



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:15 AM UTC

PDB ID : 6UPN / pdb_00006upn
EMDB ID : EMD-20842
Title : Endophilin B1 helical scaffold
Authors : Bhatt, V.S.; Sundborger-Lunna, A.C.
Deposited on : 2019-10-17
Resolution : 10.00 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

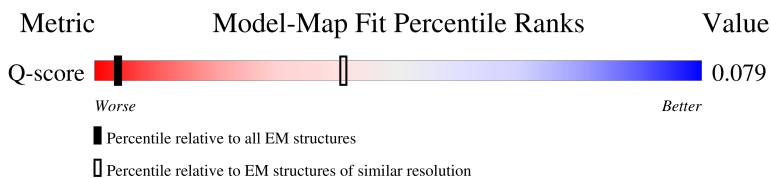
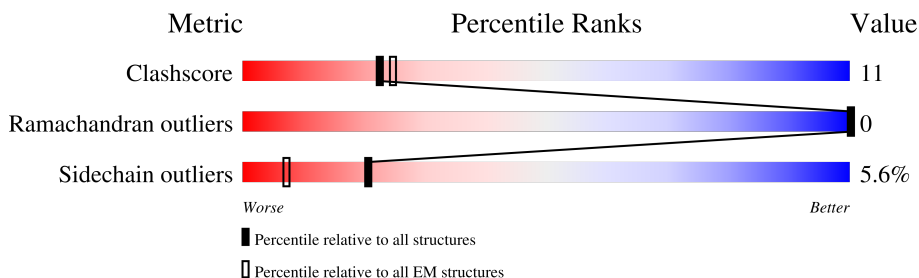
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.00 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.



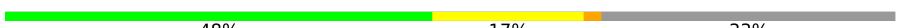
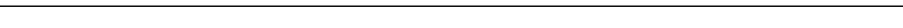
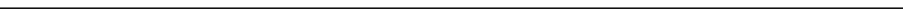
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	147 (9.50 - 10.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	365	
1	B	365	
1	C	365	
1	D	365	

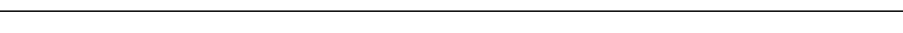
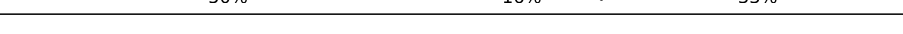
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Mol	Chain	Length	Quality of chain
1	E	365	
1	F	365	
1	G	365	
1	H	365	
1	I	365	
1	J	365	
1	K	365	
1	L	365	
1	M	365	
1	N	365	
1	O	365	
1	P	365	
1	Q	365	
1	R	365	
1	S	365	
1	T	365	
1	V	365	
1	W	365	
1	X	365	
1	Y	365	
1	a	365	
1	b	365	
1	c	365	
1	d	365	
1	e	365	

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Mol	Chain	Length	Quality of chain
1	f	365	
1	g	365	
1	h	365	
1	i	365	
1	j	365	
1	k	365	
1	l	365	
1	m	365	
1	n	365	
1	o	365	
1	p	365	
1	q	365	
1	r	365	
1	s	365	
1	t	365	
1	v	365	
1	w	365	
1	x	365	
1	y	365	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 94224 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Endophilin-B1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	B	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	C	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	D	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	E	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	F	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	G	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	H	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	I	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	J	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	K	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	L	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	M	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	N	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	O	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	P	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	Q	245	Total 1963	C 1234	N 342	O 379	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	S	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	T	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	V	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	W	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	X	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	Y	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	a	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	b	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	c	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	d	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	e	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	f	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	g	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	h	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	i	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	j	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	k	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	l	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	m	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	n	245	Total 1963	C 1234	N 342	O 379	S 8	0	0

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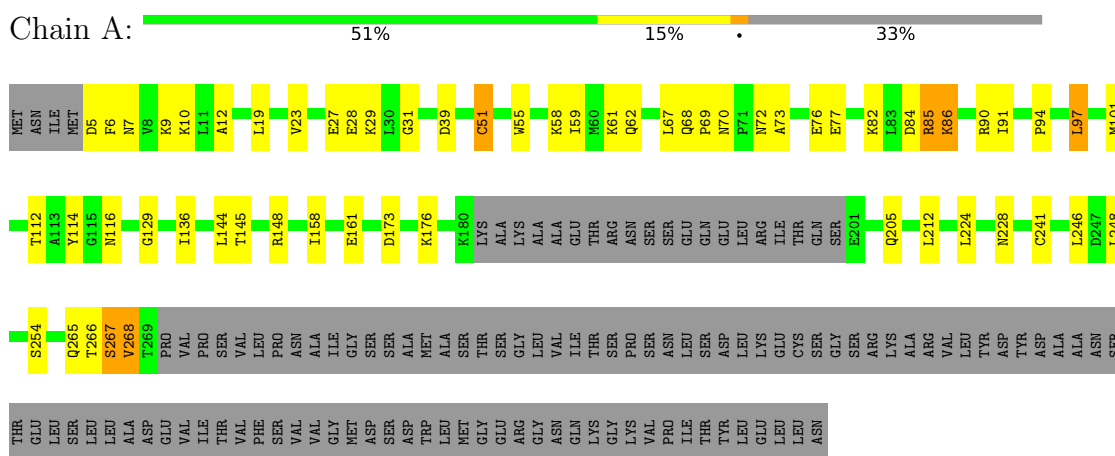
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	o	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	p	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	q	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	r	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	s	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	t	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	v	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	w	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	x	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	y	245	Total 1963	C 1234	N 342	O 379	S 8	0	0

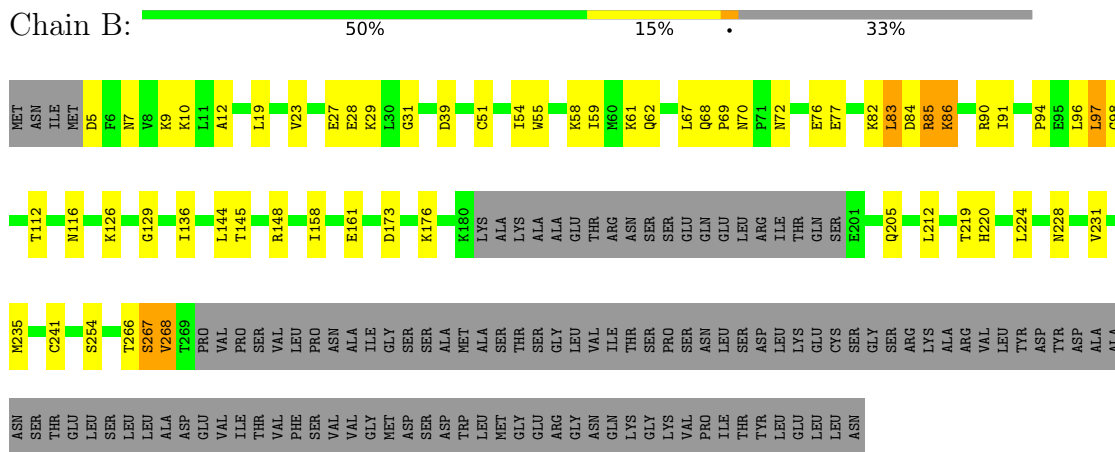
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Endophilin-B1

