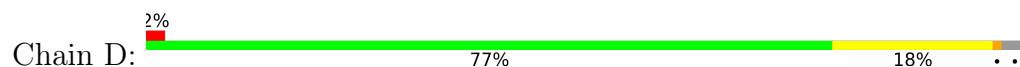


- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera

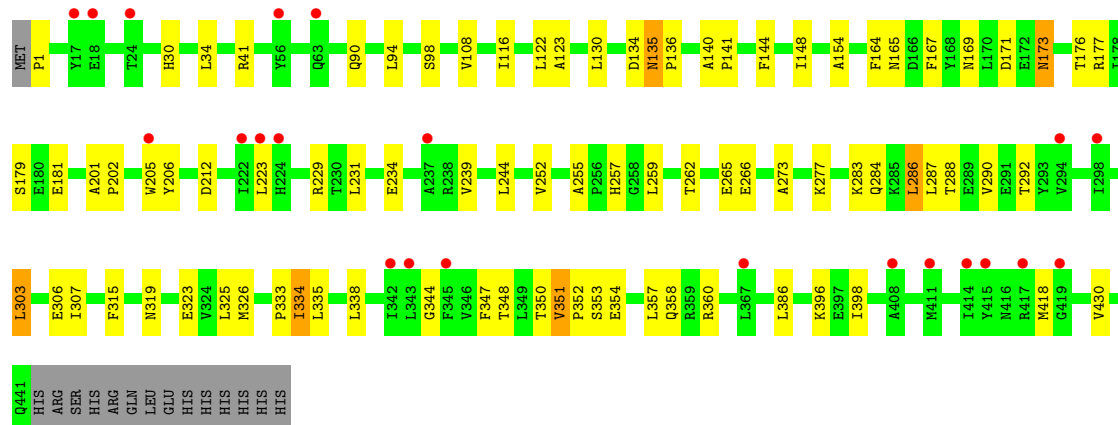
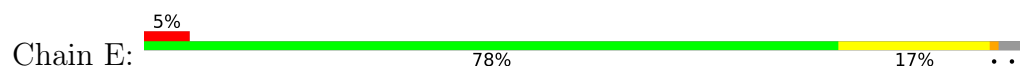




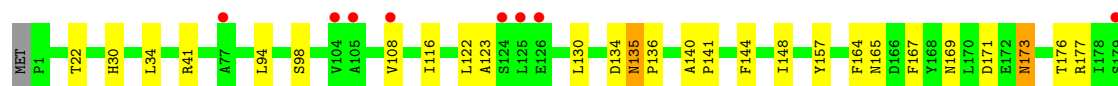
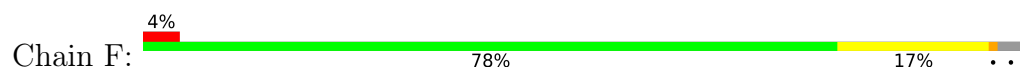
- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera



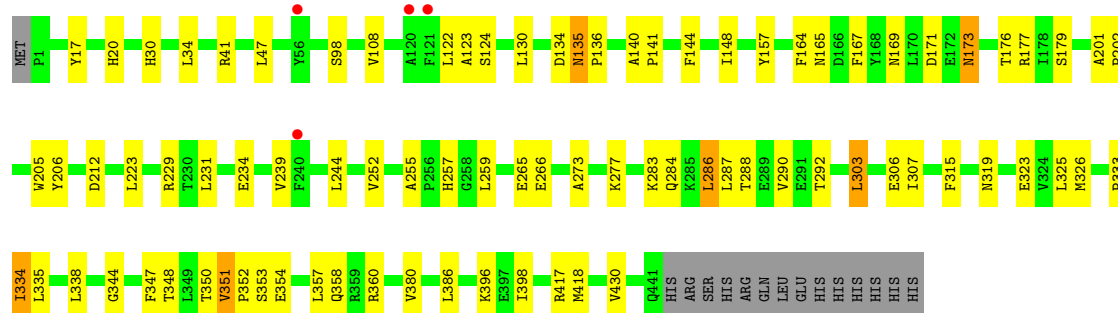
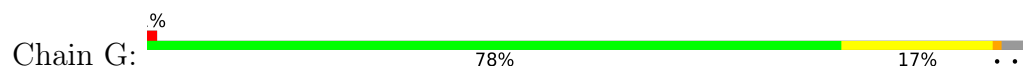
- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera



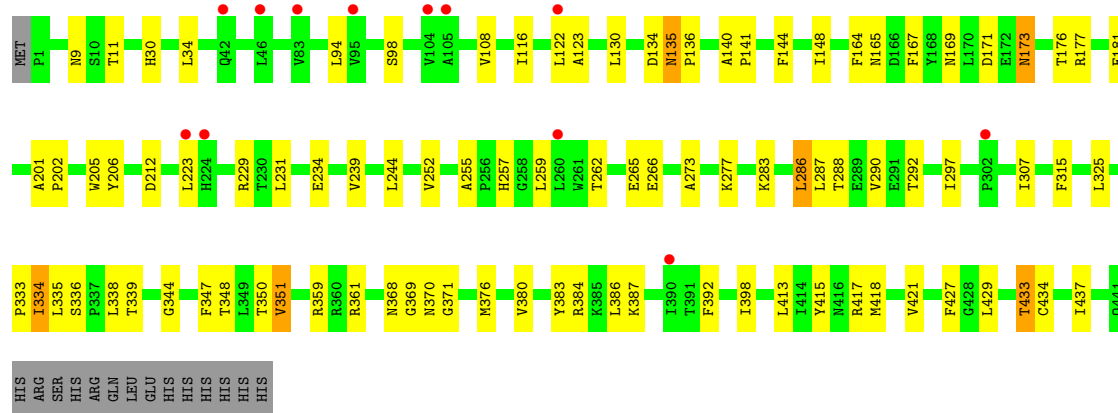
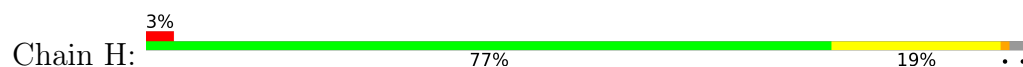
- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera



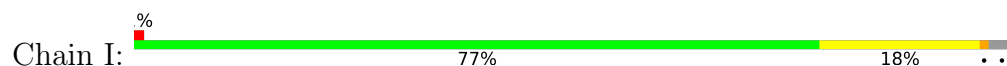
- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera

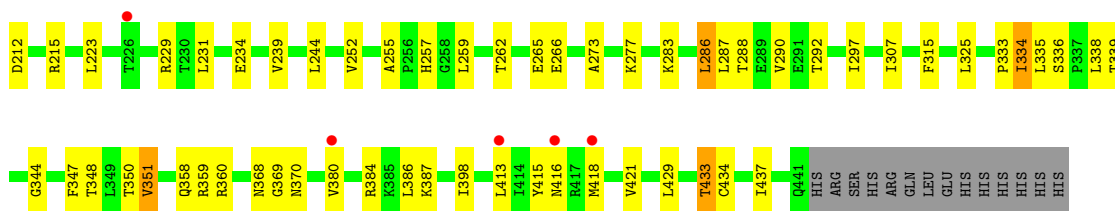


- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera

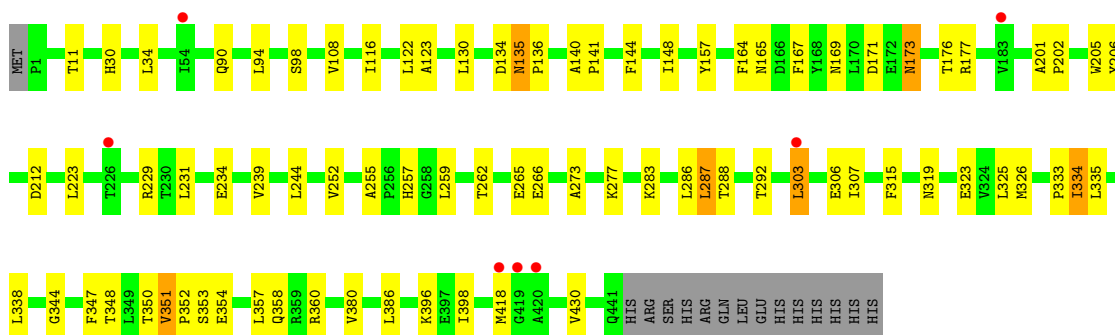
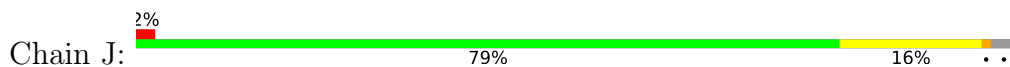


- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera

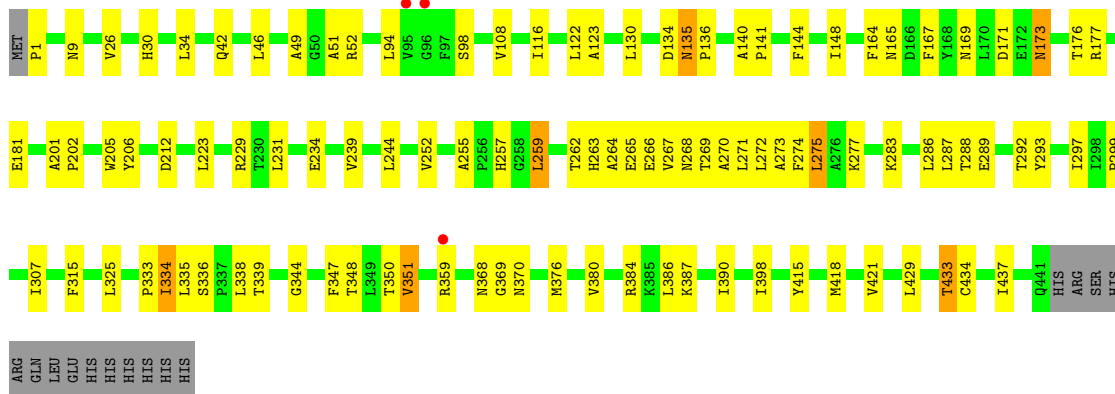
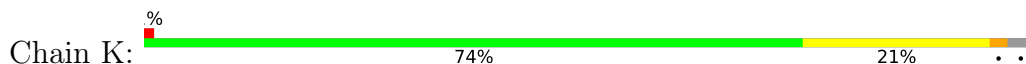




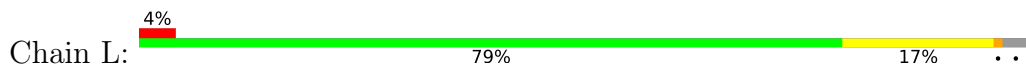
- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera



- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera



- Molecule 1: Non-haem bromoperoxidase BPO-A2, Matrix protein 1 chimera



S336	F337	L338	T339	G344	F347	T348	L349	T350	V351	R359	R360	R361	G369	N370	G371	M376	R384	K385	L386	K387	I398	Y415	M418	V421	F427	G428	L429	T433	C434	I437	Q441	HIS	ARG	SER	HIS	ARG	GLN	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	155.50Å 156.52Å 325.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.27 – 7.81 91.27 – 7.81	Depositor EDS
% Data completeness (in resolution range)	92.1 (91.27-7.81) 92.1 (91.27-7.81)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 7.43Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.288 , 0.339 0.278 , 0.314	Depositor DCC
R_{free} test set	437 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	250.0	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 379.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.057 for k,h,-l	Xtriage
F_o, F_c correlation	0.72	EDS
Total number of atoms	40512	wwPDB-VP
Average B, all atoms (Å ²)	244.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% 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	0.74	0/3452	1.06	11/4702 (0.2%)
1	B	0.75	0/3452	1.09	11/4702 (0.2%)
1	C	0.74	0/3452	1.07	11/4702 (0.2%)
1	D	0.75	0/3452	1.07	13/4702 (0.3%)
1	E	0.73	0/3452	1.05	11/4702 (0.2%)
1	F	0.75	0/3452	1.07	12/4702 (0.3%)
1	G	0.75	0/3452	1.07	12/4702 (0.3%)
1	H	0.75	0/3452	1.07	10/4702 (0.2%)
1	I	0.76	0/3452	1.08	10/4702 (0.2%)
1	J	0.75	0/3452	1.06	12/4702 (0.3%)
1	K	0.76	0/3452	1.06	8/4702 (0.2%)
1	L	0.76	0/3452	1.08	10/4702 (0.2%)
All	All	0.75	0/41424	1.07	131/56424 (0.2%)

There are no bond length outliers.