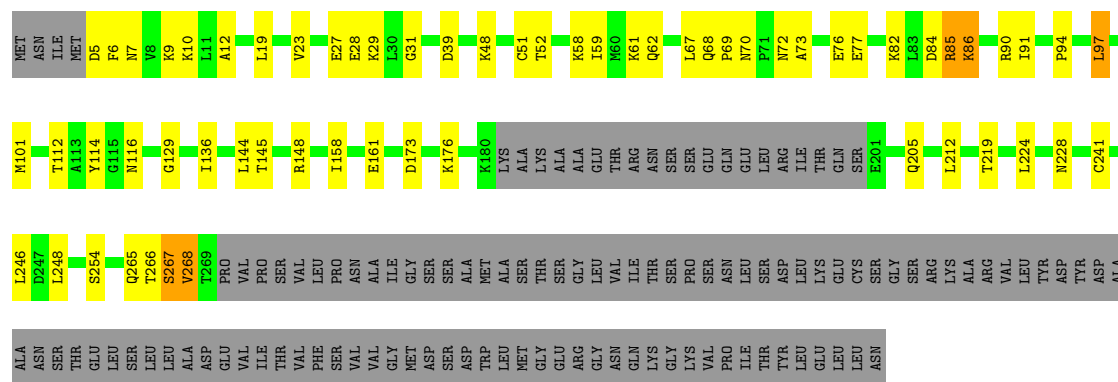


• Molecule 1: Endophilin-B1



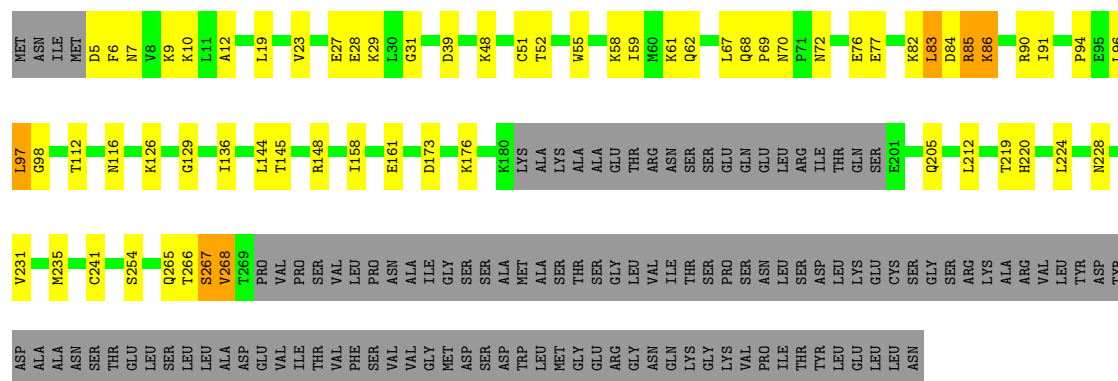
• Molecule 1: Endophilin-B1





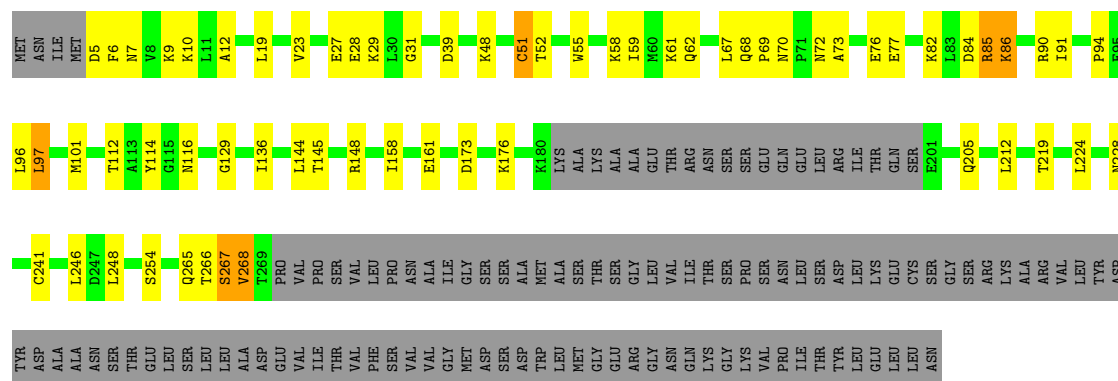
• Molecule 1: Endophilin-B1

Chain D: 49% 16% 33%



• Molecule 1: Endophilin-B1

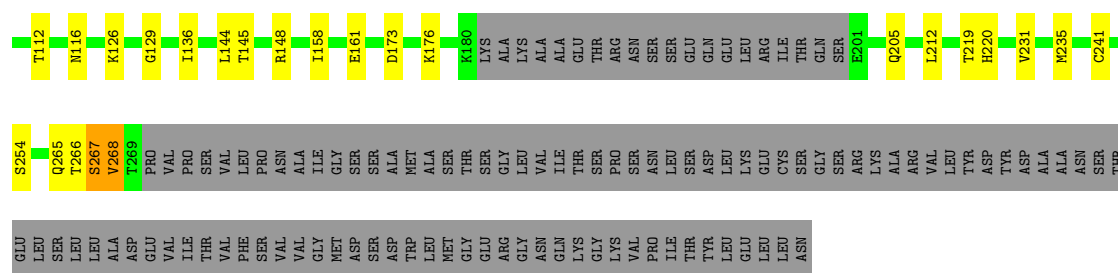
Chain E: 50% 16% 33%



• Molecule 1: Endophilin-B1

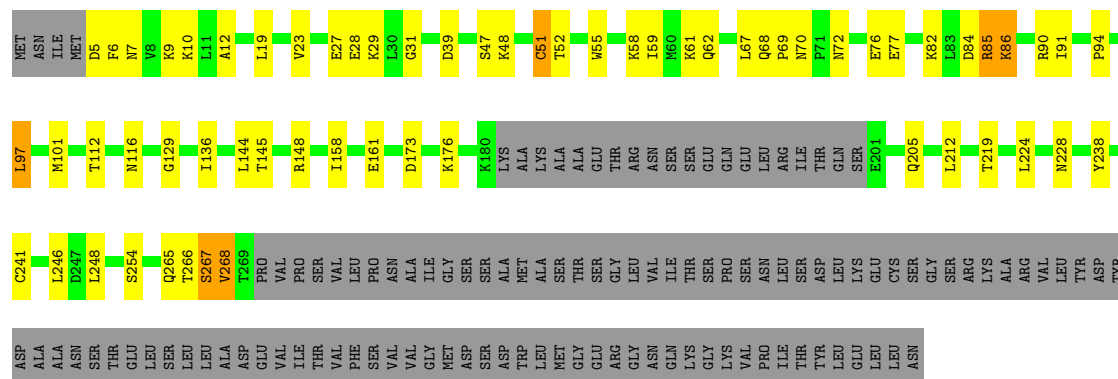
Chain F: 50% 15% 33%





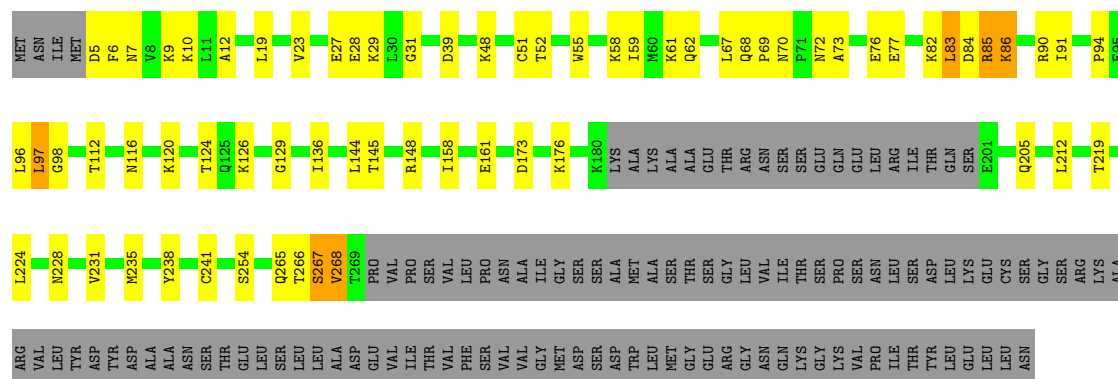
• Molecule 1: Endophilin-B1

Chain G: 50% 16% 33%



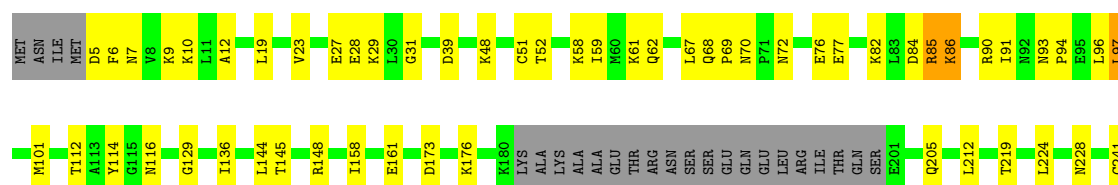
• Molecule 1: Endophilin-B1

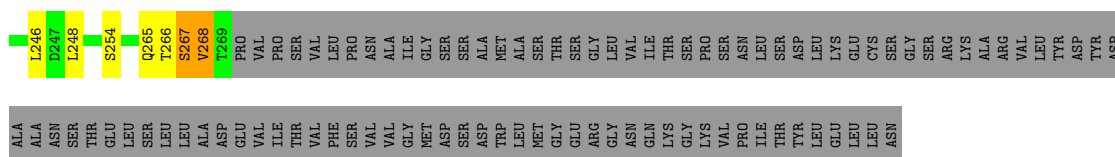
Chain H: 48% 17% 33%



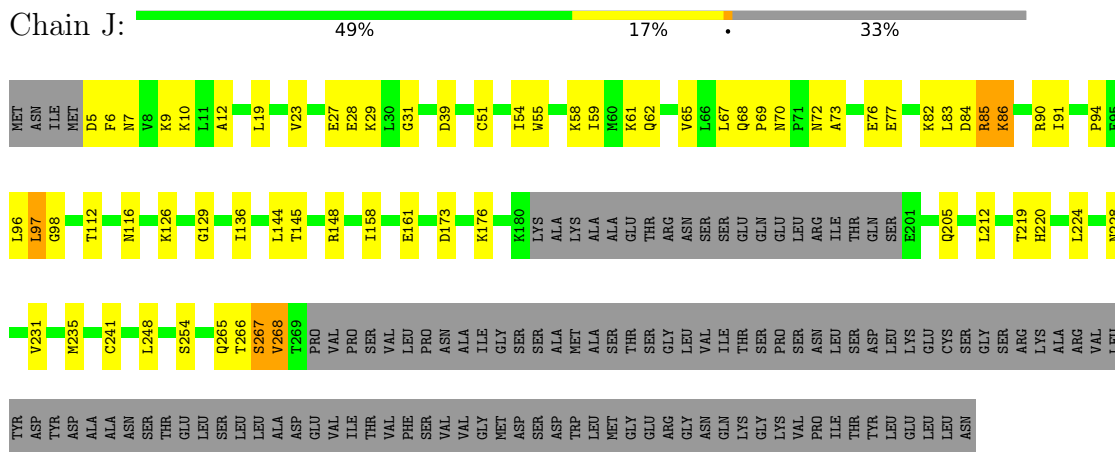
• Molecule 1: Endophilin-B1

Chain I: 50% 16% 33%

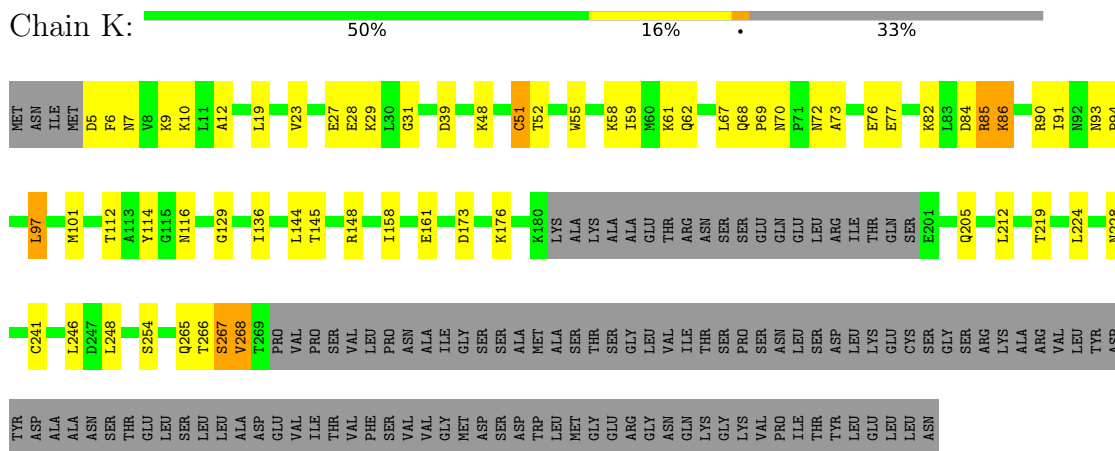




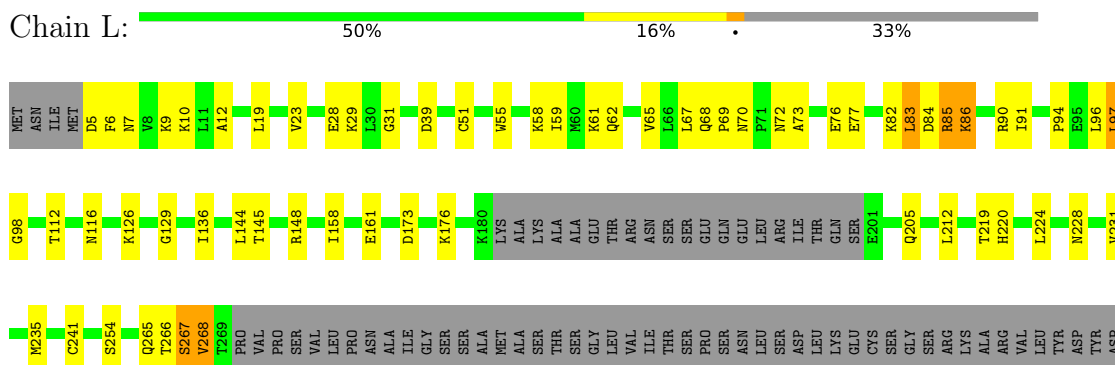
- Molecule 1: Endophilin-B1



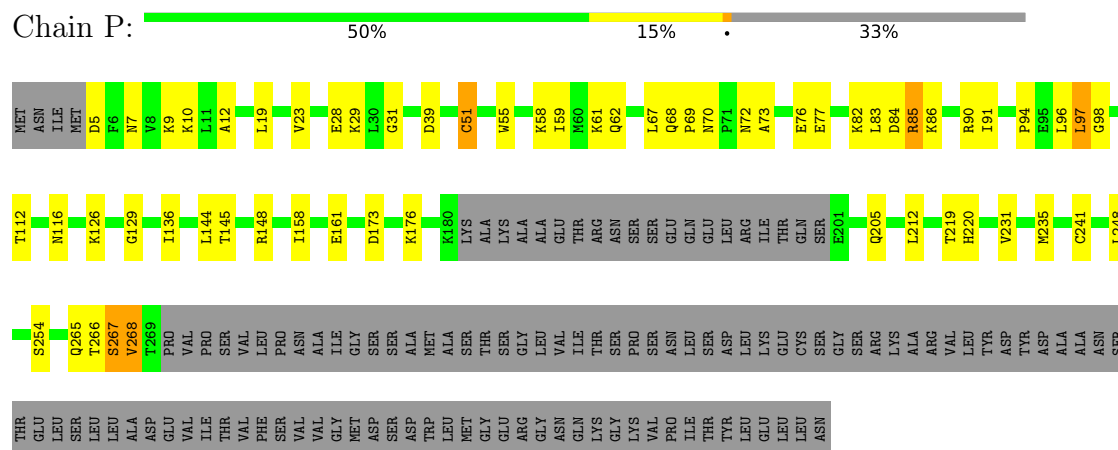
- Molecule 1: Endophilin-B1



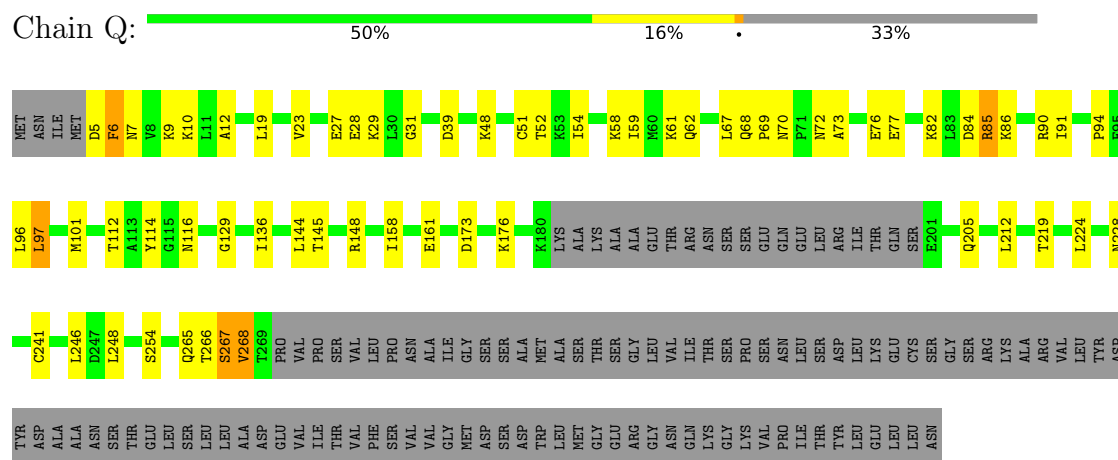
- Molecule 1: Endophilin-B1



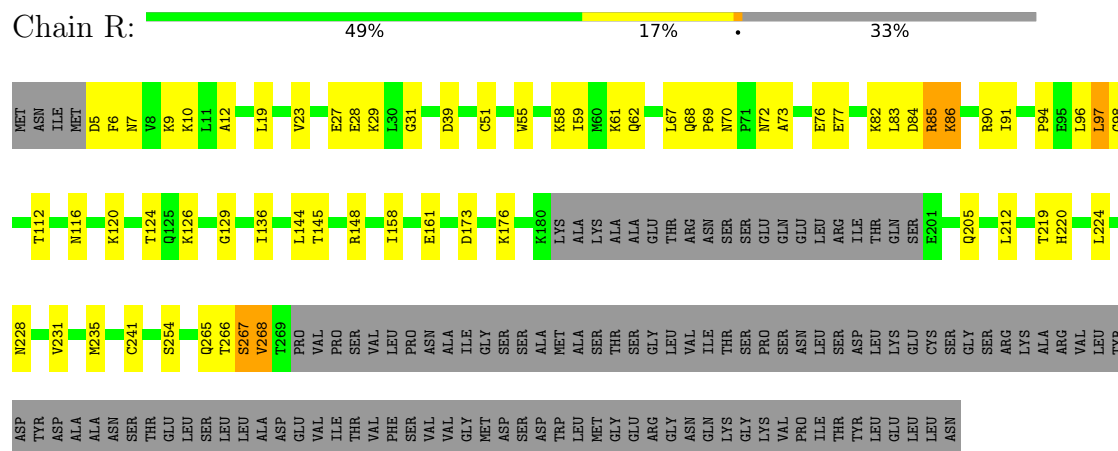
- Molecule 1: Endophilin-B1



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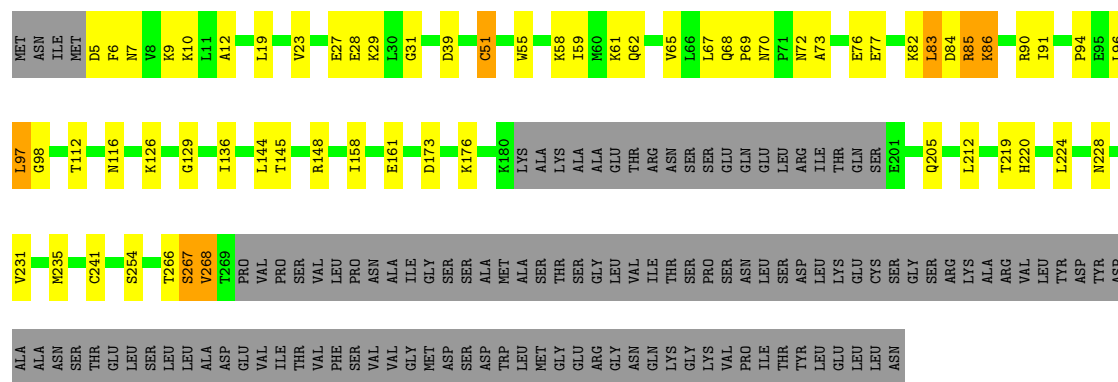


- Molecule 1: Endophilin-B1

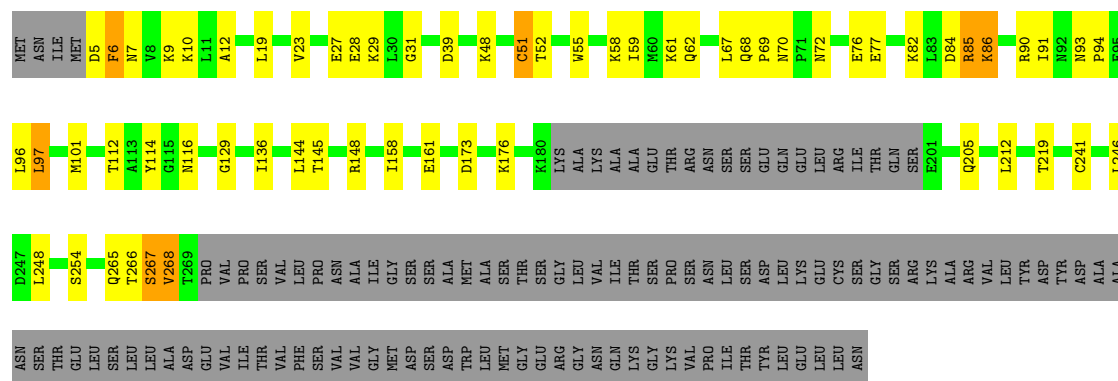
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THR		A113	ASN
GLU	S254	Y114	ILE
LEU		G115	MET
SER	Q265	N116	D5
LEU	T266	G129	F6
LEU	S267		N7
ALA	V268		V8
ASP	T269	I136	K9
GLU	PRO		K10
VAL	VAL	L144	I11
ILE	PRO	T145	A12
THR	SER		
VAL	VAL	R148	L19
PHE	LEU		
SER	PRO	I158	V23
VAL	ASN		
VAL	ALA	E161	E28
GLY	ILE		K29
MET	GLY	D173	L30
ASP	SER		G31
SER	SER	K176	
ASP	ALA		D39
TRP	MET	K180	
LEU	ALA	LYS	K48
MET	SER	ALA	
GLY	THR	LYS	C51
GLU	GLU	ALA	T52
ARG	GLY	ALA	
GLY	LEU	GLU	K58
ASN	VAL	THR	I59
GLN	ILE	ARG	M60
LYS	THR	ASN	K61
GLY	SER	SER	Q62
LYS	PRO	SER	
VAL	VAL	GLU	L67
PRO	PRO	GLN	Q68
ILE	LEU	GLU	P69
THR	SER	LEU	N70
TYR	ASP	ARG	P71
LEU	LEU	ILE	N72
GLU	LYS	THR	
LEU	LEU	GLN	E76
LEU	CYS	SER	E77
ASN	SER	E201	
	GLY		K82
	SER	Q205	L83
	ARG		D84
	LYS	L212	R85
	ALA		K86
	ARG	T219	
	VAL	L224	R90
	LEU		I91
	TYR		
	ASP	N228	P94
	TYR		
	ASP	C241	L97
	ALA		
	ALA	L246	M101
	ASN	S247	

TYR	M235	G98	MET
ASP			ASN
ALA	C241	T112	ILE
ASN		N116	MET
SER	L248		D5
THR	S254	K126	F6
GLU		G129	N7
LEU			V8
SER	Q265		K9
LEU	T266	I136	K10
LEU	S267		I11
ALA	V268	L144	A12
ASP	T269	T145	
GLU	PRO	R148	L19
VAL	VAL		V23
ILE	PRO		
THR	SER	I158	E28
VAL	VAL	E161	K29
PHE	LEU		L30
SER	PRO		G31
VAL	ASN	D173	
VAL	ALA		D39
GLY	ILE	K176	
MET	GLY		S47
ASP	SER	L180	
SER	SER	LYS	C51
ASP	ALA	ALA	
TRP	MET	LYS	M55
LEU	ALA	ALA	
MET	SER	ALA	K68
GLY	THR	GLU	I59
GLU	SER	THR	M60
ARG	GLY	ARG	K61
GLY	LEU	ASN	Q62
ASN	VAL	SER	
GLN	ILE	SER	L67
LYS	THR	GLU	Q68
GLY	SER	GLN	P69
LYS	PRO	LEU	N70
VAL	SER	LEU	P71
PRO	ASN	ARG	N72
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THR	SER	THR	
TYR	ASP	GLN	E76
LEU	LEU	SER	E77
GLU	LYS	E201	
LEU	GLY		
LEU	CYS	Q205	K82
ASN	SER		L83
	GLY	L212	D84
	SER		R85
	ARG	T219	K86
	LYS	H220	
	ALA		R90
	ARG	L224	I91
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	LEU	N228	E95
	TYR		L96
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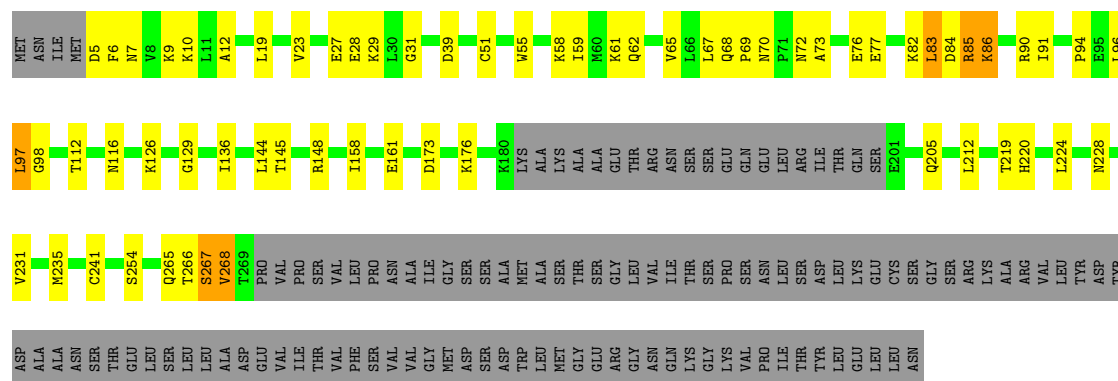
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SER	L248	T112	ASN
THR	S254	T113	ILE
GLU		Y114	MET
LEU		N116	D5
SER		G129	F6
LEU	Q265	T136	N7
LEU	T266	T144	W8
LEU	S267	T145	K9
ASP	V268	R148	K10
ASP	T269	I159	I11
GLU	PRO	E161	A12
VAL	VAL	D173	L19
VAL	PRO	K176	V23
ILE	PRO	X180	E27
THR	SER	LYS	E28
THR	SER	ALA	K29
THR	SER	LYS	K29
PHE	VAL	ALA	L30
SER	VAL	GLY	G31
SER	VAL	SER	D39
VAL	VAL	ALA	S47
VAL	VAL	THR	K48
GLY	ILE	SER	C51
MET	GLY	GLY	T52
ASP	SER	LEU	K58
SER	SER	VAL	159
SER	THR	ILE	N60
ASP	THR	THR	K61
SER	SER	ARG	Q62
ASP	PRO	ASN	L67
VAL	SER	SER	Q68
PRO	ASN	SER	P69
ILE	LEU	GLU	N70
THR	SER	GLN	P71
TYR	ASP	GLU	N72
LEU	LEU	LEU	E76
GLU	LYS	ARG	E77
LEU	GLU	ILE	
LEU	CYS	THR	
ASN	SER	GLN	
	GLY	SER	K82
	SER	E201	L83
	ARG		D84
	LYS	Q205	R85
	ALA		K86
	ARG	L212	
	VAL		R90
	LEU	L224	191
	TYR		N92
	ASP	N228	N93
	TYR		P94
	ASP	C241	
	ALA		L97
	ALA	T246	