All (131) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	287	LEU	N-CA-C	8.62	120.68	111.28
1	K	135	ASN	CA-C-N	7.52	127.16	119.19
1	K	135	ASN	C-N-CA	7.52	127.16	119.19
1	L	135	ASN	CA-C-N	7.45	127.09	119.19
1	L	135	ASN	C-N-CA	7.45	127.09	119.19
1	D	135	ASN	CA-C-N	7.45	127.08	119.19
1	D	135	ASN	C-N-CA	7.45	127.08	119.19
1	C	135	ASN	CA-C-N	7.44	127.08	119.19
1	C	135	ASN	C-N-CA	7.44	127.08	119.19
1	E	135	ASN	CA-C-N	7.42	127.06	119.19
1	E	135	ASN	C-N-CA	7.42	127.06	119.19
1	I	135	ASN	CA-C-N	7.42	127.05	119.19
1	I	135	ASN	C-N-CA	7.42	127.05	119.19
1	J	135	ASN	CA-C-N	7.42	127.05	119.19
1	J	135	ASN	C-N-CA	7.42	127.05	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	135	ASN	CA-C-N	7.41	127.05	119.19
1	B	135	ASN	C-N-CA	7.41	127.05	119.19
1	H	135	ASN	CA-C-N	7.39	127.03	119.19
1	H	135	ASN	C-N-CA	7.39	127.03	119.19
1	G	135	ASN	CA-C-N	7.39	127.02	119.19
1	G	135	ASN	C-N-CA	7.39	127.02	119.19
1	A	135	ASN	CA-C-N	7.35	126.98	119.19
1	A	135	ASN	C-N-CA	7.35	126.98	119.19
1	F	135	ASN	CA-C-N	7.35	126.98	119.19
1	F	135	ASN	C-N-CA	7.35	126.98	119.19
1	F	244	LEU	CA-C-N	6.66	126.61	119.28
1	F	244	LEU	C-N-CA	6.66	126.61	119.28
1	H	244	LEU	CA-C-N	6.63	126.58	119.28
1	H	244	LEU	C-N-CA	6.63	126.58	119.28
1	K	244	LEU	CA-C-N	6.62	126.56	119.28
1	K	244	LEU	C-N-CA	6.62	126.56	119.28
1	J	244	LEU	CA-C-N	6.62	126.56	119.28
1	J	244	LEU	C-N-CA	6.62	126.56	119.28
1	E	244	LEU	CA-C-N	6.62	126.56	119.28
1	E	244	LEU	C-N-CA	6.62	126.56	119.28
1	C	244	LEU	CA-C-N	6.61	126.56	119.28
1	C	244	LEU	C-N-CA	6.61	126.56	119.28
1	B	244	LEU	CA-C-N	6.59	126.53	119.28
1	B	244	LEU	C-N-CA	6.59	126.53	119.28
1	D	244	LEU	CA-C-N	6.59	126.53	119.28
1	D	244	LEU	C-N-CA	6.59	126.53	119.28
1	A	244	LEU	CA-C-N	6.58	126.52	119.28
1	A	244	LEU	C-N-CA	6.58	126.52	119.28
1	I	244	LEU	CA-C-N	6.58	126.52	119.28
1	I	244	LEU	C-N-CA	6.58	126.52	119.28
1	G	244	LEU	CA-C-N	6.57	126.50	119.28
1	G	244	LEU	C-N-CA	6.57	126.50	119.28
1	L	244	LEU	CA-C-N	6.55	126.49	119.28
1	L	244	LEU	C-N-CA	6.55	126.49	119.28
1	F	265	GLU	N-CA-C	6.38	117.92	110.97
1	I	265	GLU	N-CA-C	6.38	117.92	110.97
1	C	265	GLU	N-CA-C	6.37	117.91	110.97
1	B	265	GLU	N-CA-C	6.36	117.90	110.97
1	J	265	GLU	N-CA-C	6.34	117.89	110.97
1	L	265	GLU	N-CA-C	6.34	117.88	110.97
1	A	265	GLU	N-CA-C	6.33	117.87	110.97
1	E	265	GLU	N-CA-C	6.32	117.86	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	265	GLU	N-CA-C	6.30	117.84	110.97
1	H	265	GLU	N-CA-C	6.29	117.83	110.97
1	D	265	GLU	N-CA-C	6.26	117.80	110.97
1	D	282	GLN	N-CA-C	-6.02	104.80	111.36
1	J	173	ASN	N-CA-C	5.85	120.48	113.23
1	I	173	ASN	N-CA-C	5.77	120.39	113.23
1	F	173	ASN	N-CA-C	5.77	120.39	113.23
1	K	173	ASN	N-CA-C	5.76	120.38	113.23
1	D	173	ASN	N-CA-C	5.74	120.34	113.23
1	G	173	ASN	N-CA-C	5.74	120.34	113.23
1	B	173	ASN	N-CA-C	5.73	120.34	113.23
1	H	173	ASN	N-CA-C	5.72	120.32	113.23
1	E	173	ASN	N-CA-C	5.72	120.32	113.23
1	C	173	ASN	N-CA-C	5.72	120.32	113.23
1	A	173	ASN	N-CA-C	5.69	120.28	113.23
1	L	173	ASN	N-CA-C	5.67	120.27	113.23
1	A	266	GLU	N-CA-C	-5.55	105.22	111.28
1	D	266	GLU	N-CA-C	-5.55	105.23	111.28
1	L	140	ALA	N-CA-C	5.51	114.65	108.25
1	B	266	GLU	N-CA-C	-5.51	105.27	111.28
1	H	266	GLU	N-CA-C	-5.51	105.28	111.28
1	J	266	GLU	N-CA-C	-5.50	105.29	111.28
1	E	266	GLU	N-CA-C	-5.50	105.29	111.28
1	L	266	GLU	N-CA-C	-5.48	105.31	111.28
1	G	140	ALA	N-CA-C	5.47	114.59	108.25
1	K	140	ALA	N-CA-C	5.47	114.59	108.25
1	D	140	ALA	N-CA-C	5.47	114.59	108.25
1	B	140	ALA	N-CA-C	5.47	114.59	108.25
1	D	216	ILE	CB-CA-C	5.47	117.31	111.35
1	C	266	GLU	N-CA-C	-5.46	105.33	111.28
1	D	212	ASP	CA-C-N	5.46	123.68	120.24
1	D	212	ASP	C-N-CA	5.46	123.68	120.24
1	I	266	GLU	N-CA-C	-5.45	105.34	111.28
1	I	140	ALA	N-CA-C	5.45	114.57	108.25
1	C	140	ALA	N-CA-C	5.44	114.56	108.25
1	F	266	GLU	N-CA-C	-5.44	105.35	111.28
1	A	140	ALA	N-CA-C	5.43	114.55	108.25
1	E	140	ALA	N-CA-C	5.42	114.54	108.25
1	H	140	ALA	N-CA-C	5.42	114.54	108.25
1	J	140	ALA	N-CA-C	5.42	114.53	108.25
1	F	140	ALA	N-CA-C	5.41	114.53	108.25
1	E	212	ASP	CA-C-N	5.37	123.62	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	212	ASP	C-N-CA	5.37	123.62	120.24
1	H	212	ASP	CA-C-N	5.36	123.62	120.24
1	H	212	ASP	C-N-CA	5.36	123.62	120.24
1	G	266	GLU	N-CA-C	-5.35	105.45	111.28
1	I	212	ASP	CA-C-N	5.35	123.61	120.24
1	I	212	ASP	C-N-CA	5.35	123.61	120.24
1	F	430	VAL	N-CA-CB	5.32	117.77	110.54
1	C	212	ASP	CA-C-N	5.31	123.59	120.24
1	C	212	ASP	C-N-CA	5.31	123.59	120.24
1	K	212	ASP	CA-C-N	5.30	123.58	120.24
1	K	212	ASP	C-N-CA	5.30	123.58	120.24
1	G	430	VAL	N-CA-CB	5.30	117.74	110.54
1	F	212	ASP	CA-C-N	5.29	123.58	120.24
1	F	212	ASP	C-N-CA	5.29	123.58	120.24
1	J	212	ASP	CA-C-N	5.29	123.57	120.24
1	J	212	ASP	C-N-CA	5.29	123.57	120.24
1	A	212	ASP	CA-C-N	5.28	123.57	120.24
1	A	212	ASP	C-N-CA	5.28	123.57	120.24
1	D	430	VAL	N-CA-CB	5.28	117.72	110.54
1	L	212	ASP	CA-C-N	5.28	123.56	120.24
1	L	212	ASP	C-N-CA	5.28	123.56	120.24
1	G	212	ASP	CA-C-N	5.27	123.56	120.24
1	G	212	ASP	C-N-CA	5.27	123.56	120.24
1	A	430	VAL	N-CA-CB	5.27	117.70	110.54
1	B	212	ASP	CA-C-N	5.26	123.56	120.24
1	B	212	ASP	C-N-CA	5.26	123.56	120.24
1	J	430	VAL	N-CA-CB	5.25	117.69	110.54
1	E	430	VAL	N-CA-CB	5.25	117.68	110.54
1	F	275	LEU	CB-CA-C	-5.12	102.14	110.85
1	G	124	SER	N-CA-C	5.05	117.61	110.50
1	C	124	SER	N-CA-C	5.03	117.59	110.50
1	B	124	SER	N-CA-C	5.01	117.56	110.50

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	3376	0	3286	73	0
1	B	3376	0	3286	48	0
1	C	3376	0	3286	47	0
1	D	3376	0	3286	88	0
1	E	3376	0	3286	59	0
1	F	3376	0	3286	55	0
1	G	3376	0	3286	57	0
1	H	3376	0	3286	76	0
1	I	3376	0	3286	68	0
1	J	3376	0	3286	48	0
1	K	3376	0	3286	88	0
1	L	3376	0	3286	63	0
All	All	40512	0	39432	695	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 9.