• Molecule 1: Endophilin-B1

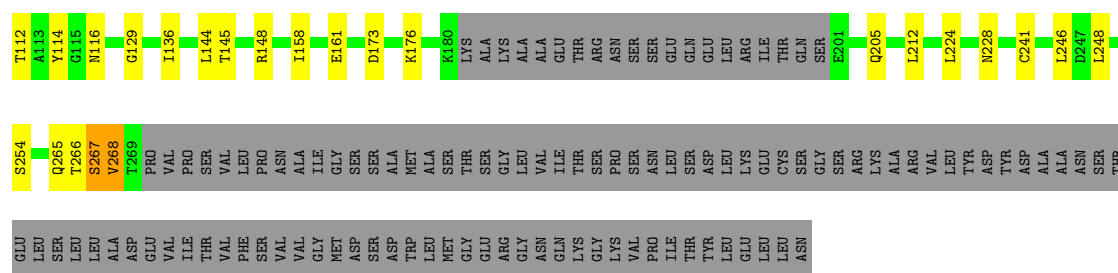


• Molecule 1: Endophilin-B1



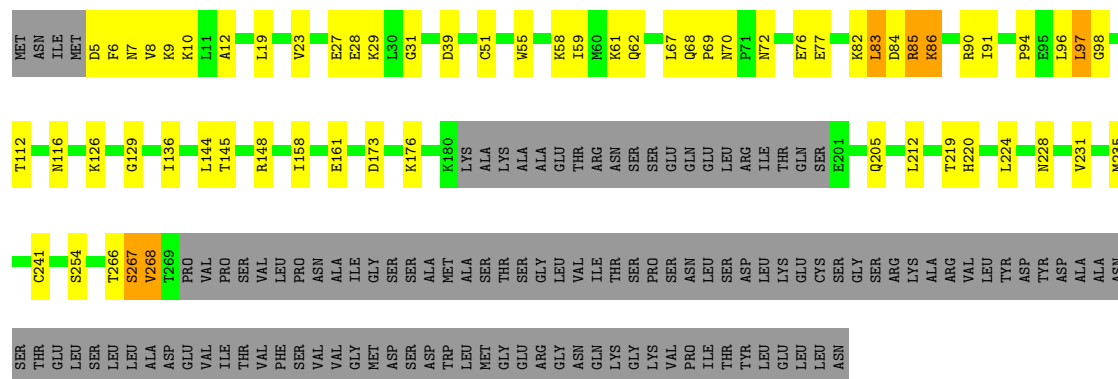
• Molecule 1: Endophilin-B1





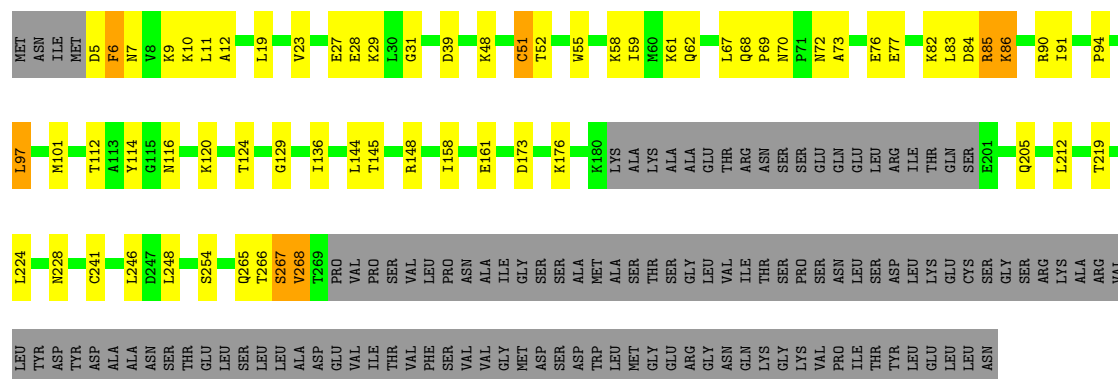
• Molecule 1: Endophilin-B1

Chain b: 50% 16% 33%



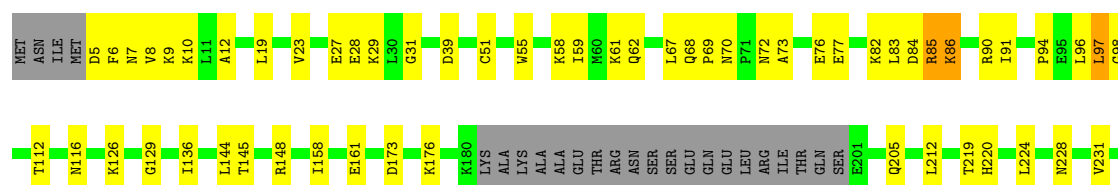
• Molecule 1: Endophilin-B1

Chain c: 49% 16% 33%

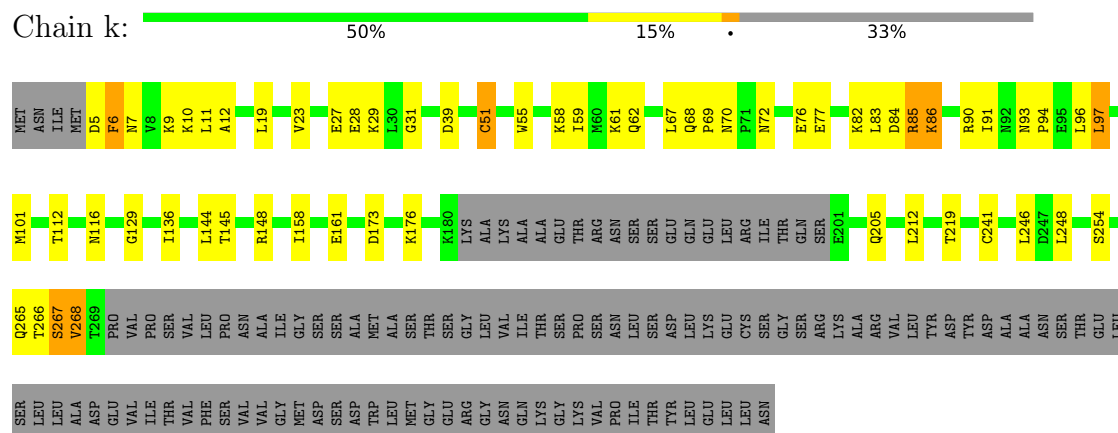


• Molecule 1: Endophilin-B1

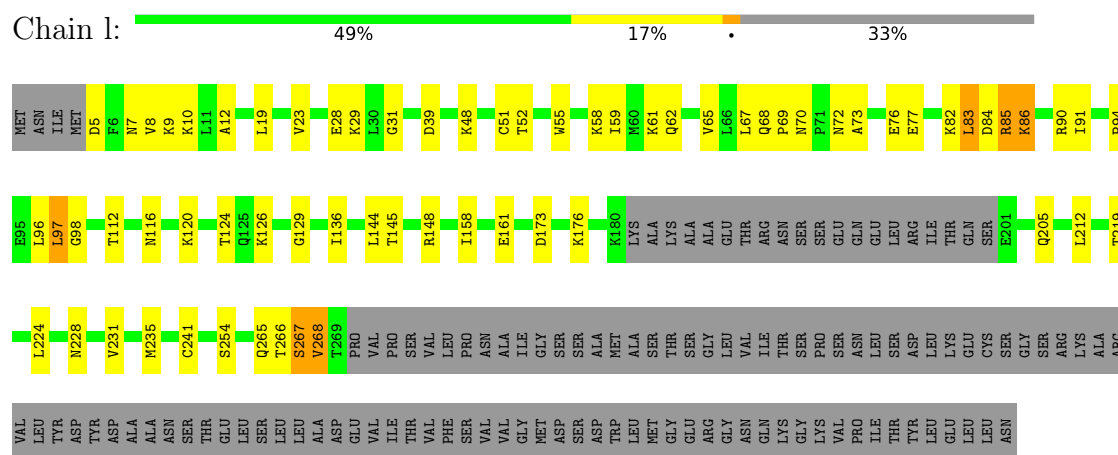
Chain d: 49% 16% 33%



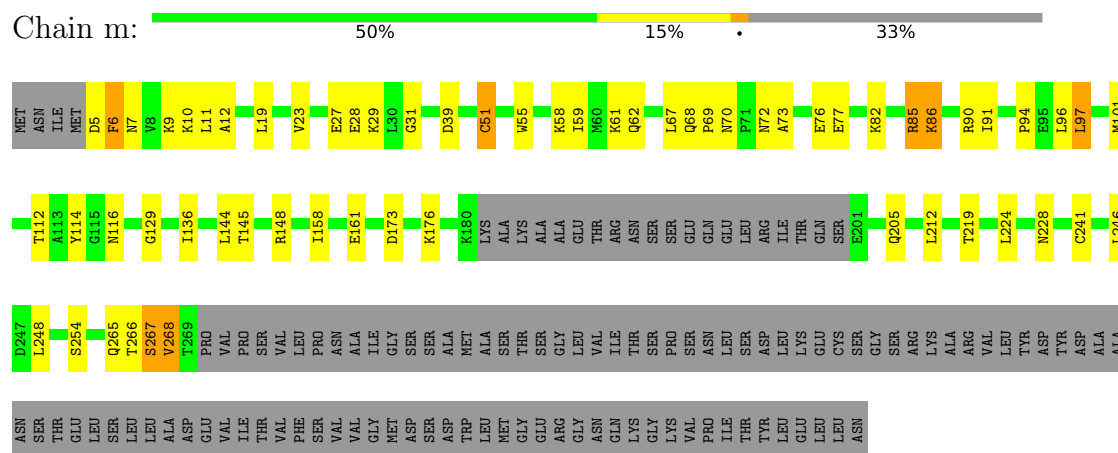
● Molecule 1: Endophilin-B1



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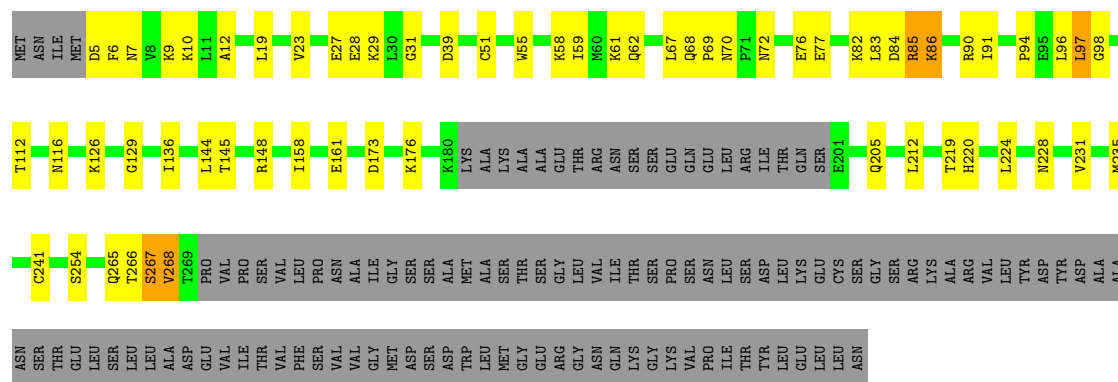