All (695) 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:418:MET:SD	1:I:418:MET:SD	2.38	1.21
1:K:264:ALA:O	1:K:268:ASN:HB2	1.39	1.19
1:L:284:GLN:HA	1:L:287:LEU:CD2	1.73	1.18
1:D:287:LEU:HD13	1:D:315:PHE:CD1	1.77	1.18
1:L:284:GLN:O	1:L:287:LEU:HG	1.41	1.16
1:C:287:LEU:HD13	1:C:315:PHE:HB3	1.16	1.13
1:B:418:MET:SD	1:J:418:MET:SD	2.47	1.12
1:I:287:LEU:HD13	1:I:315:PHE:HB3	1.32	1.12
1:K:46:LEU:HD22	1:K:275:LEU:HD22	1.21	1.10
1:D:286:LEU:CD2	1:D:424:GLU:HG3	1.85	1.07
1:I:287:LEU:HD13	1:I:315:PHE:CB	1.85	1.05
1:D:287:LEU:HB3	1:D:315:PHE:CD2	1.93	1.02
1:L:284:GLN:HA	1:L:287:LEU:HD23	1.40	1.02
1:K:266:GLU:O	1:K:269:THR:HG22	1.62	1.00
1:K:46:LEU:CD2	1:K:275:LEU:HD22	1.91	0.99
1:D:287:LEU:HD13	1:D:315:PHE:CG	1.96	0.99
1:G:418:MET:SD	1:K:418:MET:SD	2.60	0.99
1:L:286:LEU:HD13	1:L:427:PHE:HE2	1.26	0.98
1:K:42:GLN:HG3	1:K:268:ASN:OD1	1.66	0.95
1:L:287:LEU:HB2	1:L:315:PHE:CD2	2.02	0.94
1:D:90:GLN:HB3	1:D:390:ILE:HD13	1.47	0.94
1:D:287:LEU:CD1	1:D:315:PHE:HA	1.99	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:287:LEU:HB3	1:D:315:PHE:CG	2.05	0.92
1:E:287:LEU:HD13	1:E:315:PHE:HB3	1.51	0.92
1:A:368:ASN:HB2	1:H:418:MET:HA	1.51	0.91
1:K:287:LEU:HD13	1:K:315:PHE:HB3	1.53	0.90
1:D:90:GLN:HB3	1:D:390:ILE:CD1	2.01	0.90
1:A:371:GLY:HA2	1:H:418:MET:O	1.73	0.89
1:D:287:LEU:HD13	1:D:315:PHE:HA	1.54	0.89
1:I:287:LEU:CD1	1:I:315:PHE:HB3	2.02	0.89
1:F:22:THR:HG22	1:F:390:ILE:HD11	1.56	0.88
1:H:287:LEU:HD13	1:H:315:PHE:HB3	1.56	0.88
1:F:287:LEU:HD13	1:F:315:PHE:HB3	1.54	0.87
1:E:287:LEU:HD13	1:E:315:PHE:CB	2.05	0.86
1:B:287:LEU:HD13	1:B:315:PHE:HB3	1.57	0.86
1:K:264:ALA:O	1:K:268:ASN:CB	2.23	0.86
1:I:287:LEU:HD13	1:I:315:PHE:CG	2.10	0.85
1:A:418:MET:HE2	1:H:376:MET:SD	2.17	0.85
1:K:26:VAL:HG21	1:K:275:LEU:HD13	1.59	0.84
1:L:284:GLN:HA	1:L:287:LEU:HD21	1.60	0.83
1:D:287:LEU:HD22	1:D:315:PHE:CE1	2.13	0.83
1:H:287:LEU:HD13	1:H:315:PHE:CB	2.08	0.82
1:D:286:LEU:HD23	1:D:424:GLU:HG3	1.62	0.82
1:J:386:LEU:HD23	1:J:398:ILE:HD11	1.63	0.81
1:G:386:LEU:HD23	1:G:398:ILE:HD11	1.63	0.81
1:L:287:LEU:CB	1:L:315:PHE:CD2	2.63	0.81
1:L:386:LEU:HD23	1:L:398:ILE:HD11	1.63	0.81
1:A:386:LEU:HD23	1:A:398:ILE:HD11	1.63	0.81
1:I:288:THR:O	1:I:292:THR:HG23	1.81	0.80
1:E:386:LEU:HD23	1:E:398:ILE:HD11	1.63	0.80
1:D:386:LEU:HD23	1:D:398:ILE:HD11	1.63	0.80
1:F:386:LEU:HD23	1:F:398:ILE:HD11	1.63	0.80
1:H:386:LEU:HD23	1:H:398:ILE:HD11	1.63	0.80
1:B:288:THR:O	1:B:292:THR:HG23	1.82	0.79
1:F:287:LEU:HD13	1:F:315:PHE:CB	2.11	0.79
1:I:215:ARG:NH2	1:K:299:PRO:HG3	1.98	0.79
1:I:386:LEU:HD23	1:I:398:ILE:HD11	1.63	0.79
1:C:376:MET:HE1	1:E:418:MET:HE2	1.63	0.79
1:C:386:LEU:HD23	1:C:398:ILE:HD11	1.63	0.79
1:L:284:GLN:O	1:L:287:LEU:CG	2.29	0.79
1:B:386:LEU:HD23	1:B:398:ILE:HD11	1.63	0.78
1:K:263:HIS:HB3	1:K:266:GLU:HB2	1.66	0.78
1:K:386:LEU:HD23	1:K:398:ILE:HD11	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:287:LEU:HD13	1:D:315:PHE:CA	2.13	0.78
1:I:287:LEU:HB3	1:I:315:PHE:CD2	2.19	0.78
1:L:286:LEU:HD13	1:L:427:PHE:CE2	2.15	0.78
1:A:361:ARG:HH11	1:H:417:ARG:NH1	1.81	0.77
1:D:286:LEU:HG	1:D:427:PHE:CD2	2.19	0.77
1:K:288:THR:O	1:K:292:THR:HG23	1.85	0.77
1:D:287:LEU:HD13	1:D:315:PHE:CB	2.14	0.76
1:K:49:ALA:HB2	1:K:272:LEU:HD21	1.66	0.76
1:K:51:ALA:HB2	1:K:275:LEU:HD11	1.67	0.76
1:C:418:MET:SD	1:E:418:MET:SD	2.84	0.76
1:A:418:MET:O	1:H:371:GLY:HA2	1.86	0.75
1:K:223:LEU:HD21	1:K:267:VAL:HG22	1.68	0.75
1:G:287:LEU:HD13	1:G:315:PHE:HB3	1.69	0.74
1:H:9:ASN:ND2	1:I:21:GLY:O	2.20	0.74
1:H:344:GLY:O	1:H:348:THR:HG23	1.88	0.73
1:F:344:GLY:O	1:F:348:THR:HG23	1.88	0.73
1:L:287:LEU:HD12	1:L:288:THR:N	2.03	0.73
1:I:344:GLY:O	1:I:348:THR:HG23	1.88	0.73
1:A:287:LEU:HD13	1:A:315:PHE:HB3	1.71	0.73
1:A:361:ARG:HD2	1:H:417:ARG:CZ	2.19	0.73
1:B:289:GLU:HG2	1:B:293:TYR:CE2	2.23	0.73
1:D:287:LEU:CD1	1:D:315:PHE:CD1	2.67	0.73
1:J:344:GLY:O	1:J:348:THR:HG23	1.89	0.73
1:C:30:HIS:CE1	1:C:34:LEU:O	2.42	0.73
1:B:30:HIS:CE1	1:B:34:LEU:O	2.42	0.72
1:B:344:GLY:O	1:B:348:THR:HG23	1.88	0.72
1:E:30:HIS:CE1	1:E:34:LEU:O	2.42	0.72
1:L:284:GLN:C	1:L:287:LEU:HG	2.14	0.72
1:E:344:GLY:O	1:E:348:THR:HG23	1.89	0.72
1:F:30:HIS:CE1	1:F:34:LEU:O	2.43	0.72
1:H:30:HIS:CE1	1:H:34:LEU:O	2.43	0.72
1:L:344:GLY:O	1:L:348:THR:HG23	1.88	0.72
1:I:30:HIS:CE1	1:I:34:LEU:O	2.43	0.72
1:A:30:HIS:CE1	1:A:34:LEU:O	2.43	0.72
1:D:344:GLY:O	1:D:348:THR:HG23	1.89	0.72
1:G:30:HIS:CE1	1:G:34:LEU:O	2.42	0.72
1:K:30:HIS:CE1	1:K:34:LEU:O	2.42	0.72
1:C:344:GLY:O	1:C:348:THR:HG23	1.88	0.72
1:J:30:HIS:CE1	1:J:34:LEU:O	2.42	0.72
1:L:30:HIS:CE1	1:L:34:LEU:O	2.43	0.72
1:K:259:LEU:HG	1:K:267:VAL:HG21	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:344:GLY:O	1:K:348:THR:HG23	1.88	0.72
1:G:344:GLY:O	1:G:348:THR:HG23	1.89	0.71
1:A:344:GLY:O	1:A:348:THR:HG23	1.89	0.71
1:D:30:HIS:CE1	1:D:34:LEU:O	2.42	0.71
1:C:287:LEU:HD13	1:C:315:PHE:CB	2.10	0.71
1:H:286:LEU:HD13	1:H:290:VAL:CG2	2.20	0.71
1:D:273:ALA:O	1:D:277:LYS:HG2	1.91	0.71
1:L:287:LEU:HB2	1:L:315:PHE:HD2	1.55	0.70
1:D:319:ASN:HA	1:D:352:PRO:HG2	1.74	0.70
1:A:371:GLY:O	1:H:383:TYR:HE2	1.73	0.70
1:H:286:LEU:CD1	1:H:427:PHE:CD2	2.75	0.70
1:B:273:ALA:O	1:B:277:LYS:HG3	1.92	0.70
1:B:289:GLU:HG2	1:B:293:TYR:HE2	1.57	0.70
1:G:319:ASN:HA	1:G:352:PRO:HG2	1.74	0.70
1:J:319:ASN:HA	1:J:352:PRO:HG2	1.74	0.69
1:D:417:ARG:O	1:I:368:ASN:ND2	2.26	0.69
1:E:319:ASN:HA	1:E:352:PRO:HG2	1.74	0.69
1:K:286:LEU:HD13	1:K:286:LEU:C	2.17	0.69
1:A:319:ASN:HA	1:A:352:PRO:HG2	1.74	0.68
1:D:287:LEU:CD1	1:D:315:PHE:CA	2.67	0.68
1:A:376:MET:CE	1:H:413:LEU:HD22	2.23	0.68
1:C:288:THR:O	1:C:292:THR:HG23	1.93	0.68
1:F:319:ASN:HA	1:F:352:PRO:HG2	1.74	0.67
1:G:157:TYR:HB3	1:H:181:GLU:HB3	1.77	0.67
1:H:286:LEU:HD13	1:H:290:VAL:HG23	1.77	0.66
1:F:273:ALA:O	1:F:277:LYS:HG3	1.94	0.66
1:E:287:LEU:CD1	1:E:315:PHE:HB3	2.25	0.66
1:E:154:ALA:O	1:F:41:ARG:NH2	2.27	0.65
1:I:215:ARG:HH22	1:K:299:PRO:HG3	1.60	0.65
1:K:26:VAL:HG21	1:K:275:LEU:CD1	2.24	0.65
1:D:286:LEU:O	1:D:290:VAL:HG23	1.97	0.65
1:H:286:LEU:HD12	1:H:427:PHE:CD2	2.32	0.65
1:A:9:ASN:ND2	1:B:21:GLY:O	2.26	0.64
1:D:380:VAL:HG21	1:I:380:VAL:HG21	1.79	0.64
1:A:273:ALA:O	1:A:277:LYS:HG3	1.97	0.64
1:G:287:LEU:HD13	1:G:315:PHE:CB	2.28	0.64
1:J:273:ALA:O	1:J:277:LYS:HG3	1.98	0.64
1:D:287:LEU:CD1	1:D:315:PHE:CB	2.76	0.64
1:D:287:LEU:HD13	1:D:315:PHE:HD1	1.58	0.64
1:H:273:ALA:O	1:H:277:LYS:HG3	1.98	0.63
1:D:287:LEU:CD1	1:D:315:PHE:CG	2.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:LEU:HD21	1:D:424:GLU:HG3	1.77	0.63
1:E:273:ALA:O	1:E:277:LYS:HG3	1.98	0.63
1:K:269:THR:HG23	1:K:270:ALA:N	2.13	0.63
1:I:273:ALA:O	1:I:277:LYS:HG3	1.97	0.63
1:F:371:GLY:HA2	1:L:418:MET:O	1.99	0.63
1:J:283:LYS:O	1:J:287:LEU:HG	1.99	0.63
1:L:273:ALA:O	1:L:277:LYS:HG3	1.98	0.63
1:C:273:ALA:O	1:C:277:LYS:HG3	1.99	0.62
1:G:283:LYS:O	1:G:287:LEU:HG	1.99	0.62
1:H:286:LEU:O	1:H:290:VAL:HG23	2.00	0.62
1:A:371:GLY:O	1:H:383:TYR:CE2	2.53	0.61
1:H:286:LEU:HD11	1:H:427:PHE:CD2	2.35	0.61
1:H:287:LEU:HB3	1:H:315:PHE:CD2	2.35	0.61
1:F:22:THR:CG2	1:F:390:ILE:HD11	2.31	0.60
1:G:273:ALA:O	1:G:277:LYS:HG3	2.01	0.60
1:K:286:LEU:HD13	1:K:286:LEU:O	2.00	0.60
1:G:17:TYR:CZ	1:I:11:THR:HG22	2.37	0.60
1:A:326:MET:HE1	1:A:347:PHE:HB2	1.84	0.60
1:E:326:MET:HE1	1:E:347:PHE:HB2	1.84	0.60
1:A:376:MET:HE2	1:H:380:VAL:HG22	1.83	0.59
1:G:417:ARG:O	1:K:368:ASN:ND2	2.35	0.59
1:K:273:ALA:O	1:K:277:LYS:HE3	2.03	0.59
1:A:252:VAL:HG12	1:A:255:ALA:HB2	1.84	0.59
1:A:286:LEU:O	1:A:290:VAL:HG23	2.02	0.59
1:B:252:VAL:HG12	1:B:255:ALA:HB2	1.85	0.59
1:I:252:VAL:HG12	1:I:255:ALA:HB2	1.85	0.59
1:F:284:GLN:O	1:F:288:THR:HG23	2.02	0.59
1:G:252:VAL:HG12	1:G:255:ALA:HB2	1.84	0.59
1:D:252:VAL:HG12	1:D:255:ALA:HB2	1.85	0.59
1:D:286:LEU:CD2	1:D:424:GLU:CG	2.74	0.59
1:F:287:LEU:CD1	1:F:315:PHE:HB3	2.28	0.59
1:H:252:VAL:HG12	1:H:255:ALA:HB2	1.84	0.59
1:B:416:ASN:ND2	1:J:418:MET:SD	2.69	0.59
1:K:51:ALA:CB	1:K:275:LEU:HD11	2.32	0.59
1:E:333:PRO:O	1:E:334:ILE:HG12	2.03	0.59
1:G:326:MET:HE1	1:G:347:PHE:HB2	1.84	0.58
1:J:326:MET:HE1	1:J:347:PHE:HB2	1.84	0.58
1:F:326:MET:HE1	1:F:347:PHE:HB2	1.84	0.58
1:E:252:VAL:HG12	1:E:255:ALA:HB2	1.85	0.58
1:H:287:LEU:CD1	1:H:315:PHE:HB3	2.32	0.58
1:J:333:PRO:O	1:J:334:ILE:HG12	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:252:VAL:HG12	1:J:255:ALA:HB2	1.84	0.58
1:E:287:LEU:HB3	1:E:315:PHE:CD2	2.37	0.58
1:F:252:VAL:HG12	1:F:255:ALA:HB2	1.84	0.58
1:F:333:PRO:O	1:F:334:ILE:HG12	2.03	0.58
1:K:252:VAL:HG12	1:K:255:ALA:HB2	1.85	0.58
1:L:252:VAL:HG12	1:L:255:ALA:HB2	1.84	0.58
1:A:154:ALA:O	1:B:41:ARG:NH2	2.35	0.58
1:A:376:MET:HE3	1:H:413:LEU:HD22	1.85	0.58
1:D:283:LYS:O	1:D:287:LEU:HG	2.04	0.58
1:D:358:GLN:HG3	1:I:360:ARG:NH2	2.18	0.58
1:A:333:PRO:O	1:A:334:ILE:HG12	2.03	0.58
1:A:287:LEU:HD13	1:A:315:PHE:CB	2.33	0.57
1:H:333:PRO:O	1:H:334:ILE:HG12	2.04	0.57
1:C:252:VAL:HG12	1:C:255:ALA:HB2	1.84	0.57
1:C:376:MET:CE	1:E:418:MET:HE2	2.30	0.57
1:I:333:PRO:O	1:I:334:ILE:HG12	2.05	0.57
1:D:333:PRO:O	1:D:334:ILE:HG12	2.03	0.57
1:E:164:PHE:HA	1:E:167:PHE:HB3	1.87	0.57
1:E:360:ARG:HG2	1:E:360:ARG:HH11	1.70	0.57
1:G:333:PRO:O	1:G:334:ILE:HG12	2.03	0.57
1:B:333:PRO:O	1:B:334:ILE:HG12	2.05	0.57
1:D:326:MET:HE1	1:D:347:PHE:HB2	1.84	0.57
1:G:284:GLN:O	1:G:288:THR:HG23	2.05	0.57
1:L:164:PHE:HA	1:L:167:PHE:HB3	1.87	0.57
1:F:287:LEU:HB3	1:F:315:PHE:CD2	2.39	0.57
1:F:360:ARG:HG2	1:F:360:ARG:HH11	1.70	0.57
1:J:164:PHE:HA	1:J:167:PHE:HB3	1.87	0.57
1:K:283:LYS:O	1:K:287:LEU:HB2	2.05	0.57
1:K:333:PRO:O	1:K:334:ILE:HG12	2.05	0.57
1:C:333:PRO:O	1:C:334:ILE:HG12	2.05	0.57
1:A:284:GLN:O	1:A:288:THR:HG23	2.05	0.57
1:F:164:PHE:HA	1:F:167:PHE:HB3	1.87	0.57
1:I:336:SER:HB3	1:I:339:THR:HG23	1.87	0.57
1:K:164:PHE:HA	1:K:167:PHE:HB3	1.86	0.57
1:D:279:GLN:O	1:D:283:LYS:CB	2.53	0.57
1:D:164:PHE:HA	1:D:167:PHE:HB3	1.86	0.57
1:D:360:ARG:HH11	1:D:360:ARG:HG2	1.70	0.57
1:A:358:GLN:OE1	1:H:361:ARG:HB2	2.05	0.56
1:B:380:VAL:HG21	1:J:380:VAL:HG21	1.87	0.56
1:A:164:PHE:HA	1:A:167:PHE:HB3	1.87	0.56
1:C:164:PHE:HA	1:C:167:PHE:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:336:SER:HB3	1:C:339:THR:HG23	1.87	0.56
1:G:360:ARG:HH11	1:G:360:ARG:HG2	1.70	0.56
1:L:333:PRO:O	1:L:334:ILE:HG12	2.04	0.56
1:B:336:SER:HB3	1:B:339:THR:HG23	1.87	0.56
1:K:336:SER:HB3	1:K:339:THR:HG23	1.87	0.56
1:J:360:ARG:HG2	1:J:360:ARG:HH11	1.70	0.56
1:F:285:LYS:HA	1:F:288:THR:OG1	2.05	0.56
1:H:164:PHE:HA	1:H:167:PHE:HB3	1.87	0.56
1:H:287:LEU:HD13	1:H:315:PHE:CG	2.40	0.56
1:I:164:PHE:HA	1:I:167:PHE:HB3	1.87	0.56
1:L:336:SER:HB3	1:L:339:THR:HG23	1.87	0.56
1:B:164:PHE:HA	1:B:167:PHE:HB3	1.87	0.56
1:F:288:THR:O	1:F:292:THR:HG23	2.06	0.56
1:I:283:LYS:O	1:I:287:LEU:HG	2.06	0.56
1:E:284:GLN:O	1:E:288:THR:HG23	2.06	0.55
1:G:164:PHE:HA	1:G:167:PHE:HB3	1.87	0.55
1:A:360:ARG:HG2	1:A:360:ARG:HH11	1.70	0.55
1:D:274:PHE:HA	1:D:277:LYS:CG	2.36	0.55
1:D:157:TYR:HB3	1:E:181:GLU:HB3	1.87	0.55
1:K:49:ALA:CB	1:K:272:LEU:HD21	2.36	0.55
1:K:130:LEU:HB2	1:K:206:TYR:HB2	1.89	0.55
1:K:266:GLU:O	1:K:269:THR:CG2	2.45	0.55
1:K:265:GLU:O	1:K:269:THR:HB	2.07	0.55
1:D:130:LEU:HB2	1:D:206:TYR:HB2	1.89	0.55
1:H:283:LYS:O	1:H:287:LEU:HG	2.06	0.55
1:C:429:LEU:O	1:C:433:THR:HG23	2.07	0.55
1:I:130:LEU:HB2	1:I:206:TYR:HB2	1.89	0.54
1:K:429:LEU:O	1:K:433:THR:HG23	2.08	0.54
1:F:130:LEU:HB2	1:F:206:TYR:HB2	1.89	0.54
1:F:286:LEU:O	1:F:290:VAL:HG23	2.08	0.54
1:D:284:GLN:O	1:D:288:THR:HG23	2.08	0.54
1:H:336:SER:HB3	1:H:339:THR:HG23	1.87	0.54
1:B:130:LEU:HB2	1:B:206:TYR:HB2	1.89	0.54
1:B:201:ALA:HB3	1:B:202:PRO:HD3	1.90	0.54
1:H:130:LEU:HB2	1:H:206:TYR:HB2	1.89	0.54
1:B:429:LEU:O	1:B:433:THR:HG23	2.08	0.54
1:H:429:LEU:O	1:H:433:THR:HG23	2.08	0.54
1:A:283:LYS:O	1:A:287:LEU:HG	2.08	0.54
1:D:358:GLN:CB	1:I:358:GLN:HB2	2.37	0.54
1:H:286:LEU:HD13	1:H:290:VAL:HG21	1.90	0.54
1:K:223:LEU:CD2	1:K:267:VAL:HG22	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:130:LEU:HB2	1:L:206:TYR:HB2	1.89	0.54
1:D:274:PHE:HA	1:D:277:LYS:HG2	1.89	0.54
1:K:201:ALA:HB3	1:K:202:PRO:HD3	1.90	0.54
1:C:201:ALA:HB3	1:C:202:PRO:HD3	1.90	0.54
1:E:130:LEU:HB2	1:E:206:TYR:HB2	1.89	0.54
1:D:154:ALA:O	1:E:41:ARG:NH2	2.39	0.53
1:D:155:ASP:OD2	1:E:179:SER:OG	2.25	0.53
1:I:201:ALA:HB3	1:I:202:PRO:HD3	1.90	0.53
1:I:429:LEU:O	1:I:433:THR:HG23	2.08	0.53
1:G:130:LEU:HB2	1:G:206:TYR:HB2	1.89	0.53
1:B:359:ARG:NH1	1:B:415:TYR:O	2.39	0.53
1:D:201:ALA:HB3	1:D:202:PRO:HD3	1.90	0.53
1:D:418:MET:CG	1:I:416:ASN:HD22	2.21	0.53
1:G:201:ALA:HB3	1:G:202:PRO:HD3	1.90	0.53
1:H:288:THR:O	1:H:292:THR:HG23	2.07	0.53
1:K:359:ARG:NH1	1:K:415:TYR:O	2.39	0.53
1:L:429:LEU:O	1:L:433:THR:HG23	2.08	0.53
1:A:130:LEU:HB2	1:A:206:TYR:HB2	1.89	0.53
1:A:288:THR:O	1:A:292:THR:HG23	2.08	0.53
1:C:176:THR:HG22	1:C:177:ARG:N	2.24	0.53
1:E:176:THR:HG22	1:E:177:ARG:N	2.24	0.53
1:E:287:LEU:HD13	1:E:315:PHE:CG	2.43	0.53
1:G:288:THR:O	1:G:292:THR:HG23	2.08	0.53
1:C:130:LEU:HB2	1:C:206:TYR:HB2	1.90	0.53
1:F:201:ALA:HB3	1:F:202:PRO:HD3	1.90	0.53
1:I:176:THR:HG22	1:I:177:ARG:N	2.24	0.53
1:A:176:THR:HG22	1:A:177:ARG:N	2.24	0.53
1:A:201:ALA:HB3	1:A:202:PRO:HD3	1.90	0.53
1:B:176:THR:HG22	1:B:177:ARG:N	2.24	0.53
1:F:176:THR:HG22	1:F:177:ARG:N	2.24	0.53
1:D:176:THR:HG22	1:D:177:ARG:N	2.24	0.53
1:D:274:PHE:O	1:D:277:LYS:HG3	2.09	0.53
1:I:215:ARG:HH22	1:K:299:PRO:CG	2.21	0.53
1:H:201:ALA:HB3	1:H:202:PRO:HD3	1.90	0.53
1:G:286:LEU:O	1:G:290:VAL:HG23	2.09	0.53
1:E:286:LEU:O	1:E:290:VAL:HG23	2.09	0.53
1:E:288:THR:O	1:E:292:THR:HG23	2.08	0.52
1:J:130:LEU:HB2	1:J:206:TYR:HB2	1.89	0.52
1:J:201:ALA:HB3	1:J:202:PRO:HD3	1.90	0.52
1:J:288:THR:O	1:J:292:THR:HG23	2.09	0.52
1:L:176:THR:HG22	1:L:177:ARG:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:201:ALA:HB3	1:E:202:PRO:HD3	1.90	0.52
1:F:358:GLN:OE1	1:L:361:ARG:HB2	2.09	0.52
1:J:176:THR:HG22	1:J:177:ARG:N	2.24	0.52
1:K:176:THR:HG22	1:K:177:ARG:N	2.24	0.52
1:L:201:ALA:HB3	1:L:202:PRO:HD3	1.90	0.52
1:D:286:LEU:HG	1:D:427:PHE:HD2	1.71	0.52
1:D:418:MET:HE1	1:I:413:LEU:HA	1.90	0.52
1:H:176:THR:HG22	1:H:177:ARG:N	2.24	0.52
1:G:176:THR:HG22	1:G:177:ARG:N	2.24	0.52
1:I:359:ARG:NH1	1:I:415:TYR:O	2.39	0.52
1:K:266:GLU:N	1:K:266:GLU:OE1	2.42	0.52
1:K:289:GLU:O	1:K:293:TYR:HD2	1.92	0.52
1:D:287:LEU:HD22	1:D:315:PHE:CD1	2.44	0.51
1:D:418:MET:HE1	1:I:413:LEU:CA	2.40	0.51
1:K:271:LEU:O	1:K:274:PHE:N	2.40	0.51
1:A:41:ARG:NH2	1:C:154:ALA:O	2.43	0.51
1:G:98:SER:HA	1:G:123:ALA:O	2.11	0.51
1:J:98:SER:HA	1:J:123:ALA:O	2.11	0.51
1:K:98:SER:HA	1:K:123:ALA:O	2.11	0.51
1:D:359:ARG:O	1:I:358:GLN:OE1	2.28	0.51
1:L:173:ASN:HD22	1:L:177:ARG:HG3	1.76	0.51
1:A:21:GLY:O	1:C:9:ASN:ND2	2.39	0.51
1:C:98:SER:HA	1:C:123:ALA:O	2.11	0.51
1:B:98:SER:HA	1:B:123:ALA:O	2.11	0.51
1:C:130:LEU:O	1:C:135:ASN:ND2	2.38	0.51
1:F:418:MET:O	1:L:371:GLY:HA2	2.10	0.51
1:G:17:TYR:OH	1:I:11:THR:HG22	2.10	0.51
1:G:173:ASN:HD22	1:G:177:ARG:HG3	1.76	0.51
1:J:157:TYR:HB3	1:K:181:GLU:HB3	1.92	0.51
1:E:98:SER:HA	1:E:123:ALA:O	2.11	0.51
1:I:297:ILE:HD11	1:I:434:CYS:O	2.11	0.51
1:L:297:ILE:HD11	1:L:434:CYS:O	2.11	0.51
1:H:98:SER:HA	1:H:123:ALA:O	2.11	0.50
1:L:130:LEU:O	1:L:135:ASN:ND2	2.38	0.50
1:A:130:LEU:O	1:A:135:ASN:ND2	2.38	0.50
1:C:297:ILE:HD11	1:C:434:CYS:O	2.11	0.50
1:H:173:ASN:HD22	1:H:177:ARG:HG3	1.76	0.50
1:A:173:ASN:HD22	1:A:177:ARG:HG3	1.76	0.50
1:F:98:SER:HA	1:F:123:ALA:O	2.11	0.50
1:I:286:LEU:O	1:I:290:VAL:HG23	2.12	0.50
1:K:173:ASN:HD22	1:K:177:ARG:HG3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:173:ASN:HD22	1:F:177:ARG:HG3	1.76	0.50
1:L:287:LEU:CD2	1:L:315:PHE:HB3	2.41	0.50
1:B:297:ILE:HD11	1:B:434:CYS:O	2.11	0.50
1:H:297:ILE:HD11	1:H:434:CYS:O	2.12	0.50
1:I:173:ASN:HD22	1:I:177:ARG:HG3	1.76	0.50
1:J:173:ASN:HD22	1:J:177:ARG:HG3	1.76	0.50
1:K:259:LEU:HG	1:K:267:VAL:CG2	2.38	0.50
1:E:354:GLU:O	1:E:357:LEU:HG	2.12	0.50
1:L:98:SER:HA	1:L:123:ALA:O	2.11	0.50
1:D:354:GLU:O	1:D:357:LEU:HG	2.12	0.50
1:G:130:LEU:O	1:G:135:ASN:ND2	2.38	0.50
1:K:269:THR:CG2	1:K:270:ALA:N	2.74	0.50
1:I:98:SER:HA	1:I:123:ALA:O	2.11	0.50
1:J:354:GLU:O	1:J:357:LEU:HG	2.12	0.50
1:A:98:SER:HA	1:A:123:ALA:O	2.11	0.50
1:A:354:GLU:O	1:A:357:LEU:HG	2.12	0.50
1:B:173:ASN:HD22	1:B:177:ARG:HG3	1.76	0.50
1:D:98:SER:HA	1:D:123:ALA:O	2.11	0.50
1:F:354:GLU:O	1:F:357:LEU:HG	2.12	0.50
1:I:231:LEU:HD12	1:I:257:HIS:HE1	1.77	0.50
1:K:9:ASN:ND2	1:L:21:GLY:O	2.43	0.50
1:F:231:LEU:HD12	1:F:257:HIS:HE1	1.77	0.49
1:J:130:LEU:O	1:J:135:ASN:ND2	2.38	0.49
1:G:41:ARG:NH2	1:I:154:ALA:O	2.44	0.49
1:L:231:LEU:HD12	1:L:257:HIS:HE1	1.78	0.49
1:E:231:LEU:HD12	1:E:257:HIS:HE1	1.77	0.49
1:K:297:ILE:HD11	1:K:434:CYS:O	2.12	0.49
1:B:297:ILE:HD11	1:B:437:ILE:HB	1.95	0.49
1:C:359:ARG:NH1	1:C:415:TYR:O	2.39	0.49
1:D:173:ASN:HD22	1:D:177:ARG:HG3	1.77	0.49
1:F:122:LEU:CD2	1:F:223:LEU:HB3	2.43	0.49
1:G:122:LEU:CD2	1:G:223:LEU:HB3	2.42	0.49
1:G:231:LEU:HD12	1:G:257:HIS:HE1	1.77	0.49
1:G:283:LYS:O	1:G:287:LEU:N	2.32	0.49
1:J:122:LEU:CD2	1:J:223:LEU:HB3	2.43	0.49
1:K:122:LEU:CD2	1:K:223:LEU:HB3	2.43	0.49
1:A:361:ARG:NH1	1:H:417:ARG:NH1	2.57	0.49
1:C:173:ASN:HD22	1:C:177:ARG:HG3	1.76	0.49
1:D:122:LEU:CD2	1:D:223:LEU:HB3	2.43	0.49
1:I:297:ILE:HD11	1:I:437:ILE:HB	1.95	0.49
1:J:231:LEU:HD12	1:J:257:HIS:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:MET:CE	1:H:376:MET:SD	2.96	0.49
1:C:297:ILE:HD11	1:C:437:ILE:HB	1.94	0.49
1:D:231:LEU:HD12	1:D:257:HIS:HE1	1.77	0.49
1:K:287:LEU:CD1	1:K:315:PHE:HB3	2.36	0.49
1:L:287:LEU:HB3	1:L:315:PHE:CD2	2.43	0.49
1:L:297:ILE:HD11	1:L:437:ILE:HB	1.95	0.49
1:H:130:LEU:O	1:H:135:ASN:ND2	2.38	0.49
1:K:231:LEU:HD12	1:K:257:HIS:HE1	1.77	0.49
1:K:297:ILE:HD11	1:K:437:ILE:HB	1.95	0.49
1:C:122:LEU:CD2	1:C:223:LEU:HB3	2.43	0.49
1:G:354:GLU:O	1:G:357:LEU:HG	2.12	0.49
1:L:122:LEU:CD2	1:L:223:LEU:HB3	2.43	0.49
1:E:173:ASN:HD22	1:E:177:ARG:HG3	1.76	0.48
1:H:122:LEU:CD2	1:H:223:LEU:HB3	2.43	0.48
1:A:231:LEU:HD12	1:A:257:HIS:HE1	1.78	0.48
1:A:365:ASN:OD1	1:H:417:ARG:HD2	2.13	0.48
1:C:231:LEU:HD12	1:C:257:HIS:HE1	1.77	0.48
1:H:231:LEU:HD12	1:H:257:HIS:HE1	1.78	0.48
1:H:359:ARG:NH1	1:H:415:TYR:O	2.39	0.48
1:K:52:ARG:CZ	1:K:390:ILE:HD11	2.43	0.48
1:B:122:LEU:CD2	1:B:223:LEU:HB3	2.43	0.48
1:K:283:LYS:O	1:K:287:LEU:CB	2.62	0.48
1:C:376:MET:HE1	1:E:418:MET:CE	2.39	0.48
1:E:122:LEU:CD2	1:E:223:LEU:HB3	2.43	0.48
1:H:297:ILE:HD11	1:H:437:ILE:HB	1.95	0.48
1:I:122:LEU:CD2	1:I:223:LEU:HB3	2.43	0.48
1:D:181:GLU:HB3	1:F:157:TYR:HB3	1.95	0.48
1:B:231:LEU:HD12	1:B:257:HIS:HE1	1.78	0.48
1:J:347:PHE:O	1:J:351:VAL:HB	2.14	0.48
1:L:288:THR:O	1:L:292:THR:HG23	2.13	0.48
1:E:283:LYS:O	1:E:287:LEU:HG	2.14	0.47
1:A:122:LEU:CD2	1:A:223:LEU:HB3	2.43	0.47
1:E:347:PHE:O	1:E:351:VAL:HB	2.14	0.47
1:H:307:ILE:HD11	1:H:335:LEU:HD11	1.97	0.47
1:K:307:ILE:HD11	1:K:335:LEU:HD11	1.97	0.47
1:A:347:PHE:O	1:A:351:VAL:HB	2.14	0.47
1:I:286:LEU:HD13	1:I:290:VAL:HG23	1.96	0.47
1:K:369:GLY:O	1:K:370:ASN:OD1	2.33	0.47
1:L:347:PHE:O	1:L:351:VAL:HB	2.15	0.47
1:C:347:PHE:O	1:C:351:VAL:HB	2.15	0.47
1:D:418:MET:CG	1:I:416:ASN:ND2	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:173:ASN:ND2	1:E:177:ARG:HG3	2.30	0.47
1:I:173:ASN:ND2	1:I:177:ARG:HG3	2.30	0.47
1:L:359:ARG:NH1	1:L:415:TYR:O	2.39	0.47
1:D:287:LEU:CB	1:D:315:PHE:CG	2.90	0.47
1:E:134:ASP:C	1:E:136:PRO:HD3	2.40	0.47
1:F:173:ASN:ND2	1:F:177:ARG:HG3	2.30	0.47
1:F:347:PHE:O	1:F:351:VAL:HB	2.14	0.47
1:I:307:ILE:HD11	1:I:335:LEU:HD11	1.97	0.47
1:K:347:PHE:O	1:K:351:VAL:HB	2.15	0.47
1:B:369:GLY:O	1:B:370:ASN:OD1	2.33	0.47
1:C:173:ASN:ND2	1:C:177:ARG:HG3	2.30	0.47
1:L:307:ILE:HD11	1:L:335:LEU:HD11	1.97	0.47
1:A:173:ASN:ND2	1:A:177:ARG:HG3	2.30	0.47
1:A:307:ILE:HD11	1:A:335:LEU:HD11	1.97	0.47
1:D:303:LEU:HA	1:D:306:GLU:OE1	2.15	0.47
1:G:347:PHE:O	1:G:351:VAL:HB	2.14	0.47
1:C:369:GLY:O	1:C:370:ASN:OD1	2.33	0.47
1:E:303:LEU:HA	1:E:306:GLU:OE1	2.15	0.47
1:I:347:PHE:O	1:I:351:VAL:HB	2.15	0.47
1:J:30:HIS:ND1	1:J:34:LEU:O	2.48	0.47
1:J:307:ILE:HD11	1:J:335:LEU:HD11	1.97	0.47
1:A:303:LEU:HA	1:A:306:GLU:OE1	2.15	0.46
1:B:307:ILE:HD11	1:B:335:LEU:HD11	1.97	0.46
1:E:130:LEU:O	1:E:135:ASN:ND2	2.38	0.46
1:F:134:ASP:C	1:F:136:PRO:HD3	2.40	0.46
1:K:283:LYS:O	1:K:287:LEU:N	2.41	0.46
1:C:307:ILE:HD11	1:C:335:LEU:HD11	1.97	0.46
1:D:347:PHE:O	1:D:351:VAL:HB	2.15	0.46
1:F:30:HIS:ND1	1:F:34:LEU:O	2.48	0.46
1:G:173:ASN:ND2	1:G:177:ARG:HG3	2.30	0.46
1:J:134:ASP:C	1:J:136:PRO:HD3	2.40	0.46
1:J:303:LEU:HA	1:J:306:GLU:OE1	2.15	0.46
1:C:30:HIS:ND1	1:C:34:LEU:O	2.48	0.46
1:E:30:HIS:ND1	1:E:34:LEU:O	2.48	0.46
1:H:134:ASP:C	1:H:136:PRO:HD3	2.41	0.46
1:H:173:ASN:ND2	1:H:177:ARG:HG3	2.30	0.46
1:I:134:ASP:C	1:I:136:PRO:HD3	2.41	0.46
1:J:173:ASN:ND2	1:J:177:ARG:HG3	2.30	0.46
1:L:173:ASN:ND2	1:L:177:ARG:HG3	2.30	0.46
1:A:418:MET:HG2	1:H:368:ASN:CG	2.40	0.46
1:H:347:PHE:O	1:H:351:VAL:HB	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:358:GLN:CB	1:I:358:GLN:CB	2.93	0.46