● Molecule 1: Endophilin-B1



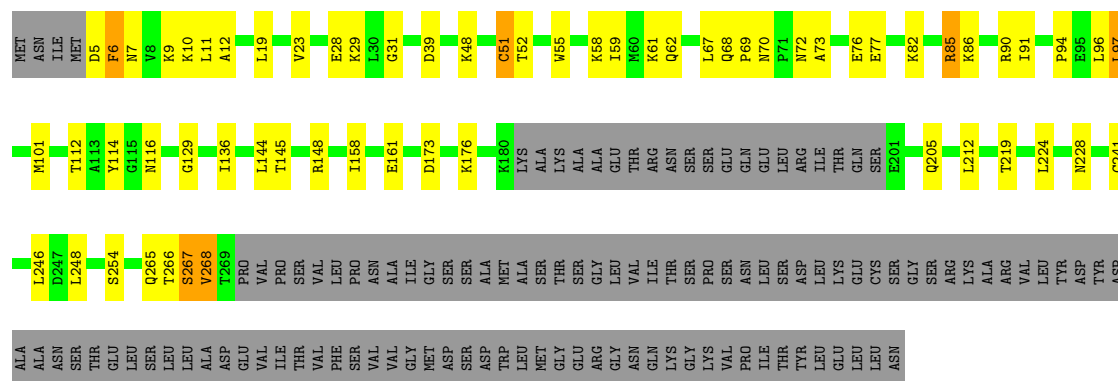
● Molecule 1: Endophilin-B1





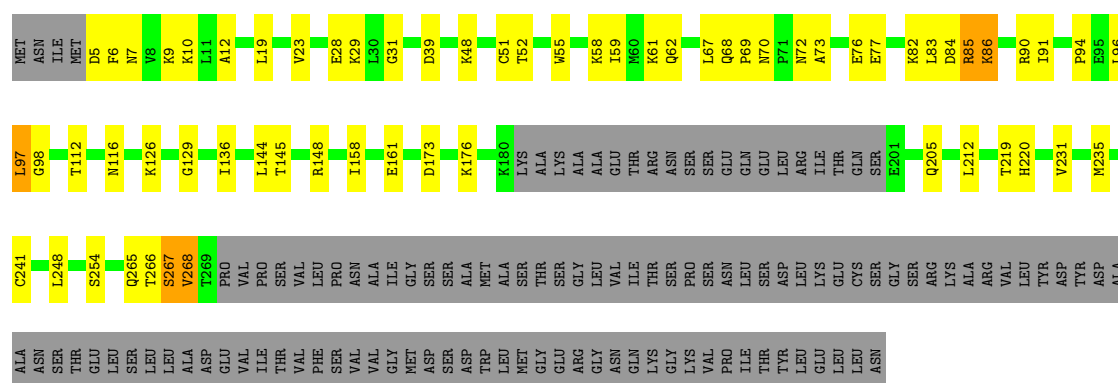
• Molecule 1: Endophilin-B1

Chain o: 50% 16% 33%



• Molecule 1: Endophilin-B1

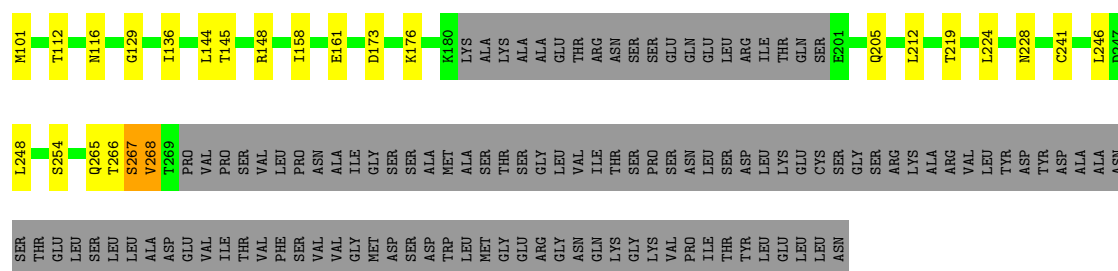
Chain p: 50% 16% 33%



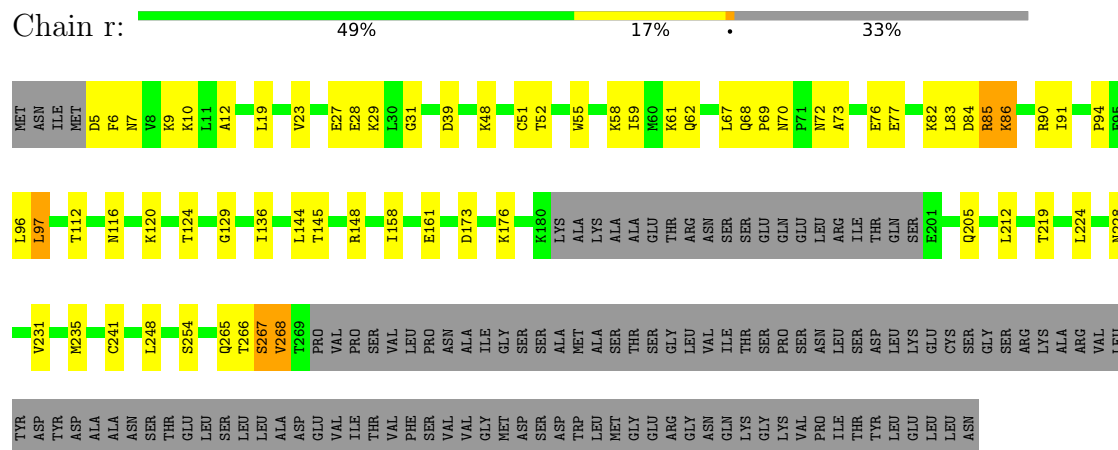
• Molecule 1: Endophilin-B1

Chain q: 50% 15% 33%

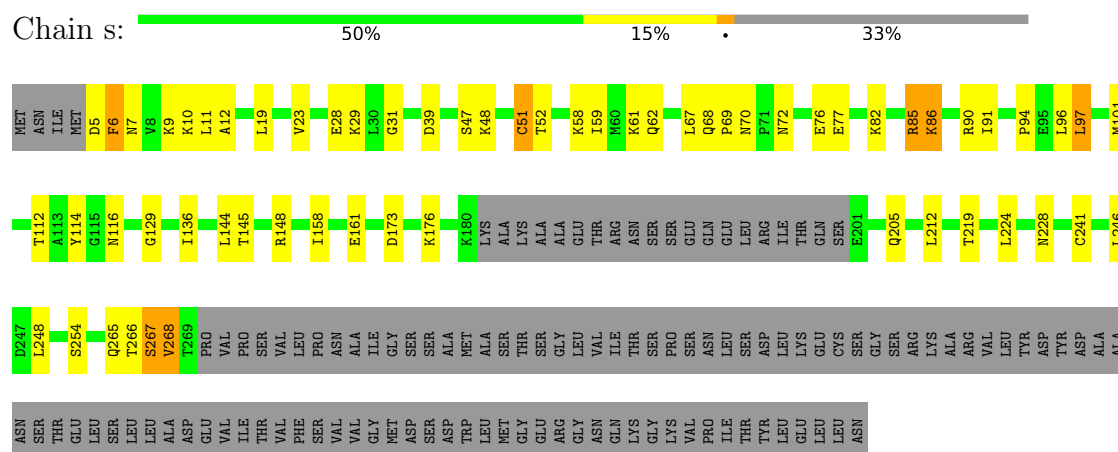




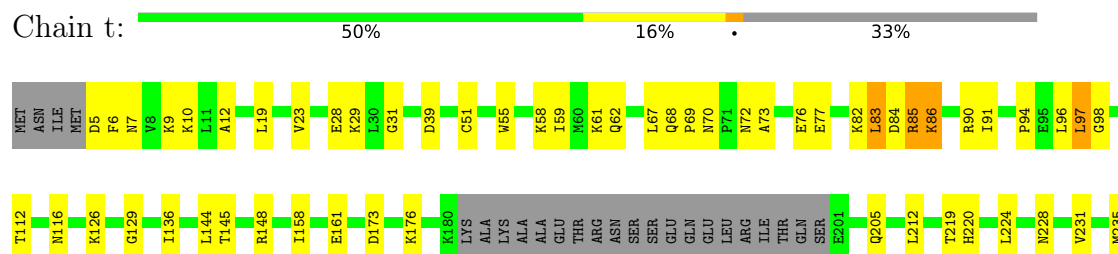
• Molecule 1: Endophilin-B1



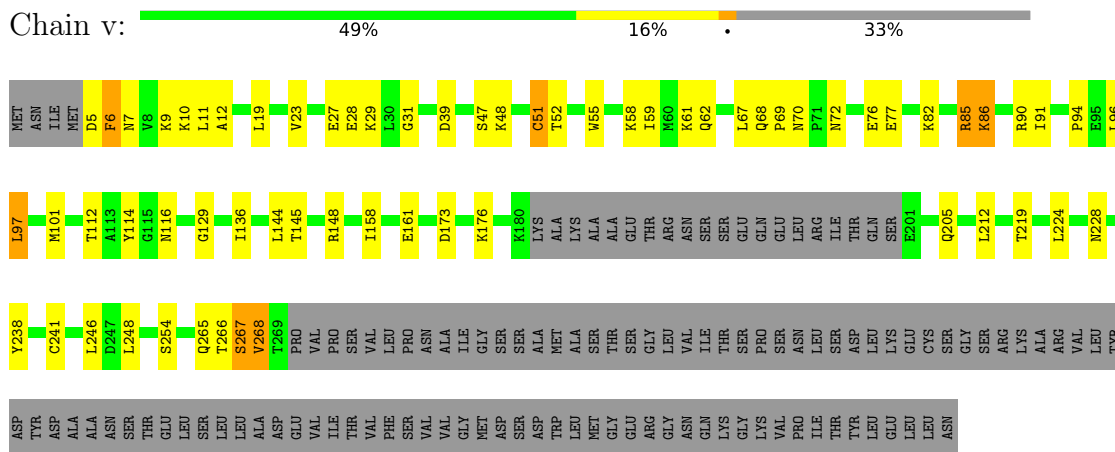
• Molecule 1: Endophilin-B1



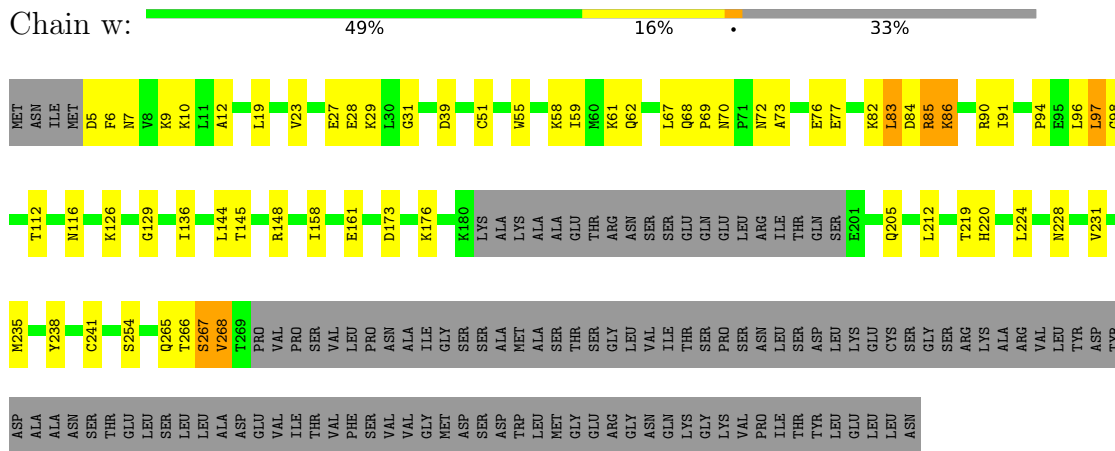
• Molecule 1: Endophilin-B1



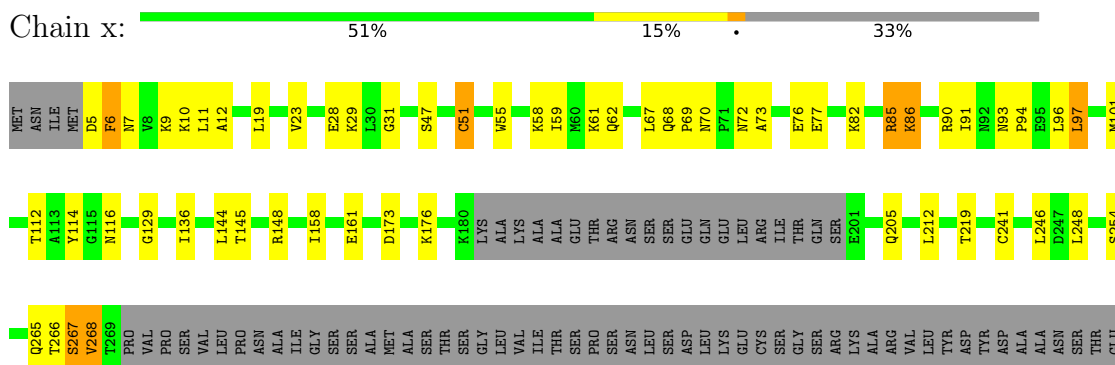
- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1

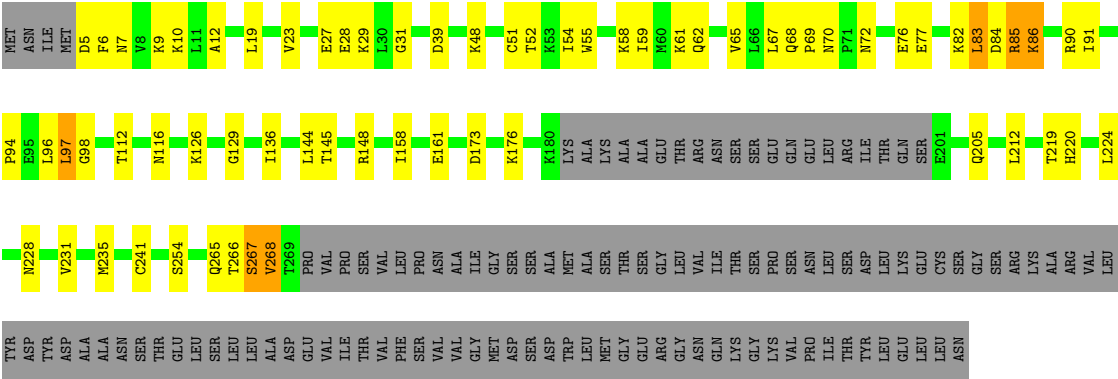


- Molecule 1: Endophilin-B1



LEU
SER
LEU
LEU
LEU
ALA
ASP
GLU
VAL
VAL
ILE
THR
VAL
PHE
SER
VAL
VAL
GLY
MET
ASP
SER
ASP
TRP
LEU
MET
GLY
GLU
ARG
GLY
ASN
GLN
LYS
GLY
LYS
VAL
PRO
ILE
THR
TYR
LEU
GLU
LEU
ASN

● Molecule 1: Endophilin-B1



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=59.1°, rise=17.8 Å, axial sym=C1	Depositor
Number of segments used	21197	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	490.9588, 490.9588, 490.9588	wwPDB
Map dimensions	214, 214, 214	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.2942, 2.2942, 2.2942	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.34	0/1993	0.76	2/2685 (0.1%)
1	B	0.35	0/1993	0.76	2/2685 (0.1%)
1	C	0.34	0/1993	0.76	2/2685 (0.1%)
1	D	0.35	0/1993	0.77	2/2685 (0.1%)
1	E	0.34	0/1993	0.76	2/2685 (0.1%)
1	F	0.35	0/1993	0.77	2/2685 (0.1%)
1	G	0.34	0/1993	0.76	2/2685 (0.1%)
1	H	0.35	0/1993	0.76	2/2685 (0.1%)
1	I	0.34	0/1993	0.76	2/2685 (0.1%)
1	J	0.35	0/1993	0.77	2/2685 (0.1%)
1	K	0.34	0/1993	0.76	2/2685 (0.1%)
1	L	0.35	0/1993	0.77	1/2685 (0.0%)
1	M	0.34	0/1993	0.76	1/2685 (0.0%)
1	N	0.35	0/1993	0.77	2/2685 (0.1%)
1	O	0.34	0/1993	0.76	2/2685 (0.1%)
1	P	0.35	0/1993	0.77	1/2685 (0.0%)
1	Q	0.34	0/1993	0.76	2/2685 (0.1%)
1	R	0.35	0/1993	0.77	2/2685 (0.1%)
1	S	0.34	0/1993	0.76	1/2685 (0.0%)
1	T	0.35	0/1993	0.77	1/2685 (0.0%)
1	V	0.34	0/1993	0.76	2/2685 (0.1%)
1	W	0.35	0/1993	0.77	2/2685 (0.1%)
1	X	0.34	0/1993	0.76	2/2685 (0.1%)
1	Y	0.35	0/1993	0.77	2/2685 (0.1%)
1	a	0.34	0/1993	0.76	2/2685 (0.1%)
1	b	0.35	0/1993	0.77	2/2685 (0.1%)
1	c	0.34	0/1993	0.76	2/2685 (0.1%)
1	d	0.35	0/1993	0.77	2/2685 (0.1%)
1	e	0.34	0/1993	0.76	2/2685 (0.1%)
1	f	0.35	0/1993	0.77	2/2685 (0.1%)
1	g	0.34	0/1993	0.76	2/2685 (0.1%)
1	h	0.35	0/1993	0.76	2/2685 (0.1%)
1	i	0.34	0/1993	0.76	1/2685 (0.0%)
1	j	0.35	0/1993	0.77	2/2685 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	k	0.34	0/1993	0.76	2/2685 (0.1%)
1	l	0.35	0/1993	0.77	1/2685 (0.0%)
1	m	0.34	0/1993	0.76	2/2685 (0.1%)
1	n	0.36	0/1993	0.77	2/2685 (0.1%)
1	o	0.34	0/1993	0.76	1/2685 (0.0%)
1	p	0.36	0/1993	0.77	1/2685 (0.0%)
1	q	0.34	0/1993	0.76	2/2685 (0.1%)
1	r	0.35	0/1993	0.77	2/2685 (0.1%)
1	s	0.34	0/1993	0.76	1/2685 (0.0%)
1	t	0.35	0/1993	0.77	1/2685 (0.0%)
1	v	0.34	0/1993	0.76	2/2685 (0.1%)
1	w	0.35	0/1993	0.77	2/2685 (0.1%)
1	x	0.34	0/1993	0.76	1/2685 (0.0%)
1	y	0.35	0/1993	0.77	2/2685 (0.1%)
All	All	0.35	0/95664	0.76	84/128880 (0.1%)

There are no bond length outliers.

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	v	254	SER	N-CA-C	-8.31	105.15	114.62
1	N	254	SER	N-CA-C	-8.30	105.16	114.62
1	c	254	SER	N-CA-C	-8.30	105.16	114.62
1	C	254	SER	N-CA-C	-8.29	105.17	114.62
1	E	254	SER	N-CA-C	-8.29	105.17	114.62
1	M	254	SER	N-CA-C	-8.29	105.17	114.62
1	X	254	SER	N-CA-C	-8.29	105.17	114.62
1	a	254	SER	N-CA-C	-8.29	105.17	114.62
1	p	254	SER	N-CA-C	-8.29	105.17	114.62
1	I	254	SER	N-CA-C	-8.29	105.17	114.62
1	Q	254	SER	N-CA-C	-8.28	105.18	114.62
1	i	254	SER	N-CA-C	-8.28	105.18	114.62
1	W	254	SER	N-CA-C	-8.28	105.18	114.62
1	g	254	SER	N-CA-C	-8.28	105.18	114.62
1	m	254	SER	N-CA-C	-8.28	105.18	114.62
1	P	254	SER	N-CA-C	-8.28	105.18	114.62
1	S	254	SER	N-CA-C	-8.28	105.18	114.62
1	R	254	SER	N-CA-C	-8.28	105.19	114.62
1	V	254	SER	N-CA-C	-8.28	105.19	114.62
1	A	254	SER	N-CA-C	-8.27	105.19	114.62
1	G	254	SER	N-CA-C	-8.27	105.19	114.62
1	H	254	SER	N-CA-C	-8.27	105.19	114.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	e	254	SER	N-CA-C	-8.27	105.19	114.62
1	Y	254	SER	N-CA-C	-8.27	105.19	114.62
1	j	254	SER	N-CA-C	-8.27	105.19	114.62
1	k	254	SER	N-CA-C	-8.27	105.19	114.62
1	w	254	SER	N-CA-C	-8.27	105.19	114.62
1	y	254	SER	N-CA-C	-8.27	105.19	114.62
1	l	254	SER	N-CA-C	-8.27	105.20	114.62
1	x	254	SER	N-CA-C	-8.27	105.20	114.62
1	n	254	SER	N-CA-C	-8.26	105.20	114.62
1	r	254	SER	N-CA-C	-8.26	105.20	114.62
1	F	254	SER	N-CA-C	-8.25	105.21	114.62
1	h	254	SER	N-CA-C	-8.25	105.21	114.62
1	q	254	SER	N-CA-C	-8.25	105.21	114.62
1	t	254	SER	N-CA-C	-8.25	105.22	114.62
1	L	254	SER	N-CA-C	-8.25	105.22	114.62
1	T	254	SER	N-CA-C	-8.25	105.22	114.62
1	B	254	SER	N-CA-C	-8.24	105.22	114.62
1	J	254	SER	N-CA-C	-8.24	105.22	114.62
1	K	254	SER	N-CA-C	-8.24	105.23	114.62
1	b	254	SER	N-CA-C	-8.24	105.23	114.62
1	s	254	SER	N-CA-C	-8.24	105.23	114.62
1	o	254	SER	N-CA-C	-8.23	105.23	114.62
1	O	254	SER	N-CA-C	-8.23	105.23	114.62
1	f	254	SER	N-CA-C	-8.23	105.24	114.62
1	d	254	SER	N-CA-C	-8.23	105.24	114.62
1	D	254	SER	N-CA-C	-8.22	105.24	114.62
1	g	27	GLU	N-CA-C	5.11	116.88	110.91
1	G	27	GLU	N-CA-C	5.09	116.86	110.91
1	j	27	GLU	N-CA-C	5.08	116.85	110.91
1	J	27	GLU	N-CA-C	5.07	116.84	110.91
1	h	27	GLU	N-CA-C	5.07	116.85	110.91
1	A	27	GLU	N-CA-C	5.06	116.83	110.91
1	a	27	GLU	N-CA-C	5.05	116.83	110.91
1	r	27	GLU	N-CA-C	5.05	116.82	110.91
1	Y	27	GLU	N-CA-C	5.05	116.81	110.91
1	d	27	GLU	N-CA-C	5.05	116.81	110.91
1	v	27	GLU	N-CA-C	5.05	116.81	110.91
1	y	27	GLU	N-CA-C	5.05	116.81	110.91
1	H	27	GLU	N-CA-C	5.04	116.81	110.91
1	n	27	GLU	N-CA-C	5.04	116.81	110.91
1	w	27	GLU	N-CA-C	5.04	116.81	110.91
1	V	27	GLU	N-CA-C	5.04	116.81	110.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	W	27	GLU	N-CA-C	5.04	116.81	110.91
1	F	27	GLU	N-CA-C	5.04	116.81	110.91
1	m	27	GLU	N-CA-C	5.04	116.81	110.91
1	Q	27	GLU	N-CA-C	5.04	116.81	110.91
1	R	27	GLU	N-CA-C	5.04	116.81	110.91
1	C	27	GLU	N-CA-C	5.04	116.80	110.91
1	q	27	GLU	N-CA-C	5.04	116.80	110.91
1	c	27	GLU	N-CA-C	5.03	116.80	110.91
1	e	27	GLU	N-CA-C	5.03	116.80	110.91
1	f	27	GLU	N-CA-C	5.03	116.80	110.91
1	D	27	GLU	N-CA-C	5.03	116.79	110.91
1	N	27	GLU	N-CA-C	5.03	116.79	110.91
1	O	27	GLU	N-CA-C	5.03	116.79	110.91
1	E	27	GLU	N-CA-C	5.03	116.79	110.91
1	b	27	GLU	N-CA-C	5.03	116.79	110.91
1	K	27	GLU	N-CA-C	5.01	116.78	110.91
1	I	27	GLU	N-CA-C	5.01	116.77	110.91
1	X	27	GLU	N-CA-C	5.01	116.77	110.91
1	k	27	GLU	N-CA-C	5.00	116.76	110.91
1	B	27	GLU	N-CA-C	5.00	116.76	110.91

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	1963	0	1963	56	0
1	B	1963	0	1963	51	0
1	C	1963	0	1963	58	0
1	D	1963	0	1963	52	0
1	E	1963	0	1963	62	0
1	F	1963	0	1963	51	0
1	G	1963	0	1963	61	0
1	H	1963	0	1963	53	0
1	I	1963	0	1963	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1963	0	1963	53	0
1	K	1963	0	1963	61	0
1	L	1963	0	1963	54	0
1	M	1963	0	1963	71	0
1	N	1963	0	1963	54	0
1	O	1963	0	1963	74	0
1	P	1963	0	1963	53	0
1	Q	1963	0	1963	73	0
1	R	1963	0	1963	53	0
1	S	1963	0	1963	69	0
1	T	1963	0	1963	54	0
1	V	1963	0	1963	70	0
1	W	1963	0	1963	54	0
1	X	1963	0	1963	73	0
1	Y	1963	0	1963	55	0
1	a	1963	0	1963	68	0
1	b	1963	0	1963	53	0
1	c	1963	0	1963	73	0
1	d	1963	0	1963	51	0
1	e	1963	0	1963	74	0
1	f	1963	0	1963	53	0
1	g	1963	0	1963	70	0
1	h	1963	0	1963	54	0
1	i	1963	0	1963	74	0
1	j	1963	0	1963	55	0
1	k	1963	0	1963	71	0
1	l	1963	0	1963	54	0
1	m	1963	0	1963	62	0
1	n	1963	0	1963	50	0
1	o	1963	0	1963	60	0
1	p	1963	0	1963	52	0
1	q	1963	0	1963	62	0
1	r	1963	0	1963	51	0
1	s	1963	0	1963	61	0
1	t	1963	0	1963	55	0
1	v	1963	0	1963	60	0
1	w	1963	0	1963	53	0
1	x	1963	0	1963	60	0
1	y	1963	0	1963	53	0
All	All	94224	0	94224	2131	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 11.

All (2131) 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:E:62:GLN:CG	1:F:97:LEU:HD22	1.43	1.49
1:s:62:GLN:CG	1:t:97:LEU:HD22	1.43	1.49
1:c:62:GLN:CG	1:d:97:LEU:HD22	1.43	1.49
1:O:62:GLN:CG	1:P:97:LEU:HD22	1.43	1.48
1:C:62:GLN:CG	1:D:97:LEU:HD22	1.43	1.48
1:V:62:GLN:CG	1:W:97:LEU:HD22	1.43	1.48
1:S:62:GLN:CG	1:T:97:LEU:HD22	1.43	1.48
1:e:62:GLN:CG	1:f:97:LEU:HD22	1.43	1.48
1:G:62:GLN:CG	1:H:97:LEU:HD22	1.43	1.47
1:v:62:GLN:CG	1:w:97:LEU:HD22	1.43	1.47
1:M:62:GLN:CG	1:N:97:LEU:HD22	1.43	1.47
1:q:62:GLN:CG	1:r:97:LEU:HD22	1.43	1.47
1:i:62:GLN:CG	1:j:97:LEU:HD22	1.43	1.47
1:m:62:GLN:CG	1:n:97:LEU:HD22	1.43	1.47
1:k:62:GLN:CG	1:l:97:LEU:HD22	1.43	1.46
1:a:62:GLN:CG	1:b:97:LEU:HD22	1.43	1.46
1:X:62:GLN:CG	1:Y:97:LEU:HD22	1.43	1.46
1:o:62:GLN:CG	1:p:97:LEU:HD22	1.43	1.46
1:K:62:GLN:CG	1:L:97:LEU:HD22	1.43	1.45
1:Q:62:GLN:CG	1:R:97:LEU:HD22	1.43	1.45
1:g:62:GLN:CG	1:h:97:LEU:HD22	1.43	1.45
1:I:62:GLN:CG	1:J:97:LEU:HD22	1.43	1.44
1:A:62:GLN:CG	1:B:97:LEU:HD22	1.43	1.44
1:x:62:GLN:CG	1:y:97:LEU:HD22	1.43	1.44
1:X:62:GLN:HG3	1:Y:97:LEU:CD2	1.56	1.35
1:x:62:GLN:HG3	1:y:97:LEU:CD2	1.56	1.35
1:E:62:GLN:HG3	1:F:97:LEU:CD2	1.56	1.34
1:I:62:GLN:HG3	1:J:97:LEU:CD2	1.56	1.34
1:k:62:GLN:HG3	1:l:97:LEU:CD2	1.56	1.34
1:m:62:GLN:HG3	1:n:97:LEU:CD2	1.56	1.34
1:M:62:GLN:HG3	1:N:97:LEU:CD2	1.56	1.34
1:c:62:GLN:HG3	1:d:97:LEU:CD2	1.56	1.34
1:e:62:GLN:HG3	1:f:97:LEU:CD2	1.56	1.34
1:O:62:GLN:HG3	1:P:97:LEU:CD2	1.56	1.33
1:s:62:GLN:HG3	1:t:97:LEU:CD2	1.56	1.33
1:v:62:GLN:HG3	1:w:97:LEU:CD2	1.56	1.33
1:C:62:GLN:HG3	1:D:97:LEU:CD2	1.56	1.33
1:q:62:GLN:HG3	1:r:97:LEU:CD2	1.56	1.33
1:i:62:GLN:HG3	1:j:97:LEU:CD2	1.56	1.33
1:a:62:GLN:HG3	1:b:97:LEU:CD2	1.56	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:62:GLN:HG3	1:R:97:LEU:CD2	1.56	1.32
1:S:62:GLN:HG3	1:T:97:LEU:CD2	1.56	1.32
1:G:62:GLN:HG3	1:H:97:LEU:CD2	1.56	1.32
1:g:62:GLN:HG3	1:h:97:LEU:CD2	1.56	1.32
1:K:62:GLN:HG3	1:L:97:LEU:CD2	1.56	1.32
1:o:62:GLN:HG3	1:p:97:LEU:CD2	1.56	1.32
1:V:62:GLN:HG3	1:W:97:LEU:CD2	1.56	1.32
1:A:62:GLN:HG3	1:B:97:LEU:CD2	1.56	1.31
1:S:84:ASP:HB3	1:s:7:ASN:OD1	1.71	0.90
1:V:84:ASP:HB3	1:v:7:ASN:OD1	1.74	0.88
1:G:84:ASP:HB3	1:g:7:ASN:OD1	1.76	0.86
1:X:6:PHE:HB2	1:k:84:ASP:N	1.90	0.86
1:V:97:LEU:HD11	1:W:59:ILE:HG23	1.58	0.85
1:I:84:ASP:HB3	1:i:7:ASN:OD1	1.76	0.85
1:v:97:LEU:HD11	1:w:59:ILE:HG23	1.58	0.85
1:S:97:LEU:HD11	1:T:59:ILE:HG23	1.58	0.85
1:c:59:ILE:HG23	1:d:97:LEU:HD11	1.59	0.85
1:C:59:ILE:HG23	1:D:97:LEU:HD11	1.59	0.85
1:i:97:LEU:HD11	1:j:59:ILE:HG23	1.58	0.85
1:m:59:ILE:HG23	1:n:97:LEU:HD11	1.59	0.85
1:s:97:LEU:HD11	1:t:59:ILE:HG23	1.58	0.85
1:G:97:LEU:HD11	1:H:59:ILE:HG23	1.58	0.85
1:O:59:ILE:HG23	1:P:97:LEU:HD11	1.59	0.85
1:g:97:LEU:HD11	1:h:59:ILE:HG23	1.58	0.85
1:I:97:LEU:HD11	1:J:59:ILE:HG23	1.59	0.85
1:K:59:ILE:HG23	1:L:97:LEU:HD11	1.59	0.84
1:G:62:GLN:HG2	1:H:97:LEU:HD22	1.60	0.84
1:k:97:LEU:HD11	1:l:59:ILE:HG23	1.58	0.84
1:E:62:GLN:HG2	1:F:97:LEU:HD22	1.60	0.84
1:V:6:PHE:HB2	1:i:84:ASP:N	1.91	0.84
1:X:97:LEU:HD11	1:Y:59:ILE:HG23	1.58	0.84
1:M:59:ILE:HG23	1:N:97:LEU:HD11	1.59	0.84
1:q:59:ILE:HG23	1:r:97:LEU:HD11	1.59	0.84
1:K:97:LEU:HD11	1:L:59:ILE:HG23	1.59	0.84
1:x:97:LEU:HD11	1:y:59:ILE:HG23	1.58	0.84
1:A:59:ILE:HG23	1:B:97:LEU:HD11	1.59	0.84
1:E:97:LEU:HD11	1:F:59:ILE:HG23	1.59	0.84
1:o:59:ILE:HG23	1:p:97:LEU:HD11	1.59	0.84
1:k:59:ILE:HG23	1:l:97:LEU:HD11	1.59	0.83
1:x:59:ILE:HG23	1:y:97:LEU:HD11	1.59	0.83
1:Q:84:ASP:HB3	1:q:7:ASN:OD1	1.77	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:97:LEU:HD11	1:f:59:ILE:HG23	1.59	0.83
1:q:97:LEU:HD11	1:r:59:ILE:HG23	1.58	0.83
1:i:59:ILE:HG23	1:j:97:LEU:HD11	1.59	0.83
1:I:59:ILE:HG23	1:J:97:LEU:HD11	1.59	0.83
1:C:97:LEU:HD11	1:D:59:ILE:HG23	1.58	0.83
1:Q:59:ILE:HG23	1:R:97:LEU:HD11	1.59	0.83
1:S:59:ILE:HG23	1:T:97:LEU:HD11	1.59	0.83
1:V:59:ILE:HG23	1:W:97:LEU:HD11	1.59	0.83
1:s:59:ILE:HG23	1:t:97:LEU:HD11	1.59	0.83
1:E:59:ILE:HG23	1:F:97:LEU:HD11	1.59	0.83
1:M:97:LEU:HD11	1:N:59:ILE:HG23	1.58	0.83
1:Q:97:LEU:HD11	1:R:59:ILE:HG23	1.58	0.83
1:m:97:LEU:HD11	1:n:59:ILE:HG23	1.58	0.83
1:a:59:ILE:HG23	1:b:97:LEU:HD11	1.59	0.83
1:g:59:ILE:HG23	1:h:97:LEU:HD11	1.59	0.83
1:E:84:ASP:HB3	1:e:7:ASN:OD1	1.78	0.82
1:a:97:LEU:HD11	1:b:59:ILE:HG23	1.58	0.82
1:c:97:LEU:HD11	1:d:59:ILE:HG23	1.58	0.82
1:o:62:GLN:HG2	1:p:97:LEU:HD22	1.60	0.82
1:v:59:ILE:HG23	1:w:97:LEU:HD11	1.59	0.82
1:A:97:LEU:HD11	1:B:59:ILE:HG23	1.58	0.82
1:X:59:ILE:HG23	1:Y:97:LEU:HD11	1.59	0.82
1:O:97:LEU:HD11	1:P:59:ILE:HG23	1.58	0.82
1:o:97:LEU:HD11	1:p:59:ILE:HG23	1.58	0.82
1:q:62:GLN:HG2	1:r:97:LEU:HD22	1.60	0.82
1:e:59:ILE:HG23	1:f:97:LEU:HD11	1.59	0.82
1:G:59:ILE:HG23	1:H:97:LEU:HD11	1.59	0.82
1:s:62:GLN:HG2	1:t:97:LEU:HD22	1.60	0.81
1:M:62:GLN:HG2	1:N:97:LEU:HD22	1.60	0.81
1:v:62:GLN:HG2	1:w:97:LEU:HD22	1.60	0.81
1:K:84:ASP:HB3	1:k:7:ASN:OD1	1.81	0.81
1:S:6:PHE:HB2	1:g:84:ASP:N	1.96	0.81
1:A:84:ASP:HB3	1:a:7:ASN:OD1	1.81	0.81
1:O:62:GLN:HG2	1:P:97:LEU:HD22	1.60	0.80
1:M:6:PHE:HB2	1:a:84:ASP:N	1.96	0.80
1:C:84:ASP:HB3	1:c:7:ASN:OD1	1.81	0.80
1:Q:62:GLN:HG2	1:R:97:LEU:HD22	1.60	0.80
1:S:62:GLN:HG2	1:T:97:LEU:HD22	1.60	0.80
1:a:62:GLN:HG2	1:b:97:LEU:HD22	1.60	0.80
1:X:84:ASP:HB3	1:x:7:ASN:OD1	1.83	0.79
1:A:62:GLN:HG2	1:B:97:LEU:HD22	1.60	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:62:GLN:HG2	1:y:97:LEU:HD22	1.60	0.79
1:V:62:GLN:HG2	1:W:97:LEU:HD22	1.60	0.79
1:V:97:LEU:HD22	1:W:62:GLN:HG3	1.65	0.79
1:A:97:LEU:HD22	1:B:62:GLN:HG3	1.65	0.79
1:K:62:GLN:HG2	1:L:97:LEU:HD22	1.60	0.79
1:o:97:LEU:HD22	1:p:62:GLN:HG3	1.65	0.79
1:v:97:LEU:HD22	1:w:62:GLN:HG3	1.65	0.79
1:G:97:LEU:HD22	1:H:62:GLN:HG3	1.65	0.79
1:i:62:GLN:CG	1:j:97:LEU:CD2	2.36	0.79
1:x:62:GLN:CG	1:y:97:LEU:CD2	2.36	0.79
1:K:97:LEU:HD22	1:L:62:GLN:HG3	1.65	0.78
1:O:97:LEU:HD22	1:P:62:GLN:HG3	1.65	0.78
1:m:62:GLN:HG2	1:n:97:LEU:HD22	1.60	0.78
1:e:97:LEU:HD22	1:f:62:GLN:HG3	1.65	0.78
1:e:62:GLN:CG	1:f:97:LEU:CD2	2.36	0.78
1:Q:97:LEU:HD22	1:R:62:GLN:HG3	1.65	0.78
1:a:97:LEU:HD22	1:b:62:GLN:HG3	1.65	0.78
1:k:97:LEU:HD22	1:l:62:GLN:HG3	1.65	0.78
1:O:84:ASP:HB3	1:o:7:ASN:OD1	1.84	0.78
1:c:62:GLN:HG2	1:d:97:LEU:HD22	1.60	0.78
1:s:97:LEU:HD22	1:t:62:GLN:HG3	1.65	0.78
1:i:97:LEU:HD22	1:j:62:GLN:HG3	1.65	0.78
1:E:97:LEU:HD22	1:F:62:GLN:HG3	1.65	0.78
1:m:97:LEU:O	1:m:97:LEU:HD12	1.84	0.78
1:X:97:LEU:HD12	1:X:97:LEU:O	1.84	0.78
1:x:97:LEU:O	1:x:97:LEU:HD12	1.84	0.78
1:M:97:LEU:HD12	1:M:97:LEU:O	1.84	0.78
1:a:97:LEU:HD12	1:a:97:LEU:O	1.84	0.78
1:c:97:LEU:HD22	1:d:62:GLN:HG3	1.65	0.78
1:g:97:LEU:HD22	1:h:62:GLN:HG3	1.65	0.78
1:k:97:LEU:HD12	1:k:97:LEU:O	1.84	0.77
1:K:97:LEU:HD12	1:K:97:LEU:O	1.84	0.77
1:A:97:LEU:HD12	1:A:97:LEU:O	1.84	0.77
1:m:97:LEU:HD22	1:n:62:GLN:HG3	1.65	0.77
1:E:97:LEU:HD12	1:E:97:LEU:O	1.84	0.77
1:G:97:LEU:HD12	1:G:97:LEU:O	1.84	0.77
1:e:62:GLN:HG2	1:f:97:LEU:HD22	1.60	0.77
1:C:97:LEU:HD22	1:D:62:GLN:HG3	1.65	0.77
1:X:97:LEU:HD22	1:Y:62:GLN:HG3	1.65	0.77
1:g:62:GLN:HG2	1:h:97:LEU:HD22	1.60	0.77
1:g:97:LEU:HD12	1:g:97:LEU:O	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:62:GLN:CG	1:l:97:LEU:CD2	2.36	0.77
1:q:97:LEU:HD22	1:r:62:GLN:HG3	1.65	0.77
1:v:97:LEU:HD12	1:v:97:LEU:O	1.84	0.77
1:M:97:LEU:HD22	1:N:62:GLN:HG3	1.65	0.77
1:e:97:LEU:O	1:e:97:LEU:HD12	1.84	0.77
1:V:97:LEU:HD12	1:V:97:LEU:O	1.84	0.77
1:X:62:GLN:HG2	1:Y:97:LEU:HD22	1.60	0.77
1:s:62:GLN:CG	1:t:97:LEU:CD2	2.36	0.77
1:S:97:LEU:HD12	1:S:97:LEU:O	1.84	0.77
1:x:97:LEU:HD22	1:y:62:GLN:HG3	1.65	0.77
1:I:97:LEU:HD22	1:J:62:GLN:HG3	1.65	0.76
1:Q:97:LEU:HD12	1:Q:97:LEU:O	1.84	0.76
1:S:97:LEU:HD22	1:T:62:GLN:HG3	1.65	0.76
1:i:62:GLN:HG2	1:j:97:LEU:HD22	1.60	0.76
1:o:97:LEU:HD12	1:o:97:LEU:O	1.84	0.76
1:M:84:ASP:HB3	1:m:7:ASN:OD1	1.85	0.76
1:O:6:PHE:HB2	1:c:84:ASP:N	2.00	0.76
1:i:97:LEU:HD12	1:i:97:LEU:O	1.84	0.76
1:o:62:GLN:CG	1:p:97:LEU:CD2	2.36	0.76
1:s:97:LEU:HD12	1:s:97:LEU:O	1.84	0.76
1:K:62:GLN:CG	1:L:97:LEU:CD2	2.36	0.76
1:I:97:LEU:HD12	1:I:97:LEU:O	1.84	0.76
1:q:97:LEU:HD12	1:q:97:LEU:O	1.84	0.76
1:O:97:LEU:HD12	1:O:97:LEU:O	1.84	0.76
1:I:62:GLN:HG2	1:J:97:LEU:HD22	1.60	0.76
1:c:97:LEU:HD12	1:c:97:LEU:O	1.84	0.76
1:C:97:LEU:HD12	1:C:97:LEU:O	1.84	0.76
1:O:62:GLN:CG	1:P:97:LEU:CD2	2.36	0.76
1:a:62:GLN:CG	1:b:97:LEU:CD2	2.36	0.75
1:C:62:GLN:HG2	1:D:97:LEU:HD22	1.60	0.75
1:v:62:GLN:CG	1:w:97:LEU:CD2	2.36	0.75
1:G:62:GLN:CG	1:H:97:LEU:CD2	2.36	0.75
1:Q:6:PHE:HB2	1:e:84:ASP:N	2.02	0.75
1:k:62:GLN:HG2	1:l:97:LEU:HD22	1.60	0.74
1:V:62:GLN:CG	1:W:97:LEU:CD2	2.36	0.74
1:C:62:GLN:CG	1:D:97:LEU:CD2	2.36	0.73
1:L:7:ASN:HB2	1:k:11:LEU:HD22	1.71	0.73
1:b:85:ARG:HG2	1:b:85:ARG:HH21	1.53	0.73
1:B:85:ARG:HG2	1:B:85:ARG:HH21	1.54	0.73
1:N:85:ARG:HH21	1:N:85:ARG:HG2	1.54	0.73
1:n:85:ARG:HH21	1:n:85:ARG:HG2	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:7:ASN:HB2	1:x:11:LEU:HD22	1.70	0.73
1:p:85:ARG:HG2	1:p:85:ARG:HH21	1.53	0.72
1:P:85:ARG:HG2	1:P:85:ARG:HH21	1.54	0.72