1:G:134:ASP:C	1:G:136:PRO:HD3	2.40	0.46
1:D:30:HIS:ND1	1:D:34:LEU:O	2.48	0.46
1:D:307:ILE:HD11	1:D:335:LEU:HD11	1.97	0.46
1:G:30:HIS:ND1	1:G:34:LEU:O	2.48	0.46
1:G:303:LEU:HA	1:G:306:GLU:OE1	2.15	0.46
1:G:307:ILE:HD11	1:G:335:LEU:HD11	1.97	0.46
1:K:30:HIS:ND1	1:K:34:LEU:O	2.48	0.46
1:K:173:ASN:ND2	1:K:177:ARG:HG3	2.30	0.46
1:B:173:ASN:ND2	1:B:177:ARG:HG3	2.30	0.46
1:F:287:LEU:HD13	1:F:315:PHE:CG	2.50	0.46
1:K:134:ASP:C	1:K:136:PRO:HD3	2.41	0.46
1:L:134:ASP:C	1:L:136:PRO:HD3	2.41	0.46
1:A:134:ASP:C	1:A:136:PRO:HD3	2.40	0.46
1:F:303:LEU:HA	1:F:306:GLU:OE1	2.15	0.46
1:B:30:HIS:ND1	1:B:34:LEU:O	2.48	0.46
1:B:134:ASP:C	1:B:136:PRO:HD3	2.40	0.46
1:D:173:ASN:ND2	1:D:177:ARG:HG3	2.30	0.46
1:H:369:GLY:O	1:H:370:ASN:OD1	2.33	0.46
1:L:315:PHE:HE1	1:L:350:THR:HG21	1.81	0.46
1:B:347:PHE:O	1:B:351:VAL:HB	2.15	0.46
1:D:134:ASP:C	1:D:136:PRO:HD3	2.41	0.46
1:I:30:HIS:ND1	1:I:34:LEU:O	2.49	0.46
1:L:287:LEU:HB3	1:L:315:PHE:CG	2.51	0.46
1:F:307:ILE:HD11	1:F:335:LEU:HD11	1.97	0.45
1:G:319:ASN:CA	1:G:352:PRO:HG2	2.46	0.45
1:L:284:GLN:CA	1:L:287:LEU:CD2	2.67	0.45
1:C:141:PRO:O	1:C:144:PHE:HB3	2.17	0.45
1:D:141:PRO:O	1:D:144:PHE:HB3	2.17	0.45
1:A:141:PRO:O	1:A:144:PHE:HB3	2.17	0.45
1:B:141:PRO:O	1:B:144:PHE:HB3	2.17	0.45
1:E:307:ILE:HD11	1:E:335:LEU:HD11	1.98	0.45
1:I:369:GLY:O	1:I:370:ASN:OD1	2.33	0.45
1:L:30:HIS:ND1	1:L:34:LEU:O	2.49	0.45
1:A:365:ASN:OD1	1:H:417:ARG:CD	2.65	0.45
1:G:141:PRO:O	1:G:144:PHE:HB3	2.17	0.45
1:H:141:PRO:O	1:H:144:PHE:HB3	2.17	0.45
1:D:130:LEU:O	1:D:135:ASN:ND2	2.38	0.45
1:E:315:PHE:HE1	1:E:350:THR:HG21	1.82	0.45
1:G:283:LYS:O	1:G:287:LEU:CB	2.64	0.45
1:H:30:HIS:ND1	1:H:34:LEU:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:141:PRO:O	1:J:144:PHE:HB3	2.17	0.45
1:A:30:HIS:ND1	1:A:34:LEU:O	2.48	0.45
1:A:315:PHE:HE1	1:A:350:THR:HG21	1.81	0.45
1:B:130:LEU:O	1:B:135:ASN:ND2	2.38	0.45
1:F:141:PRO:O	1:F:144:PHE:HB3	2.17	0.45
1:I:315:PHE:HE1	1:I:350:THR:HG21	1.82	0.45
1:K:315:PHE:HE1	1:K:350:THR:HG21	1.82	0.45
1:L:369:GLY:O	1:L:370:ASN:OD1	2.33	0.45
1:C:134:ASP:C	1:C:136:PRO:HD3	2.40	0.45
1:F:319:ASN:CA	1:F:352:PRO:HG2	2.46	0.45
1:H:315:PHE:HE1	1:H:350:THR:HG21	1.82	0.45
1:D:171:ASP:CG	1:D:229:ARG:HH22	2.24	0.45
1:E:141:PRO:O	1:E:144:PHE:HB3	2.17	0.45
1:A:358:GLN:O	1:A:360:ARG:NH1	2.50	0.45
1:B:122:LEU:HD23	1:B:223:LEU:HB3	1.99	0.45
1:G:122:LEU:HD23	1:G:223:LEU:HB3	1.99	0.45
1:G:315:PHE:HE1	1:G:350:THR:HG21	1.82	0.45
1:D:122:LEU:HD23	1:D:223:LEU:HB3	1.99	0.44
1:E:358:GLN:O	1:E:360:ARG:NH1	2.50	0.44
1:H:122:LEU:HD23	1:H:223:LEU:HB3	1.99	0.44
1:K:171:ASP:CG	1:K:229:ARG:HH22	2.24	0.44
1:A:171:ASP:CG	1:A:229:ARG:HH22	2.24	0.44
1:D:319:ASN:CA	1:D:352:PRO:HG2	2.46	0.44
1:I:141:PRO:O	1:I:144:PHE:HB3	2.17	0.44
1:K:269:THR:C	1:K:271:LEU:H	2.24	0.44
1:L:287:LEU:HD12	1:L:288:THR:CA	2.47	0.44
1:B:171:ASP:CG	1:B:229:ARG:HH22	2.24	0.44
1:E:319:ASN:CA	1:E:352:PRO:HG2	2.46	0.44
1:F:315:PHE:HE1	1:F:350:THR:HG21	1.82	0.44
1:K:141:PRO:O	1:K:144:PHE:HB3	2.17	0.44
1:A:361:ARG:HD2	1:H:417:ARG:NH2	2.32	0.44
1:B:286:LEU:O	1:B:290:VAL:HG23	2.18	0.44
1:B:289:GLU:O	1:B:293:TYR:HD2	2.00	0.44
1:G:358:GLN:O	1:G:360:ARG:NH1	2.50	0.44
1:F:171:ASP:CG	1:F:229:ARG:HH22	2.24	0.44
1:F:358:GLN:O	1:F:360:ARG:NH1	2.50	0.44
1:J:315:PHE:HE1	1:J:350:THR:HG21	1.81	0.44
1:J:358:GLN:O	1:J:360:ARG:NH1	2.50	0.44
1:A:285:LYS:O	1:A:289:GLU:HG3	2.18	0.44
1:C:315:PHE:HE1	1:C:350:THR:HG21	1.82	0.44
1:K:122:LEU:HD23	1:K:223:LEU:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:358:GLN:O	1:D:360:ARG:NH1	2.51	0.44
1:E:171:ASP:CG	1:E:229:ARG:HH22	2.24	0.43
1:F:122:LEU:HD23	1:F:223:LEU:HB3	1.99	0.43
1:G:418:MET:HE2	1:K:376:MET:HE1	1.99	0.43
1:L:141:PRO:O	1:L:144:PHE:HB3	2.17	0.43
1:L:284:GLN:CA	1:L:287:LEU:HD21	2.39	0.43
1:A:122:LEU:HD23	1:A:223:LEU:HB3	2.00	0.43
1:D:315:PHE:HE1	1:D:350:THR:HG21	1.83	0.43
1:E:122:LEU:HD23	1:E:223:LEU:HB3	1.99	0.43
1:I:122:LEU:HD23	1:I:223:LEU:HB3	1.99	0.43
1:J:122:LEU:HD23	1:J:223:LEU:HB3	1.99	0.43
1:K:42:GLN:O	1:K:46:LEU:HG	2.17	0.43
1:L:171:ASP:CG	1:L:229:ARG:HH22	2.24	0.43
1:D:358:GLN:HB3	1:I:358:GLN:CB	2.48	0.43
1:G:171:ASP:CG	1:G:229:ARG:HH22	2.25	0.43
1:J:171:ASP:CG	1:J:229:ARG:HH22	2.24	0.43
1:B:315:PHE:HE1	1:B:350:THR:HG21	1.82	0.43
1:G:169:ASN:HA	1:G:229:ARG:NH1	2.33	0.43
1:I:130:LEU:O	1:I:135:ASN:ND2	2.38	0.43
1:D:90:GLN:HB3	1:D:390:ILE:HD11	1.92	0.43
1:F:130:LEU:O	1:F:135:ASN:ND2	2.38	0.43
1:J:11:THR:HG21	1:K:1:PRO:HG2	2.01	0.43
1:K:130:LEU:O	1:K:135:ASN:ND2	2.38	0.43
1:L:122:LEU:HD23	1:L:223:LEU:HB3	1.99	0.43
1:L:284:GLN:HA	1:L:287:LEU:CG	2.41	0.43
1:C:122:LEU:HD23	1:C:223:LEU:HB3	1.99	0.43
1:G:20:HIS:CE1	1:I:66:GLN:O	2.72	0.43
1:G:47:LEU:HD11	1:I:68:THR:HG21	2.01	0.43
1:H:171:ASP:CG	1:H:229:ARG:HH22	2.24	0.43
1:J:319:ASN:CA	1:J:352:PRO:HG2	2.46	0.43
1:C:283:LYS:O	1:C:287:LEU:HG	2.19	0.42
1:A:169:ASN:HA	1:A:229:ARG:NH1	2.35	0.42
1:A:319:ASN:CA	1:A:352:PRO:HG2	2.46	0.42
1:B:286:LEU:C	1:B:286:LEU:HD13	2.44	0.42
1:D:252:VAL:CG1	1:D:255:ALA:HB2	2.50	0.42
1:K:252:VAL:CG1	1:K:255:ALA:HB2	2.50	0.42
1:A:416:ASN:O	1:H:368:ASN:ND2	2.53	0.42
1:D:144:PHE:CZ	1:D:148:ILE:HD11	2.55	0.42
1:E:202:PRO:HA	1:E:205:TRP:CD2	2.55	0.42
1:E:252:VAL:CG1	1:E:255:ALA:HB2	2.50	0.42
1:J:360:ARG:HG2	1:J:360:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:ASN:HA	1:B:229:ARG:NH1	2.35	0.42
1:C:202:PRO:HA	1:C:205:TRP:CD2	2.55	0.42
1:H:286:LEU:HD21	1:H:392:PHE:CD1	2.55	0.42
1:L:202:PRO:HA	1:L:205:TRP:CD2	2.54	0.42
1:F:202:PRO:HA	1:F:205:TRP:CD2	2.55	0.42
1:I:252:VAL:CG1	1:I:255:ALA:HB2	2.50	0.42
1:L:252:VAL:CG1	1:L:255:ALA:HB2	2.49	0.42
1:D:202:PRO:HA	1:D:205:TRP:CD2	2.55	0.42
1:I:202:PRO:HA	1:I:205:TRP:CD2	2.54	0.42
1:G:360:ARG:HG2	1:G:360:ARG:NH1	2.34	0.42
1:K:272:LEU:C	1:K:274:PHE:N	2.76	0.42
1:A:360:ARG:HG2	1:A:360:ARG:NH1	2.34	0.42
1:B:202:PRO:HA	1:B:205:TRP:CD2	2.55	0.42
1:F:323:GLU:HB2	1:F:357:LEU:HD11	2.02	0.42
1:J:144:PHE:CZ	1:J:148:ILE:HD11	2.55	0.42
1:K:169:ASN:HA	1:K:229:ARG:NH1	2.35	0.42
1:K:202:PRO:HA	1:K:205:TRP:CD2	2.55	0.42
1:A:202:PRO:HA	1:A:205:TRP:CD2	2.54	0.41
1:A:323:GLU:HB2	1:A:357:LEU:HD11	2.02	0.41
1:G:144:PHE:CZ	1:G:148:ILE:HD11	2.55	0.41
1:H:144:PHE:CZ	1:H:148:ILE:HD11	2.55	0.41
1:J:169:ASN:HA	1:J:229:ARG:NH1	2.35	0.41
1:K:144:PHE:CZ	1:K:148:ILE:HD11	2.55	0.41
1:B:144:PHE:CZ	1:B:148:ILE:HD11	2.55	0.41
1:C:169:ASN:HA	1:C:229:ARG:NH1	2.35	0.41
1:D:169:ASN:HA	1:D:229:ARG:NH1	2.35	0.41
1:G:252:VAL:CG1	1:G:255:ALA:HB2	2.49	0.41
1:I:169:ASN:HA	1:I:229:ARG:NH1	2.35	0.41
1:J:202:PRO:HA	1:J:205:TRP:CD2	2.54	0.41
1:A:155:ASP:OD2	1:B:179:SER:OG	2.35	0.41
1:F:169:ASN:HA	1:F:229:ARG:NH1	2.35	0.41
1:H:11:THR:HG23	1:I:19:ASP:HB3	2.02	0.41
1:A:144:PHE:CZ	1:A:148:ILE:HD11	2.55	0.41
1:G:202:PRO:HA	1:G:205:TRP:CD2	2.55	0.41
1:G:323:GLU:HB2	1:G:357:LEU:HD11	2.02	0.41
1:I:144:PHE:CZ	1:I:148:ILE:HD11	2.56	0.41
1:J:323:GLU:HB2	1:J:357:LEU:HD11	2.02	0.41
1:K:52:ARG:NH1	1:K:390:ILE:HD11	2.36	0.41
1:L:297:ILE:CD1	1:L:437:ILE:HB	2.51	0.41
1:B:177:ARG:HD3	1:B:262:THR:O	2.21	0.41
1:C:297:ILE:CD1	1:C:437:ILE:HB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:202:PRO:HA	1:H:205:TRP:CD2	2.54	0.41
1:K:263:HIS:O	1:K:266:GLU:HB2	2.21	0.41
1:C:94:LEU:HG	1:C:116:ILE:HD12	2.03	0.41
1:H:94:LEU:HG	1:H:116:ILE:HD12	2.03	0.41
1:J:252:VAL:CG1	1:J:255:ALA:HB2	2.49	0.41
1:K:94:LEU:HG	1:K:116:ILE:HD12	2.02	0.41
1:K:286:LEU:C	1:K:286:LEU:CD1	2.88	0.41
1:L:169:ASN:HA	1:L:229:ARG:NH1	2.35	0.41
1:H:169:ASN:HA	1:H:229:ARG:NH1	2.35	0.41
1:I:177:ARG:HD3	1:I:262:THR:O	2.21	0.41
1:I:297:ILE:CD1	1:I:437:ILE:HB	2.51	0.41
1:J:360:ARG:HH11	1:J:360:ARG:CG	2.34	0.41
1:A:94:LEU:HG	1:A:116:ILE:HD12	2.03	0.41
1:D:130:LEU:HD12	1:D:130:LEU:HA	1.95	0.41
1:E:94:LEU:HG	1:E:116:ILE:HD12	2.03	0.41
1:E:144:PHE:CZ	1:E:148:ILE:HD11	2.55	0.41
1:E:169:ASN:HA	1:E:229:ARG:NH1	2.35	0.41
1:G:179:SER:OG	1:I:155:ASP:OD2	2.32	0.41
1:I:286:LEU:HD13	1:I:290:VAL:CG2	2.51	0.41
1:A:177:ARG:HD3	1:A:262:THR:O	2.21	0.41
1:A:361:ARG:HD2	1:H:417:ARG:NH1	2.36	0.41
1:C:144:PHE:CZ	1:C:148:ILE:HD11	2.55	0.41
1:D:286:LEU:HD21	1:D:424:GLU:CG	2.49	0.41
1:E:360:ARG:HG2	1:E:360:ARG:NH1	2.34	0.41
1:G:380:VAL:HG21	1:K:380:VAL:HG21	2.03	0.41
1:H:177:ARG:HD3	1:H:262:THR:O	2.21	0.41
1:L:144:PHE:CZ	1:L:148:ILE:HD11	2.55	0.41
1:A:360:ARG:HH11	1:A:360:ARG:CG	2.34	0.41
1:E:323:GLU:HB2	1:E:357:LEU:HD11	2.02	0.41
1:J:94:LEU:HG	1:J:116:ILE:HD12	2.03	0.41
1:D:323:GLU:HB2	1:D:357:LEU:HD11	2.02	0.40
1:F:144:PHE:CZ	1:F:148:ILE:HD11	2.55	0.40
1:H:297:ILE:CD1	1:H:437:ILE:HB	2.51	0.40
1:K:52:ARG:CZ	1:K:390:ILE:CD1	3.00	0.40
1:K:177:ARG:HD3	1:K:262:THR:O	2.21	0.40
1:K:263:HIS:O	1:K:266:GLU:N	2.54	0.40
1:A:358:GLN:OE1	1:H:361:ARG:CB	2.69	0.40
1:C:90:GLN:NE2	1:C:90:GLN:HA	2.37	0.40
1:J:177:ARG:HD3	1:J:262:THR:O	2.21	0.40
1:L:32:PHE:HA	1:L:33:PRO:HA	1.95	0.40
1:L:177:ARG:HD3	1:L:262:THR:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:LEU:HG	1:B:116:ILE:HD12	2.03	0.40
1:C:130:LEU:HD12	1:C:130:LEU:HA	1.95	0.40
1:D:11:THR:HB	1:E:1:PRO:HG3	2.03	0.40
1:E:177:ARG:HD3	1:E:262:THR:O	2.21	0.40
1:G:283:LYS:O	1:G:287:LEU:HB2	2.22	0.40
1:L:286:LEU:HD22	1:L:427:PHE:CD2	2.56	0.40
1:A:418:MET:HE2	1:H:376:MET:CE	2.52	0.40
1:C:177:ARG:HD3	1:C:262:THR:O	2.21	0.40
1:D:360:ARG:HG2	1:D:360:ARG:NH1	2.34	0.40
1:F:94:LEU:HG	1:F:116:ILE:HD12	2.03	0.40
1:F:177:ARG:HD3	1:F:262:THR:O	2.21	0.40
1:F:360:ARG:HH11	1:F:360:ARG:CG	2.34	0.40
1:F:418:MET:HE2	1:L:376:MET:HE1	2.03	0.40
1:J:90:GLN:NE2	1:J:90:GLN:HA	2.37	0.40
1:K:297:ILE:CD1	1:K:437:ILE:HB	2.51	0.40
1:E:90:GLN:NE2	1:E:90:GLN:HA	2.37	0.40
1:E:287:LEU:HD13	1:E:315:PHE:CA	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	439/456 (96%)	428 (98%)	10 (2%)	1 (0%)	43	78
1	B	439/456 (96%)	426 (97%)	12 (3%)	1 (0%)	43	78
1	C	439/456 (96%)	426 (97%)	12 (3%)	1 (0%)	43	78
1	D	439/456 (96%)	427 (97%)	11 (2%)	1 (0%)	43	78
1	E	439/456 (96%)	428 (98%)	10 (2%)	1 (0%)	43	78
1	F	439/456 (96%)	427 (97%)	11 (2%)	1 (0%)	43	78
1	G	439/456 (96%)	428 (98%)	10 (2%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	439/456 (96%)	426 (97%)	12 (3%)	1 (0%)	43	78
1	I	439/456 (96%)	425 (97%)	13 (3%)	1 (0%)	43	78
1	J	439/456 (96%)	427 (97%)	11 (2%)	1 (0%)	43	78
1	K	439/456 (96%)	424 (97%)	14 (3%)	1 (0%)	43	78
1	L	439/456 (96%)	426 (97%)	12 (3%)	1 (0%)	43	78
All	All	5268/5472 (96%)	5118 (97%)	138 (3%)	12 (0%)	43	78