1:j:85:ARG:HG2	1:j:85:ARG:HH21	1.53	0.72
1:D:85:ARG:HG2	1:D:85:ARG:HH21	1.54	0.72
1:J:85:ARG:HG2	1:J:85:ARG:HH21	1.53	0.72
1:Q:62:GLN:CG	1:R:97:LEU:CD2	2.36	0.72
1:w:85:ARG:HG2	1:w:85:ARG:HH21	1.53	0.72
1:I:62:GLN:CG	1:J:97:LEU:CD2	2.36	0.72
1:N:7:ASN:HB2	1:m:11:LEU:HD22	1.72	0.72
1:W:85:ARG:HG2	1:W:85:ARG:HH21	1.54	0.72
1:d:85:ARG:HG2	1:d:85:ARG:HH21	1.54	0.72
1:t:85:ARG:HH21	1:t:85:ARG:HG2	1.54	0.72
1:L:85:ARG:HG2	1:L:85:ARG:HH21	1.53	0.72
1:T:85:ARG:HG2	1:T:85:ARG:HH21	1.54	0.72
1:X:6:PHE:HB3	1:k:83:LEU:HA	1.72	0.72
1:h:85:ARG:HG2	1:h:85:ARG:HH21	1.54	0.72
1:l:85:ARG:HG2	1:l:85:ARG:HH21	1.53	0.72
1:H:85:ARG:HH21	1:H:85:ARG:HG2	1.54	0.71
1:M:62:GLN:CG	1:N:97:LEU:CD2	2.36	0.71
1:Y:85:ARG:HH21	1:Y:85:ARG:HG2	1.54	0.71
1:y:85:ARG:HH21	1:y:85:ARG:HG2	1.54	0.71
1:V:6:PHE:HB3	1:i:83:LEU:HA	1.73	0.71
1:v:69:PRO:HG2	1:w:69:PRO:HG2	1.73	0.71
1:I:69:PRO:HG2	1:J:69:PRO:HG2	1.73	0.71
1:J:7:ASN:HB2	1:i:11:LEU:HD22	1.72	0.71
1:S:62:GLN:CG	1:T:97:LEU:CD2	2.36	0.71
1:V:69:PRO:HG2	1:W:69:PRO:HG2	1.73	0.71
1:g:69:PRO:HG2	1:h:69:PRO:HG2	1.73	0.71
1:V:6:PHE:HB2	1:i:84:ASP:HB2	1.73	0.71
1:S:69:PRO:HG2	1:T:69:PRO:HG2	1.73	0.71
1:m:62:GLN:CG	1:n:97:LEU:CD2	2.36	0.71
1:r:85:ARG:HG2	1:r:85:ARG:HH21	1.54	0.71
1:s:69:PRO:HG2	1:t:69:PRO:HG2	1.73	0.71
1:R:85:ARG:HG2	1:R:85:ARG:HH21	1.54	0.71
1:S:6:PHE:HB2	1:g:84:ASP:HB2	1.71	0.71
1:X:62:GLN:CG	1:Y:97:LEU:CD2	2.36	0.71
1:i:69:PRO:HG2	1:j:69:PRO:HG2	1.73	0.71
1:F:85:ARG:HH21	1:F:85:ARG:HG2	1.54	0.71
1:G:69:PRO:HG2	1:H:69:PRO:HG2	1.73	0.71
1:X:69:PRO:HG2	1:Y:69:PRO:HG2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:85:ARG:HH21	1:f:85:ARG:HG2	1.54	0.71
1:E:69:PRO:HG2	1:F:69:PRO:HG2	1.73	0.70
1:Q:69:PRO:HG2	1:R:69:PRO:HG2	1.73	0.70
1:x:62:GLN:HG3	1:y:97:LEU:HD22	0.72	0.70
1:k:69:PRO:HG2	1:l:69:PRO:HG2	1.73	0.70
1:x:69:PRO:HG2	1:y:69:PRO:HG2	1.73	0.70
1:e:62:GLN:HG3	1:f:97:LEU:HD22	0.72	0.70
1:o:62:GLN:HG3	1:p:97:LEU:HD22	0.72	0.70
1:q:69:PRO:HG2	1:r:69:PRO:HG2	1.73	0.70
1:I:62:GLN:HG3	1:J:97:LEU:HD22	0.72	0.70
1:K:69:PRO:HG2	1:L:69:PRO:HG2	1.73	0.70
1:e:69:PRO:HG2	1:f:69:PRO:HG2	1.73	0.70
1:g:62:GLN:HG3	1:h:97:LEU:HD22	0.72	0.70
1:I:84:ASP:O	1:i:10:LYS:HG3	1.92	0.70
1:Q:62:GLN:HG3	1:R:97:LEU:HD22	0.72	0.70
1:A:62:GLN:CG	1:B:97:LEU:CD2	2.36	0.69
1:V:84:ASP:O	1:v:10:LYS:HG3	1.92	0.69
1:c:69:PRO:HG2	1:d:69:PRO:HG2	1.73	0.69
1:X:84:ASP:O	1:x:10:LYS:HG3	1.93	0.69
1:g:62:GLN:CG	1:h:97:LEU:CD2	2.36	0.69
1:A:62:GLN:HG3	1:B:97:LEU:HD22	0.72	0.69
1:o:69:PRO:HG2	1:p:69:PRO:HG2	1.73	0.69
1:M:69:PRO:HG2	1:N:69:PRO:HG2	1.73	0.69
1:O:69:PRO:HG2	1:P:69:PRO:HG2	1.73	0.69
1:q:62:GLN:CG	1:r:97:LEU:CD2	2.36	0.69
1:A:69:PRO:HG2	1:B:69:PRO:HG2	1.73	0.69
1:G:62:GLN:HG3	1:H:97:LEU:HD22	0.72	0.69
1:i:62:GLN:HG3	1:j:97:LEU:HD22	0.72	0.69
1:m:69:PRO:HG2	1:n:69:PRO:HG2	1.73	0.69
1:C:69:PRO:HG2	1:D:69:PRO:HG2	1.73	0.69
1:H:7:ASN:HB2	1:g:11:LEU:HD22	1.75	0.69
1:a:69:PRO:HG2	1:b:69:PRO:HG2	1.73	0.69
1:q:62:GLN:HG3	1:r:97:LEU:HD22	0.72	0.69
1:C:62:GLN:HG3	1:D:97:LEU:HD22	0.72	0.69
1:S:62:GLN:HG3	1:T:97:LEU:HD22	0.72	0.69
1:V:62:GLN:HG3	1:W:97:LEU:HD22	0.72	0.69
1:W:7:ASN:HB2	1:v:11:LEU:HD22	1.75	0.68
1:a:62:GLN:HG3	1:b:97:LEU:HD22	0.72	0.68
1:K:62:GLN:HG3	1:L:97:LEU:HD22	0.72	0.68
1:X:6:PHE:HB2	1:k:84:ASP:HB2	1.76	0.68
1:v:62:GLN:HG3	1:w:97:LEU:HD22	0.72	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:ASN:HB2	1:a:11:LEU:HD22	1.76	0.68
1:E:62:GLN:CG	1:F:97:LEU:CD2	2.36	0.68
1:G:84:ASP:O	1:g:10:LYS:HG3	1.95	0.67
1:K:84:ASP:O	1:k:10:LYS:HG3	1.94	0.67
1:M:62:GLN:HG3	1:N:97:LEU:HD22	0.72	0.67
1:k:62:GLN:HG3	1:l:97:LEU:HD22	0.72	0.67
1:c:62:GLN:HG3	1:d:97:LEU:HD22	0.72	0.67
1:s:62:GLN:HG3	1:t:97:LEU:HD22	0.72	0.67
1:P:7:ASN:HB2	1:o:11:LEU:HD22	1.75	0.67
1:c:62:GLN:CG	1:d:97:LEU:CD2	2.36	0.67
1:X:62:GLN:HG3	1:Y:97:LEU:HD22	0.72	0.67
1:E:62:GLN:HG3	1:F:97:LEU:HD22	0.72	0.66
1:F:7:ASN:HB2	1:e:11:LEU:HD22	1.77	0.66
1:S:6:PHE:HB3	1:g:83:LEU:HA	1.78	0.66
1:m:62:GLN:HG3	1:n:97:LEU:HD22	0.72	0.66
1:M:6:PHE:HB3	1:a:83:LEU:HA	1.77	0.66
1:O:62:GLN:HG3	1:P:97:LEU:HD22	0.72	0.66
1:R:7:ASN:HB2	1:q:11:LEU:HD22	1.78	0.65
1:D:7:ASN:HB2	1:c:11:LEU:HD22	1.78	0.65
1:S:84:ASP:O	1:s:10:LYS:HG3	1.96	0.65
1:O:6:PHE:HB3	1:c:83:LEU:HA	1.79	0.65
1:Q:6:PHE:HB2	1:e:84:ASP:HB2	1.77	0.65
1:M:6:PHE:HB2	1:a:84:ASP:HB2	1.77	0.65
1:T:7:ASN:HB2	1:s:11:LEU:HD22	1.78	0.63
1:O:7:ASN:OD1	1:c:84:ASP:HB3	1.98	0.63
1:M:84:ASP:HB2	1:m:6:PHE:HB2	1.82	0.62
1:M:84:ASP:O	1:m:10:LYS:HG3	1.99	0.62
1:X:6:PHE:CB	1:k:84:ASP:N	2.63	0.62
1:E:84:ASP:O	1:e:10:LYS:HG3	2.00	0.62
1:O:84:ASP:HB2	1:o:6:PHE:HB2	1.81	0.62
1:e:85:ARG:HH21	1:e:85:ARG:CG	2.13	0.62
1:E:85:ARG:HH21	1:E:85:ARG:CG	2.13	0.61
1:C:85:ARG:HH21	1:C:85:ARG:CG	2.14	0.61
1:Q:85:ARG:HH21	1:Q:85:ARG:CG	2.14	0.61
1:c:85:ARG:HH21	1:c:85:ARG:CG	2.13	0.61
1:q:85:ARG:HH21	1:q:85:ARG:CG	2.14	0.61
1:G:85:ARG:HH21	1:G:85:ARG:CG	2.13	0.61
1:O:85:ARG:HH21	1:O:85:ARG:CG	2.13	0.61
1:Q:6:PHE:HB3	1:e:83:LEU:HA	1.82	0.61
1:A:85:ARG:HH21	1:A:85:ARG:CG	2.13	0.61
1:S:85:ARG:HH21	1:S:85:ARG:CG	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:85:ARG:HH21	1:g:85:ARG:CG	2.14	0.61
1:o:85:ARG:HH21	1:o:85:ARG:CG	2.14	0.61
1:s:85:ARG:HH21	1:s:85:ARG:CG	2.13	0.61
1:x:85:ARG:HH21	1:x:85:ARG:CG	2.13	0.61
1:a:85:ARG:HH21	1:a:85:ARG:CG	2.13	0.61
1:I:85:ARG:HH21	1:I:85:ARG:CG	2.13	0.61
1:S:6:PHE:HD2	1:g:84:ASP:OD1	1.83	0.61
1:X:85:ARG:HH21	1:X:85:ARG:CG	2.13	0.61
1:M:85:ARG:HH21	1:M:85:ARG:CG	2.13	0.61
1:V:6:PHE:CB	1:i:84:ASP:N	2.63	0.61
1:i:85:ARG:HH21	1:i:85:ARG:CG	2.13	0.61
1:K:85:ARG:HH21	1:K:85:ARG:CG	2.13	0.61
1:k:85:ARG:HH21	1:k:85:ARG:CG	2.13	0.61
1:O:6:PHE:HB2	1:c:84:ASP:HB2	1.83	0.60
1:V:85:ARG:HH21	1:V:85:ARG:CG	2.14	0.60
1:v:85:ARG:HH21	1:v:85:ARG:CG	2.14	0.60
1:V:6:PHE:HD2	1:i:84:ASP:OD1	1.84	0.60
1:Q:84:ASP:O	1:q:10:LYS:HG3	2.01	0.60
1:A:84:ASP:O	1:a:10:LYS:HG3	2.01	0.60
1:E:101:MET:SD	1:F:55:TRP:NE1	2.74	0.59
1:m:85:ARG:HH21	1:m:85:ARG:CG	2.13	0.59
1:M:101:MET:SD	1:N:55:TRP:NE1	2.74	0.59
1:a:101:MET:SD	1:b:55:TRP:NE1	2.74	0.59
1:c:101:MET:SD	1:d:55:TRP:NE1	2.74	0.59
1:Q:84:ASP:HB2	1:q:7:ASN:N	2.18	0.59
1:C:84:ASP:HB2	1:c:6:PHE:HB2	1.85	0.58
1:M:7:ASN:OD1	1:a:84:ASP:HB3	2.03	0.58
1:O:84:ASP:O	1:o:10:LYS:HG3	2.03	0.58
1:m:101:MET:SD	1:n:55:TRP:NE1	2.74	0.58
1:A:84:ASP:HB2	1:a:6:PHE:HB2	1.85	0.58
1:O:101:MET:SD	1:P:55:TRP:NE1	2.74	0.58
1:A:101:MET:SD	1:B:55:TRP:NE1	2.74	0.58
1:C:84:ASP:O	1:c:10:LYS:HG3	2.03	0.58
1:q:101:MET:SD	1:r:55:TRP:NE1	2.74	0.58
1:C:101:MET:SD	1:D:55:TRP:NE1	2.74	0.58
1:S:84:ASP:HB2	1:s:7:ASN:N	2.19	0.58
1:B:7:ASN:HA	1:B:10:LYS:HB3	1.86	0.58
1:F:7:ASN:HA	1:F:10:LYS:HB3	1.86	0.58
1:b:7:ASN:HA	1:b:10:LYS:HB3	1.86	0.58
1:f:7:ASN:HA	1:f:10:LYS:HB3	1.86	0.58
1:n:7:ASN:HA	1:n:10:LYS:HB3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:7:ASN:HA	1:r:10:LYS:HB3	1.86	0.58
1:D:7:ASN:HA	1:D:10:LYS:HB3	1.86	0.58
1:h:7:ASN:HA	1:h:10:LYS:HB3	1.86	0.58
1:G:7:ASN:HA	1:G:10:LYS:HB3	1.86	0.58
1:S:7:ASN:HA	1:S:10:LYS:HB3	1.86	0.58
1:X:6:PHE:HD2	1:k:84:ASP:OD1	1.87	0.58
1:d:7:ASN:HA	1:d:10:LYS:HB3	1.86	0.58
1:p:7:ASN:HA	1:p:10:LYS:HB3	1.86	0.58
1:L:7:ASN:HA	1:L:10:LYS:HB3	1.86	0.57
1:N:7:ASN:HA	1:N:10:LYS:HB3	1.86	0.57
1:s:7:ASN:HA	1:s:10:LYS:HB3	1.86	0.57
1:y:7:ASN:HA	1:y:10:LYS:HB3	1.86	0.57
1:R:7:ASN:HA	1:R:10:LYS:HB3	1.86	0.57
1:T:7:ASN:HA	1:T:10:LYS:HB3	1.86	0.57
1:l:7:ASN:HA	1:l:10:LYS:HB3	1.86	0.57
1:t:7:ASN:HA	1:t:10:LYS:HB3	1.86	0.57
1:H:7:ASN:HA	1:H:10:LYS:HB3	1.86	0.57
1:I:7:ASN:HA	1:I:10:LYS:HB3	1.86	0.57
1:J:7:ASN:HA	1:J:10:LYS:HB3	1.86	0.57
1:P:7:ASN:HA	1:P:10:LYS:HB3	1.86	0.57
1:e:7:ASN:HA	1:e:10:LYS:HB3	1.86	0.57
1:o:101:MET:SD	1:p:55:TRP:NE1	2.74	0.57
1:Q:7:ASN:HA	1:Q:10:LYS:HB3	1.86	0.57
1:W:7:ASN:HA	1:W:10:LYS:HB3	1.86	0.57
1:Y:7:ASN:HA	1:Y:10:LYS:HB3	1.86	0.57
1:g:7:ASN:HA	1:g:10:LYS:HB3	1.86	0.57
1:i:7:ASN:HA	1:i:10:LYS:HB3	1.86	0.57
1:v:7:ASN:HA	1:v:10:LYS:HB3	1.86	0.57
1:q:7:ASN:HA	1:q:10:LYS:HB3	1.86	0.57
1:D:31:GLY:O	1:D:58:LYS:NZ	2.38	0.57
1:E:7:ASN:HA	1:E:10:LYS:HB3	1.86	0.57
1:F:31:GLY:O	1:F:58:LYS:NZ	2.38	0.57
1:d:31:GLY:O	1:d:58:LYS:NZ	2.38	0.57
1:w:7:ASN:HA	1:w:10:LYS:HB3	1.86	0.57
1:V:7:ASN:HA	1:V:10:LYS:HB3	1.86	0.57
1:f:31:GLY:O	1:f:58:LYS:NZ	2.38	0.57
1:j:7:ASN:HA	1:j:10:LYS:HB3	1.86	0.57
1:K:101:MET:SD	1:L:55:TRP:NE1	2.74	0.57
1:N:31:GLY:O	1:N:58:LYS:NZ	2.38	0.57
1:P:31:GLY:O	1:P:58:LYS:NZ	2.38	0.57
1:a:31:GLY:O	1:a:58:LYS:NZ	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:31:GLY:O	1:b:58:LYS:NZ	2.38	0.57
1:A:31:GLY:O	1:A:58:LYS:NZ	2.38	0.57
1:H:31:GLY:O	1:H:58:LYS:NZ	2.38	0.57
1:M:31:GLY:O	1:M:58:LYS:NZ	2.38	0.57
1:B:31:GLY:O	1:B:58:LYS:NZ	2.38	0.56
1:R:31:GLY:O	1:R:58:LYS:NZ	2.38	0.56
1:S:101:MET:SD	1:T:55:TRP:NE1	2.74	0.56
1:Q:84:ASP:HB2	1:q:6:PHE:HB2	1.87	0.56
1:Q:101:MET:SD	1:R:55:TRP:NE1	2.74	0.56
1:A:7:ASN:HA	1:A:10:LYS:HB3	1.86	0.56
1:C:7:ASN:HA	1:C:10:LYS:HB3	1.86	0.56
1:G:84:ASP:HB2	1:g:7:ASN:N	2.20	0.56
1:K:31:GLY:O	1:K:58:LYS:NZ	2.38	0.56
1:O:84:ASP:HB2	1:o:7:ASN:N	2.20	0.56
1:Q:7:ASN:OD1	1:e:84:ASP:HB3	2.05	0.56
1:S:6:PHE:CB	1:g:84:ASP:N	2.67	0.56
1:S:31:GLY:O	1:S:58:LYS:NZ	2.38	0.56
1:c:7:ASN:HA	1:c:10:LYS:HB3	1.86	0.56
1:h:31:GLY:O	1:h:58:LYS:NZ	2.38	0.56
1:m:31:GLY:O	1:m:58:LYS:NZ	2.38	0.56
1:n:31:GLY:O	1:n:58:LYS:NZ	2.38	0.56
1:s:31:GLY:O	1:s:58:LYS:NZ	2.38	0.56
1:E:31:GLY:O	1:E:58:LYS:NZ	2.38	0.56
1:l:31:GLY:O	1:l:58:LYS:NZ	2.38	0.56
1:o:7:ASN:HA	1:o:10:LYS:HB3	1.86	0.56
1:w:31:GLY:O	1:w:58:LYS:NZ	2.38	0.56
1:x:31:GLY:O	1:x:58:LYS:NZ	2.38	0.56
1:K:84:ASP:HB2	1:k:6:PHE:HB2	1.88	0.56
1:M:6:PHE:HD2	1:a:84:ASP:OD1	1.88	0.56
1:g:31:GLY:O	1:g:58:LYS:NZ	2.38	0.56
1:k:7:ASN:HA	1:k:10:LYS:HB3	1.86	0.56
1:n:145:THR:HG23	1:n:148:ARG:HH11	1.71	0.56
1:p:31:GLY:O	1:p:58:LYS:NZ	2.38	0.56
1:x:7:ASN:HA	1:x:10:LYS:HB3	1.86	0.56
1:L:31:GLY:O	1:L:58:LYS:NZ	2.38	0.56
1:O:31:GLY:O	1:O:58:LYS:NZ	2.38	0.56
1:c:31:GLY:O	1:c:58:LYS:NZ	2.38	0.56
1:h:145:THR:HG23	1:h:148:ARG:HH11	1.71	0.56
1:m:7:ASN:HA	1:m:10:LYS:HB3	1.86	0.56
1:p:145:THR:HG23	1:p:148:ARG:HH11	1.71	0.56
1:s:158:ILE:HG12	1:s:212:LEU:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:t:31:GLY:O	1:t:58:LYS:NZ	2.38	0.56
1:B:145:THR:HG23	1:B:148:ARG:HH11	1.71	0.56
1:K:145:THR:HG23	1:K:148:ARG:HH11	1.71	0.56
1:R:145:THR:HG23	1:R:148:ARG:HH11	1.71	0.56
1:V:158:ILE:HG12	1:V:212:LEU:HB3	1.88	0.56
1:r:31:GLY:O	1:r:58:LYS:NZ	2.38	0.56
1:v:158:ILE:HG12	1:v:212:LEU:HB3	1.88	0.56
1:C:31:GLY:O	1:C:58:LYS:NZ	2.38	0.56
1:G:158:ILE:HG12	1:G:212:LEU:HB3	1.88	0.56
1:H:145:THR:HG23	1:H:148:ARG:HH11	1.71	0.56
1:J:145:THR:HG23	1:J:148:ARG:HH11	1.71	0.56
1:K:7:ASN:HA	1:K:10:LYS:HB3	1.86	0.56
1:O:7:ASN:HA	1:O:10:LYS:HB3	1.86	0.56
1:T:145:THR:HG23	1:T:148:ARG:HH11	1.71	0.56
1:W:31:GLY:O	1:W:58:LYS:NZ	2.38	0.56
1:X:7:ASN:HA	1:X:10:LYS:HB3	1.86	0.56
1:a:145:THR:HG23	1:a:148:ARG:HH11	1.71	0.56
1:e:31:GLY:O	1:e:58:LYS:NZ	2.38	0.56
1:i:158:ILE:HG12	1:i:212:LEU:HB3	1.88	0.56
1:r:145:THR:HG23	1:r:148:ARG:HH11	1.71	0.56
1:N:145:THR:HG23	1:N:148:ARG:HH11	1.71	0.56
1:Q:6:PHE:HD2	1:e:84:ASP:OD1	1.88	0.56
1:S:158:ILE:HG12	1:S:212:LEU:HB3	1.88	0.56
1:a:7:ASN:HA	1:a:10:LYS:HB3	1.86	0.56
1:l:145:THR:HG23	1:l:148:ARG:HH11	1.71	0.56
1:o:31:GLY:O	1:o:58:LYS:NZ	2.38	0.56
1:q:31:GLY:O	1:q:58:LYS:NZ	2.38	0.56
1:x:145:THR:HG23	1:x:148:ARG:HH11	1.71	0.56
1:D:145:THR:HG23	1:D:148:ARG:HH11	1.71	0.56
1:G:31:GLY:O	1:G:58:LYS:NZ	2.38	0.56
1:K:158:ILE:HG12	1:K:212:LEU:HB3	1.88	0.56
1:L:145:THR:HG23	1:L:148:ARG:HH11	1.71	0.56
1:M:6:PHE:CB	1:a:84:ASP:N	2.68	0.56
1:X:31:GLY:O	1:X:58:LYS:NZ	2.38	0.56
1:X:158:ILE:HG12	1:X:212:LEU:HB3	1.88	0.56
1:k:31:GLY:O	1:k:58:LYS:NZ	2.38	0.56
1:x:158:ILE:HG12	1:x:212:LEU:HB3	1.88	0.56
1:A:145:THR:HG23	1:A:148:ARG:HH11	1.71	0.55
1:I:84:ASP:HB2	1:i:7:ASN:N	2.21	0.55
1:g:158:ILE:HG12	1:g:212:LEU:HB3	1.88	0.55
1:k:145:THR:HG23	1:k:148:ARG:HH11	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:158:ILE:HG12	1:k:212:LEU:HB3	1.88	0.55
1:n:158:ILE:HG12	1:n:212:LEU:HB3	1.88	0.55
1:C:91:ILE:HG12	1:D:19:LEU:HG	1.89	0.55
1:F:145:THR:HG23	1:F:148:ARG:HH11	1.71	0.55
1:b:145:THR:HG23	1:b:148:ARG:HH11	1.71	0.55
1:i:31:GLY:O	1:i:58:LYS:NZ	2.38	0.55
1:i:145:THR:HG23	1:i:148:ARG:HH11	1.71	0.55
1:t:145:THR:HG23	1:t:148:ARG:HH11	1.71	0.55
1:v:101:MET:SD	1:w:55:TRP:NE1	2.74	0.55
1:E:84:ASP:HB2	1:e:6:PHE:HB2	1.88	0.55
1:I:31:GLY:O	1:I:58:LYS:NZ	2.38	0.55
1:I:158:ILE:HG12	1:I:212:LEU:HB3	1.88	0.55
1:M:84:ASP:HB2	1:m:6:PHE:C	2.32	0.55
1:M:145:THR:HG23	1:M:148:ARG:HH11	1.71	0.55
1:N:158:ILE:HG12	1:N:212:LEU:HB3	1.88	0.55
1:P:145:THR:HG23	1:P:148:ARG:HH11	1.71	0.55
1:P:161:GLU:OE1	1:P:205:GLN:NE2	2.40	0.55
1:v:31:GLY:O	1:v:58:LYS:NZ	2.38	0.55
1:v:145:THR:HG23	1:v:148:ARG:HH11	1.71	0.55
1:y:31:GLY:O	1:y:58:LYS:NZ	2.38	0.55
1:M:91:ILE:HG12	1:N:19:LEU:HG	1.89	0.55
1:V:31:GLY:O	1:V:58:LYS:NZ	2.38	0.55
1:X:84:ASP:HB2	1:x:6:PHE:HB2	1.89	0.55
1:Y:31:GLY:O	1:Y:58:LYS:NZ	2.38	0.55
1:Y:145:THR:HG23	1:Y:148:ARG:HH11	1.71	0.55
1:f:145:THR:HG23	1:f:148:ARG:HH11	1.71	0.55
1:f:161:GLU:OE1	1:f:205:GLN:NE2	2.40	0.55
1:j:31:GLY:O	1:j:58:LYS:NZ	2.38	0.55
1:j:145:THR:HG23	1:j:148:ARG:HH11	1.71	0.55
1:k:161:GLU:OE1	1:k:205:GLN:NE2	2.40	0.55
1:m:161:GLU:OE1	1:m:205:GLN:NE2	2.40	0.55
1:o:267:SER:OG	1:o:268:VAL:N	2.39	0.55
1:q:91:ILE:HG12	1:r:19:LEU:HG	1.89	0.55
1:x:101:MET:SD	1:y:55:TRP:NE1	2.74	0.55
1:K:161:GLU:OE1	1:K:205:GLN:NE2	2.40	0.55
1:M:7:ASN:HA	1:M:10:LYS:HB3	1.86	0.55
1:Q:31:GLY:O	1:Q:58:LYS:NZ	2.38	0.55
1:S:267:SER:OG	1:S:268:VAL:N	2.39	0.55
1:V:101:MET:SD	1:W:55:TRP:NE1	2.74	0.55
1:V:145:THR:HG23	1:V:148:ARG:HH11	1.71	0.55
1:X:7:ASN:OD1	1:k:84:ASP:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:91:ILE:HG12	1:b:19:LEU:HG	1.89	0.55
1:c:91:ILE:HG12	1:d:19:LEU:HG	1.89	0.55
1:d:158:ILE:HG12	1:d:212:LEU:HB3	1.88	0.55
1:t:161:GLU:OE1	1:t:205:GLN:NE2	2.40	0.55
1:A:161:GLU:OE1	1:A:205:GLN:NE2	2.40	0.55
1:B:161:GLU:OE1	1:B:205:GLN:NE2	2.40	0.55
1:C:267:SER:OG	1:C:268:VAL:N	2.39	0.55
1:E:91:ILE:HG12	1:F:19:LEU:HG	1.89	0.55
1:F:161:GLU:OE1	1:F:205:GLN:NE2	2.40	0.55
1:H:158:ILE:HG12	1:H:212:LEU:HB3	1.88	0.55
1:I:101:MET:SD	1:J:55:TRP:NE1	2.74	0.55
1:I:161:GLU:OE1	1:I:205:GLN:NE2	2.40	0.55
1:I:267:SER:OG	1:I:268:VAL:N	2.39	0.55
1:P:158:ILE:HG12	1:P:212:LEU:HB3	1.88	0.55
1:S:91:ILE:HG12	1:T:19:LEU:HG	1.89	0.55
1:T:31:GLY:O	1:T:58:LYS:NZ	2.38	0.55
1:X:145:THR:HG23	1:X:148:ARG:HH11	1.71	0.55
1:b:267:SER:OG	1:b:268:VAL:N	2.39	0.55
1:e:158:ILE:HG12	1:e:212:LEU:HB3	1.88	0.55
1:h:158:ILE:HG12	1:h:212:LEU:HB3	1.88	0.55
1:p:161:GLU:OE1	1:p:205:GLN:NE2	2.40	0.55
1:r:161:GLU:OE1	1:r:205:GLN:NE2	2.40	0.55
1:s:91:ILE:HG12	1:t:19:LEU:HG	1.89	0.55
1:t:158:ILE:HG12	1:t:212:LEU:HB3	1.88	0.55
1:A:267:SER:OG	1:A:268:VAL:N	2.39	0.55
1:E:158:ILE:HG12	1:E:212:LEU:HB3	1.88	0.55
1:H:161:GLU:OE1	1:H:205:GLN:NE2	2.40	0.55
1:J:31:GLY:O	1:J:58:LYS:NZ	2.38	0.55
1:Q:158:ILE:HG12	1:Q:212:LEU:HB3	1.88	0.55
1:Q:161:GLU:OE1	1:Q:205:GLN:NE2	2.40	0.55
1:Q:267:SER:OG	1:Q:268:VAL:N	2.39	0.55
1:S:161:GLU:OE1	1:S:205:GLN:NE2	2.40	0.55
1:m:267:SER:OG	1:m:268:VAL:N	2.39	0.55
1:n:267:SER:OG	1:n:268:VAL:N	2.39	0.55
1:q:158:ILE:HG12	1:q:212:LEU:HB3	1.88	0.55
1:A:84:ASP:HB2	1:a:7:ASN:N	2.22	0.55
1:D:158:ILE:HG12	1:D:212:LEU:HB3	1.88	0.55
1:G:267:SER:OG	1:G:268:VAL:N	2.39	0.55
1:I:145:THR:HG23	1:I:148:ARG:HH11	1.71	0.55
1:O:84:ASP:HB2	1:o:6:PHE:C	2.31	0.55
1:Y:158:ILE:HG12	1:Y:212:LEU:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:158:ILE:HG12	1:a:212:LEU:HB3	1.88	0.55
1:d:161:GLU:OE1	1:d:205:GLN:NE2	2.40	0.55
1:l:267:SER:OG	1:l:268:VAL:N	2.39	0.55
1:m:91:ILE:HG12	1:n:19:LEU:HG	1.89	0.55
1:n:161:GLU:OE1	1:n:205:GLN:NE2	2.40	0.55
1:y:145:THR:HG23	1:y:148:ARG:HH11	1.71	0.55
1:y:158:ILE:HG12	1:y:212:LEU:HB3	1.88	0.55
1:C:161:GLU:OE1	1:C:205:GLN:NE2	2.40	0.55
1:O:145:THR:HG23	1:O:148:ARG:HH11	1.71	0.55
1:R:161:GLU:OE1	1:R:205:GLN:NE2	2.40	0.55
1:T:158:ILE:HG12	1:T:212:LEU:HB3	1.88	0.55
1:c:145:THR:HG23	1:c:148:ARG:HH11	1.71	0.55
1:e:161:GLU:OE1	1:e:205:GLN:NE2	2.40	0.55
1:g:161:GLU:OE1	1:g:205:GLN:NE2	2.40	0.55
1:m:158:ILE:HG12	1:m:212:LEU:HB3	1.88	0.55
1:q:161:GLU:OE1	1:q:205:GLN:NE2	2.40	0.55
1:s:161:GLU:OE1	1:s:205:GLN:NE2	2.40	0.55
1:C:145:THR:HG23	1:C:148:ARG:HH11	1.71	0.55
1:L:267:SER:OG	1:L:268:VAL:N	2.39	0.55
1:P:267:SER:OG	1:P:268:VAL:N	2.39	0.55
1:Q:84:ASP:HB2	1:q:6:PHE:C	2.32	0.55
1:W:158:ILE:HG12	1:W:212:LEU:HB3	1.88	0.55
1:X:161:GLU:OE1	1:X:205:GLN:NE2	2.40	0.55
1:Y:267:SER:OG	1:Y:268:VAL:N	2.39	0.55
1:b:158:ILE:HG12	1:b:212:LEU:HB3	1.88	0.55
1:g:91:ILE:HG12	1:h:19:LEU:HG	1.89	0.55
1:g:267:SER:OG	1:g:268:VAL:N	2.39	0.55
1:t:267:SER:OG	1:t:268:VAL:N	2.39	0.55
1:w:145:THR:HG23	1:w:148:ARG:HH11	1.71	0.55
1:A:91:ILE:HG12	1:B:19:LEU:HG	1.89	0.54
1:B:267:SER:OG	1:B:268:VAL:N	2.39	0.54
1:M:161:GLU:OE1	1:M:205:GLN:NE2	2.40	0.54
1:M:267:SER:OG	1:M:268:VAL:N	2.39	0.54
1:N:267:SER:OG	1:N:268:VAL:N	2.39	0.54
1:O:84:ASP:OD1	1:o:6:PHE:HD2	1.90	0.54
1:O:91:ILE:HG12	1:P:19:LEU:HG	1.89	0.54
1:O:267:SER:OG	1:O:268:VAL:N	2.39	0.54
1:Q:145:THR:HG23	1:Q:148:ARG:HH11	1.71	0.54
1:W:145:THR:HG23	1:W:148:ARG:HH11	1.71	0.54
1:c:267:SER:OG	1:c:268:VAL:N	2.39	0.54
1:i:161:GLU:OE1	1:i:205:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:161:GLU:OE1	1:j:205:GLN:NE2	2.40	0.54
1:w:158:ILE:HG12	1:w:212:LEU:HB3	1.88	0.54
1:y:161:GLU:OE1	1:y:205:GLN:NE2	2.40	0.54
1:G:101:MET:SD	1:H:55:TRP:NE1	2.74	0.54
1:M:158:ILE:HG12	1:M:212:LEU:HB3	1.88	0.54
1:Q:91:ILE:HG12	1:R:19:LEU:HG	1.89	0.54
1:T:161:GLU:OE1	1:T:205:GLN:NE2	2.40	0.54
1:Y:161:GLU:OE1	1:Y:205:GLN:NE2	2.40	0.54
1:j:158:ILE:HG12	1:j:212:LEU:HB3	1.88	0.54
1:m:145:THR:HG23	1:m:148:ARG:HH11	1.71	0.54
1:o:161:GLU:OE1	1:o:205:GLN:NE2	2.40	0.54
1:r:5:ASP:N	1:r:5:ASP:OD1	2.40	0.54
1:s:267:SER:OG	1:s:268:VAL:N	2.39	0.54
1:t:5:ASP:N	1:t:5:ASP:OD1	2.40	0.54
1:v:161:GLU:OE1	1:v:205:GLN:NE2	2.40	0.54
1:y:267:SER:OG	1:y:268:VAL:N	2.39	0.54