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	334	ILE
1	B	334	ILE
1	D	334	ILE
1	F	334	ILE
1	G	334	ILE
1	H	334	ILE
1	I	334	ILE
1	J	334	ILE
1	K	334	ILE
1	L	334	ILE
1	C	334	ILE
1	E	334	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	348/369 (94%)	336 (97%)	12 (3%)	32	54
1	B	348/369 (94%)	336 (97%)	12 (3%)	32	54
1	C	348/369 (94%)	335 (96%)	13 (4%)	30	51
1	D	348/369 (94%)	337 (97%)	11 (3%)	34	56
1	E	348/369 (94%)	336 (97%)	12 (3%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	348/369 (94%)	336 (97%)	12 (3%)	32	54
1	G	348/369 (94%)	336 (97%)	12 (3%)	32	54
1	H	348/369 (94%)	335 (96%)	13 (4%)	30	51
1	I	348/369 (94%)	335 (96%)	13 (4%)	30	51
1	J	348/369 (94%)	336 (97%)	12 (3%)	32	54
1	K	348/369 (94%)	335 (96%)	13 (4%)	30	51
1	L	348/369 (94%)	336 (97%)	12 (3%)	32	54
All	All	4176/4428 (94%)	4029 (96%)	147 (4%)	32	53

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	VAL
1	A	165	ASN
1	A	234	GLU
1	A	239	VAL
1	A	259	LEU
1	A	286	LEU
1	A	303	LEU
1	A	325	LEU
1	A	338	LEU
1	A	351	VAL
1	A	353	SER
1	A	396	LYS
1	B	108	VAL
1	B	165	ASN
1	B	234	GLU
1	B	239	VAL
1	B	259	LEU
1	B	325	LEU
1	B	338	LEU
1	B	351	VAL
1	B	384	ARG
1	B	387	LYS
1	B	421	VAL
1	B	433	THR
1	C	108	VAL
1	C	165	ASN
1	C	234	GLU
1	C	239	VAL

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Mol	Chain	Res	Type
1	C	259	LEU
1	C	286	LEU
1	C	325	LEU
1	C	338	LEU
1	C	351	VAL
1	C	384	ARG
1	C	387	LYS
1	C	421	VAL
1	C	433	THR
1	D	165	ASN
1	D	234	GLU
1	D	239	VAL
1	D	259	LEU
1	D	286	LEU
1	D	303	LEU
1	D	325	LEU
1	D	338	LEU
1	D	351	VAL
1	D	353	SER
1	D	396	LYS
1	E	108	VAL
1	E	165	ASN
1	E	234	GLU
1	E	239	VAL
1	E	259	LEU
1	E	286	LEU
1	E	303	LEU
1	E	325	LEU
1	E	338	LEU
1	E	351	VAL
1	E	353	SER
1	E	396	LYS
1	F	108	VAL
1	F	165	ASN
1	F	234	GLU
1	F	239	VAL
1	F	259	LEU
1	F	286	LEU
1	F	303	LEU
1	F	325	LEU
1	F	338	LEU
1	F	351	VAL

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Mol	Chain	Res	Type
1	F	353	SER
1	F	396	LYS
1	G	108	VAL
1	G	165	ASN
1	G	234	GLU
1	G	239	VAL
1	G	259	LEU
1	G	286	LEU
1	G	303	LEU
1	G	325	LEU
1	G	338	LEU
1	G	351	VAL
1	G	353	SER
1	G	396	LYS
1	H	108	VAL
1	H	165	ASN
1	H	234	GLU
1	H	239	VAL
1	H	259	LEU
1	H	286	LEU
1	H	325	LEU
1	H	338	LEU
1	H	351	VAL
1	H	384	ARG
1	H	387	LYS
1	H	421	VAL
1	H	433	THR
1	I	108	VAL
1	I	165	ASN
1	I	234	GLU
1	I	239	VAL
1	I	259	LEU
1	I	286	LEU
1	I	325	LEU
1	I	338	LEU
1	I	351	VAL
1	I	384	ARG
1	I	387	LYS
1	I	421	VAL
1	I	433	THR
1	J	108	VAL
1	J	165	ASN

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Mol	Chain	Res	Type
1	J	234	GLU
1	J	239	VAL
1	J	259	LEU
1	J	286	LEU
1	J	303	LEU
1	J	325	LEU
1	J	338	LEU
1	J	351	VAL
1	J	353	SER
1	J	396	LYS
1	K	108	VAL
1	K	165	ASN
1	K	234	GLU
1	K	239	VAL
1	K	259	LEU
1	K	275	LEU
1	K	325	LEU
1	K	338	LEU
1	K	351	VAL
1	K	384	ARG
1	K	387	LYS
1	K	421	VAL
1	K	433	THR
1	L	108	VAL
1	L	165	ASN
1	L	234	GLU
1	L	239	VAL
1	L	259	LEU
1	L	325	LEU
1	L	338	LEU
1	L	351	VAL
1	L	384	ARG
1	L	387	LYS
1	L	421	VAL
1	L	433	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	GLN
1	A	173	ASN
1	A	188	ASN

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Mol	Chain	Res	Type
1	A	319	ASN
1	B	90	GLN
1	B	173	ASN
1	B	188	ASN
1	B	375	ASN
1	C	90	GLN
1	C	173	ASN
1	C	188	ASN
1	C	375	ASN
1	D	173	ASN
1	D	188	ASN
1	D	319	ASN
1	E	90	GLN
1	E	173	ASN
1	E	188	ASN
1	E	319	ASN
1	F	90	GLN
1	F	173	ASN
1	F	185	ASN
1	F	188	ASN
1	F	319	ASN
1	F	374	ASN
1	G	90	GLN
1	G	173	ASN
1	G	188	ASN
1	G	374	ASN
1	H	90	GLN
1	H	173	ASN
1	H	188	ASN
1	H	375	ASN
1	I	90	GLN
1	I	173	ASN
1	I	188	ASN
1	I	375	ASN
1	J	90	GLN
1	J	173	ASN
1	J	188	ASN
1	K	90	GLN
1	K	173	ASN
1	K	188	ASN
1	K	375	ASN
1	L	90	GLN

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Mol	Chain	Res	Type
1	L	173	ASN
1	L	188	ASN
1	L	375	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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	441/456 (96%)	-0.17	6 (1%) 73 62	120, 209, 300, 386	0
1	B	441/456 (96%)	-0.09	14 (3%) 50 45	93, 191, 267, 346	0
1	C	441/456 (96%)	0.08	23 (5%) 33 35	114, 196, 263, 325	0
1	D	441/456 (96%)	-0.08	9 (2%) 65 56	110, 223, 370, 443	0
1	E	441/456 (96%)	0.02	22 (4%) 34 35	122, 196, 275, 336	0
1	F	441/456 (96%)	-0.13	17 (3%) 43 42	117, 208, 305, 393	0
1	G	441/456 (96%)	-0.18	4 (0%) 81 70	142, 284, 420, 498	0
1	H	441/456 (96%)	-0.09	12 (2%) 56 48	130, 228, 310, 365	0
1	I	441/456 (96%)	-0.28	6 (1%) 73 62	179, 269, 364, 453	0
1	J	441/456 (96%)	-0.27	7 (1%) 70 59	127, 225, 323, 448	0
1	K	441/456 (96%)	-0.29	3 (0%) 84 74	194, 329, 412, 474	0
1	L	441/456 (96%)	0.00	18 (4%) 41 41	179, 305, 412, 500	0
All	All	5292/5472 (96%)	-0.12	141 (2%) 56 48	93, 233, 368, 500	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	302	PRO	6.7
1	F	224	HIS	6.7
1	C	80	LEU	6.5
1	C	56	TYR	6.2
1	C	103	GLU	5.9
1	F	237	ALA	5.7
1	L	124	SER	5.7
1	F	105	ALA	5.7
1	B	56	TYR	5.7
1	H	260	LEU	5.1
1	B	83	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
1	L	123	ALA	5.0
1	E	411	MET	4.8
1	G	121	PHE	4.6
1	H	390	ILE	4.5
1	C	102	GLY	4.5
1	E	414	ILE	4.4
1	E	223	LEU	4.4
1	G	120	ALA	4.4
1	C	77	ALA	4.3
1	J	419	GLY	4.0
1	L	120	ALA	4.0
1	I	418	MET	3.9
1	I	413	LEU	3.8
1	E	222	ILE	3.7
1	F	125	LEU	3.7
1	F	126	GLU	3.6
1	C	73	TYR	3.5
1	A	34	LEU	3.5
1	L	101	THR	3.5
1	J	418	MET	3.4
1	D	15	LEU	3.4
1	C	83	VAL	3.4
1	L	294	VAL	3.3
1	L	121	PHE	3.3
1	E	345	PHE	3.3
1	C	84	LEU	3.3
1	C	125	LEU	3.2
1	L	126	GLU	3.2
1	E	56	TYR	3.2
1	H	105	ALA	3.1
1	J	420	ALA	3.1
1	B	339	THR	3.1
1	L	98	SER	3.1
1	K	95	VAL	3.0
1	A	211	ALA	3.0
1	E	419	GLY	3.0
1	H	95	VAL	3.0
1	C	260	LEU	2.9
1	C	153	LYS	2.9
1	H	46	LEU	2.9
1	A	56	TYR	2.9
1	K	359	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	L	122	LEU	2.9
1	F	124	SER	2.9
1	D	56	TYR	2.9
1	F	223	LEU	2.9
1	A	267	VAL	2.8
1	E	237	ALA	2.8
1	C	107	TYR	2.7
1	E	342	ILE	2.7
1	L	224	HIS	2.7
1	C	294	VAL	2.7
1	B	29	ILE	2.7
1	D	279	GLN	2.7
1	F	179	SER	2.7
1	J	226	THR	2.6
1	C	33	PRO	2.6
1	J	54	ILE	2.6
1	E	294	VAL	2.6
1	L	95	VAL	2.6
1	E	415	TYR	2.6
1	C	415	TYR	2.6
1	L	209	PHE	2.5
1	J	303	LEU	2.5
1	B	84	LEU	2.5
1	G	56	TYR	2.5
1	H	122	LEU	2.5
1	E	224	HIS	2.5
1	A	404	ALA	2.5
1	D	65	SER	2.5
1	B	358	GLN	2.5
1	E	298	ILE	2.5
1	I	83	VAL	2.4
1	B	335	LEU	2.4
1	L	54	ILE	2.4
1	D	376	MET	2.4
1	B	376	MET	2.4
1	C	348	THR	2.4
1	E	17	TYR	2.4
1	H	223	LEU	2.4
1	C	205	TRP	2.4
1	F	231	LEU	2.3
1	E	63	GLN	2.3
1	B	329	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	125	LEU	2.3
1	F	240	PHE	2.3
1	K	96	GLY	2.3
1	F	77	ALA	2.3
1	C	94	LEU	2.3
1	E	408	ALA	2.3
1	B	357	LEU	2.3
1	F	343	LEU	2.3
1	F	342	ILE	2.3
1	I	416	ASN	2.2
1	I	380	VAL	2.2
1	G	240	PHE	2.2
1	D	153	LYS	2.2
1	E	417	ARG	2.2
1	C	175	GLY	2.2
1	C	42	GLN	2.2
1	J	183	VAL	2.2
1	D	24	THR	2.2
1	I	226	THR	2.2
1	C	27	VAL	2.2
1	F	108	VAL	2.2
1	B	418	MET	2.2
1	F	195	PHE	2.1
1	E	367	LEU	2.1
1	A	252	VAL	2.1
1	H	104	VAL	2.1
1	L	223	LEU	2.1
1	L	246	SER	2.1
1	B	316	ALA	2.1
1	B	383	TYR	2.1
1	L	96	GLY	2.1
1	E	205	TRP	2.1
1	H	224	HIS	2.1
1	L	292	THR	2.1
1	E	343	LEU	2.1
1	H	42	GLN	2.1
1	B	343	LEU	2.1
1	E	18	GLU	2.0
1	E	24	THR	2.0
1	F	104	VAL	2.0
1	F	433	THR	2.0
1	H	83	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	360	ARG	2.0
1	C	32	PHE	2.0
1	C	427	PHE	2.0
1	D	144	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.