1:A:158:ILE:HG12	1:A:212:LEU:HB3	1.88	0.54
1:C:158:ILE:HG12	1:C:212:LEU:HB3	1.88	0.54
1:E:84:ASP:HB2	1:e:7:ASN:N	2.21	0.54
1:F:158:ILE:HG12	1:F:212:LEU:HB3	1.88	0.54
1:J:158:ILE:HG12	1:J:212:LEU:HB3	1.88	0.54
1:O:161:GLU:OE1	1:O:205:GLN:NE2	2.40	0.54
1:Q:70:ASN:ND2	1:R:69:PRO:O	2.41	0.54
1:a:267:SER:OG	1:a:268:VAL:N	2.39	0.54
1:b:161:GLU:OE1	1:b:205:GLN:NE2	2.40	0.54
1:c:161:GLU:OE1	1:c:205:GLN:NE2	2.40	0.54
1:i:267:SER:OG	1:i:268:VAL:N	2.39	0.54
1:o:158:ILE:HG12	1:o:212:LEU:HB3	1.88	0.54
1:q:70:ASN:ND2	1:r:69:PRO:O	2.41	0.54
1:q:267:SER:OG	1:q:268:VAL:N	2.39	0.54
1:B:158:ILE:HG12	1:B:212:LEU:HB3	1.88	0.54
1:E:70:ASN:ND2	1:F:69:PRO:O	2.41	0.54
1:N:161:GLU:OE1	1:N:205:GLN:NE2	2.40	0.54
1:O:158:ILE:HG12	1:O:212:LEU:HB3	1.88	0.54
1:S:70:ASN:ND2	1:T:69:PRO:O	2.41	0.54
1:T:5:ASP:N	1:T:5:ASP:OD1	2.40	0.54
1:V:161:GLU:OE1	1:V:205:GLN:NE2	2.40	0.54
1:W:161:GLU:OE1	1:W:205:GLN:NE2	2.40	0.54
1:e:70:ASN:ND2	1:f:69:PRO:O	2.41	0.54
1:e:145:THR:HG23	1:e:148:ARG:HH11	1.71	0.54
1:g:70:ASN:ND2	1:h:69:PRO:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:145:THR:HG23	1:o:148:ARG:HH11	1.71	0.54
1:p:158:ILE:HG12	1:p:212:LEU:HB3	1.88	0.54
1:q:145:THR:HG23	1:q:148:ARG:HH11	1.71	0.54
1:s:70:ASN:ND2	1:t:69:PRO:O	2.41	0.54
1:x:91:ILE:HG12	1:y:19:LEU:HG	1.89	0.54
1:G:70:ASN:ND2	1:H:69:PRO:O	2.41	0.54
1:I:91:ILE:HG12	1:J:19:LEU:HG	1.89	0.54
1:J:161:GLU:OE1	1:J:205:GLN:NE2	2.40	0.54
1:L:161:GLU:OE1	1:L:205:GLN:NE2	2.40	0.54
1:R:5:ASP:OD1	1:R:5:ASP:N	2.40	0.54
1:X:91:ILE:HG12	1:Y:19:LEU:HG	1.89	0.54
1:a:161:GLU:OE1	1:a:205:GLN:NE2	2.40	0.54
1:d:145:THR:HG23	1:d:148:ARG:HH11	1.71	0.54
1:d:267:SER:OG	1:d:268:VAL:N	2.39	0.54
1:f:158:ILE:HG12	1:f:212:LEU:HB3	1.88	0.54
1:h:161:GLU:OE1	1:h:205:GLN:NE2	2.40	0.54
1:i:101:MET:SD	1:j:55:TRP:NE1	2.74	0.54
1:l:158:ILE:HG12	1:l:212:LEU:HB3	1.88	0.54
1:s:145:THR:HG23	1:s:148:ARG:HH11	1.71	0.54
1:D:161:GLU:OE1	1:D:205:GLN:NE2	2.40	0.54
1:F:5:ASP:N	1:F:5:ASP:OD1	2.40	0.54
1:F:267:SER:OG	1:F:268:VAL:N	2.39	0.54
1:G:161:GLU:OE1	1:G:205:GLN:NE2	2.40	0.54
1:K:267:SER:OG	1:K:268:VAL:N	2.39	0.54
1:M:84:ASP:HB2	1:m:7:ASN:N	2.23	0.54
1:R:158:ILE:HG12	1:R:212:LEU:HB3	1.88	0.54
1:S:145:THR:HG23	1:S:148:ARG:HH11	1.71	0.54
1:X:5:ASP:OD1	1:X:5:ASP:N	2.40	0.54
1:c:158:ILE:HG12	1:c:212:LEU:HB3	1.88	0.54
1:e:91:ILE:HG12	1:f:19:LEU:HG	1.89	0.54
1:e:101:MET:SD	1:f:55:TRP:NE1	2.74	0.54
1:g:101:MET:SD	1:h:55:TRP:NE1	2.74	0.54
1:x:161:GLU:OE1	1:x:205:GLN:NE2	2.40	0.54
1:I:5:ASP:N	1:I:5:ASP:OD1	2.40	0.54
1:I:84:ASP:HB2	1:i:6:PHE:C	2.33	0.54
1:x:267:SER:OG	1:x:268:VAL:N	2.39	0.54
1:E:145:THR:HG23	1:E:148:ARG:HH11	1.71	0.54
1:G:91:ILE:HG12	1:H:19:LEU:HG	1.89	0.54
1:V:267:SER:OG	1:V:268:VAL:N	2.39	0.54
1:k:5:ASP:OD1	1:k:5:ASP:N	2.40	0.54
1:l:161:GLU:OE1	1:l:205:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:5:ASP:OD1	1:p:5:ASP:N	2.40	0.54
1:r:158:ILE:HG12	1:r:212:LEU:HB3	1.88	0.54
1:A:70:ASN:ND2	1:B:69:PRO:O	2.41	0.54
1:E:161:GLU:OE1	1:E:205:GLN:NE2	2.40	0.54
1:H:5:ASP:OD1	1:H:5:ASP:N	2.40	0.54
1:M:70:ASN:ND2	1:N:69:PRO:O	2.41	0.54
1:X:70:ASN:ND2	1:Y:69:PRO:O	2.41	0.54
1:X:267:SER:OG	1:X:268:VAL:N	2.39	0.54
1:a:70:ASN:ND2	1:b:69:PRO:O	2.41	0.54
1:i:5:ASP:N	1:i:5:ASP:OD1	2.40	0.54
1:i:91:ILE:HG12	1:j:19:LEU:HG	1.89	0.54
1:k:70:ASN:ND2	1:l:69:PRO:O	2.41	0.54
1:m:70:ASN:ND2	1:n:69:PRO:O	2.41	0.54
1:o:91:ILE:HG12	1:p:19:LEU:HG	1.89	0.54
1:p:267:SER:OG	1:p:268:VAL:N	2.39	0.54
1:x:70:ASN:ND2	1:y:69:PRO:O	2.41	0.54
1:C:70:ASN:ND2	1:D:69:PRO:O	2.41	0.54
1:G:84:ASP:HB2	1:g:6:PHE:C	2.34	0.54
1:K:70:ASN:ND2	1:L:69:PRO:O	2.41	0.54
1:P:5:ASP:OD1	1:P:5:ASP:N	2.40	0.54
1:V:84:ASP:HB2	1:v:7:ASN:N	2.23	0.54
1:g:145:THR:HG23	1:g:148:ARG:HH11	1.71	0.54
1:k:91:ILE:HG12	1:l:19:LEU:HG	1.89	0.54
1:s:101:MET:SD	1:t:55:TRP:NE1	2.74	0.54
1:w:5:ASP:N	1:w:5:ASP:OD1	2.40	0.54
1:w:161:GLU:OE1	1:w:205:GLN:NE2	2.40	0.54
1:F:85:ARG:HH21	1:F:85:ARG:CG	2.22	0.53
1:L:158:ILE:HG12	1:L:212:LEU:HB3	1.88	0.53
1:c:70:ASN:ND2	1:d:69:PRO:O	2.41	0.53
1:f:85:ARG:HH21	1:f:85:ARG:CG	2.22	0.53
1:x:5:ASP:OD1	1:x:5:ASP:N	2.40	0.53
1:B:85:ARG:HH21	1:B:85:ARG:CG	2.21	0.53
1:D:5:ASP:N	1:D:5:ASP:OD1	2.40	0.53
1:D:85:ARG:HH21	1:D:85:ARG:CG	2.22	0.53
1:O:70:ASN:ND2	1:P:69:PRO:O	2.41	0.53
1:C:84:ASP:HB2	1:c:7:ASN:N	2.23	0.53
1:D:267:SER:OG	1:D:268:VAL:N	2.39	0.53
1:K:84:ASP:HB2	1:k:6:PHE:C	2.33	0.53
1:M:84:ASP:OD1	1:m:6:PHE:HD2	1.91	0.53
1:P:85:ARG:HH21	1:P:85:ARG:CG	2.21	0.53
1:V:5:ASP:N	1:V:5:ASP:OD1	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:70:ASN:ND2	1:W:69:PRO:O	2.41	0.53
1:X:101:MET:SD	1:Y:55:TRP:NE1	2.74	0.53
1:b:85:ARG:HH21	1:b:85:ARG:CG	2.21	0.53
1:o:70:ASN:ND2	1:p:69:PRO:O	2.41	0.53
1:v:70:ASN:ND2	1:w:69:PRO:O	2.41	0.53
1:w:267:SER:OG	1:w:268:VAL:N	2.39	0.53
1:d:85:ARG:HH21	1:d:85:ARG:CG	2.22	0.53
1:f:5:ASP:OD1	1:f:5:ASP:N	2.40	0.53
1:h:5:ASP:OD1	1:h:5:ASP:N	2.40	0.53
1:i:70:ASN:ND2	1:j:69:PRO:O	2.41	0.53
1:k:267:SER:OG	1:k:268:VAL:N	2.39	0.53
1:v:5:ASP:OD1	1:v:5:ASP:N	2.40	0.53
1:I:70:ASN:ND2	1:J:69:PRO:O	2.41	0.53
1:K:5:ASP:OD1	1:K:5:ASP:N	2.40	0.53
1:W:5:ASP:N	1:W:5:ASP:OD1	2.40	0.53
1:p:85:ARG:HH21	1:p:85:ARG:CG	2.21	0.53
1:V:91:ILE:HG12	1:W:19:LEU:HG	1.89	0.53
1:a:5:ASP:N	1:a:5:ASP:OD1	2.40	0.53
1:v:267:SER:OG	1:v:268:VAL:N	2.39	0.53
1:J:5:ASP:OD1	1:J:5:ASP:N	2.40	0.53
1:M:5:ASP:OD1	1:M:5:ASP:N	2.40	0.53
1:N:85:ARG:HH21	1:N:85:ARG:CG	2.21	0.53
1:k:101:MET:SD	1:l:55:TRP:NE1	2.74	0.53
1:K:91:ILE:HG12	1:L:19:LEU:HG	1.89	0.53
1:W:267:SER:OG	1:W:268:VAL:N	2.39	0.53
1:v:91:ILE:HG12	1:w:19:LEU:HG	1.89	0.53
1:A:5:ASP:N	1:A:5:ASP:OD1	2.40	0.53
1:J:267:SER:OG	1:J:268:VAL:N	2.39	0.53
1:O:84:ASP:CB	1:o:6:PHE:HB2	2.39	0.53
1:X:6:PHE:O	1:k:83:LEU:CD1	2.56	0.53
1:d:5:ASP:N	1:d:5:ASP:OD1	2.40	0.53
1:j:267:SER:OG	1:j:268:VAL:N	2.39	0.53
1:G:84:ASP:HB2	1:g:6:PHE:HB2	1.91	0.53
1:G:145:THR:HG23	1:G:148:ARG:HH11	1.71	0.53
1:N:5:ASP:N	1:N:5:ASP:OD1	2.40	0.53
1:n:85:ARG:HH21	1:n:85:ARG:CG	2.21	0.53
1:s:5:ASP:OD1	1:s:5:ASP:N	2.40	0.53
1:E:84:ASP:HB2	1:e:6:PHE:C	2.35	0.52
1:A:84:ASP:HB2	1:a:6:PHE:C	2.34	0.52
1:K:84:ASP:HB2	1:k:7:ASN:N	2.23	0.52
1:S:5:ASP:OD1	1:S:5:ASP:N	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:6:PHE:HB3	1:k:83:LEU:CA	2.38	0.52
1:n:5:ASP:OD1	1:n:5:ASP:N	2.40	0.52
1:G:5:ASP:N	1:G:5:ASP:OD1	2.40	0.52
1:V:6:PHE:HB2	1:i:84:ASP:CB	2.39	0.52
1:g:5:ASP:N	1:g:5:ASP:OD1	2.40	0.52
1:j:5:ASP:N	1:j:5:ASP:OD1	2.40	0.52
1:e:267:SER:OG	1:e:268:VAL:N	2.39	0.52
1:v:97:LEU:HA	1:w:62:GLN:HG2	1.92	0.52
1:y:5:ASP:N	1:y:5:ASP:OD1	2.40	0.52
1:A:97:LEU:HA	1:B:62:GLN:HG2	1.92	0.52
1:B:23:VAL:HG13	1:B:28:GLU:HB3	1.92	0.52
1:L:5:ASP:N	1:L:5:ASP:OD1	2.40	0.52
1:M:69:PRO:O	1:N:70:ASN:ND2	2.43	0.52
1:O:69:PRO:O	1:P:70:ASN:ND2	2.43	0.52
1:a:69:PRO:O	1:b:70:ASN:ND2	2.43	0.52
1:m:5:ASP:OD1	1:m:5:ASP:N	2.40	0.52
1:m:69:PRO:O	1:n:70:ASN:ND2	2.43	0.52
1:o:69:PRO:O	1:p:70:ASN:ND2	2.43	0.52
1:r:23:VAL:HG13	1:r:28:GLU:HB3	1.92	0.52
1:A:69:PRO:O	1:B:70:ASN:ND2	2.43	0.52
1:C:5:ASP:OD1	1:C:5:ASP:N	2.40	0.52
1:C:69:PRO:O	1:D:70:ASN:ND2	2.43	0.52
1:I:84:ASP:HB2	1:i:6:PHE:HB2	1.92	0.52
1:R:23:VAL:HG13	1:R:28:GLU:HB3	1.92	0.52
1:T:267:SER:OG	1:T:268:VAL:N	2.39	0.52
1:V:97:LEU:HA	1:W:62:GLN:HG2	1.92	0.52
1:X:6:PHE:O	1:k:83:LEU:HD12	2.10	0.52
1:a:112:THR:O	1:a:116:ASN:ND2	2.43	0.52
1:c:69:PRO:O	1:d:70:ASN:ND2	2.43	0.52
1:m:97:LEU:HA	1:n:62:GLN:HG2	1.92	0.52
1:n:23:VAL:HG13	1:n:28:GLU:HB3	1.92	0.52
1:p:23:VAL:HG13	1:p:28:GLU:HB3	1.92	0.52
1:r:267:SER:OG	1:r:268:VAL:N	2.39	0.52
1:I:97:LEU:HA	1:J:62:GLN:HG2	1.92	0.52
1:O:6:PHE:O	1:c:83:LEU:CD1	2.58	0.52
1:O:97:LEU:HA	1:P:62:GLN:HG2	1.92	0.52
1:P:23:VAL:HG13	1:P:28:GLU:HB3	1.92	0.52
1:S:6:PHE:HB2	1:g:84:ASP:CB	2.39	0.52
1:b:5:ASP:N	1:b:5:ASP:OD1	2.40	0.52
1:e:112:THR:O	1:e:116:ASN:ND2	2.43	0.52
1:h:23:VAL:HG13	1:h:28:GLU:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:112:THR:O	1:n:116:ASN:ND2	2.43	0.52
1:o:97:LEU:HA	1:p:62:GLN:HG2	1.92	0.52
1:s:23:VAL:HG13	1:s:28:GLU:HB3	1.92	0.52
1:x:69:PRO:O	1:y:70:ASN:ND2	2.43	0.52
1:A:85:ARG:HH21	1:A:85:ARG:HG2	1.75	0.52
1:D:23:VAL:HG13	1:D:28:GLU:HB3	1.92	0.52
1:F:23:VAL:HG13	1:F:28:GLU:HB3	1.92	0.52
1:G:23:VAL:HG13	1:G:28:GLU:HB3	1.92	0.52
1:G:97:LEU:HA	1:H:62:GLN:HG2	1.92	0.52
1:K:85:ARG:HH21	1:K:85:ARG:HG2	1.75	0.52
1:T:23:VAL:HG13	1:T:28:GLU:HB3	1.92	0.52
1:X:69:PRO:O	1:Y:70:ASN:ND2	2.43	0.52
1:X:97:LEU:HA	1:Y:62:GLN:HG2	1.92	0.52
1:a:97:LEU:HA	1:b:62:GLN:HG2	1.92	0.52
1:b:23:VAL:HG13	1:b:28:GLU:HB3	1.92	0.52
1:c:112:THR:O	1:c:116:ASN:ND2	2.43	0.52
1:g:97:LEU:HA	1:h:62:GLN:HG2	1.92	0.52
1:A:112:THR:O	1:A:116:ASN:ND2	2.43	0.52
1:H:23:VAL:HG13	1:H:28:GLU:HB3	1.92	0.52
1:L:112:THR:O	1:L:116:ASN:ND2	2.43	0.52
1:M:112:THR:O	1:M:116:ASN:ND2	2.43	0.52
1:N:23:VAL:HG13	1:N:28:GLU:HB3	1.92	0.52
1:N:112:THR:O	1:N:116:ASN:ND2	2.43	0.52
1:Q:112:THR:O	1:Q:116:ASN:ND2	2.43	0.52
1:S:112:THR:O	1:S:116:ASN:ND2	2.43	0.52
1:T:112:THR:O	1:T:116:ASN:ND2	2.43	0.52
1:V:248:LEU:HD23	1:W:231:VAL:HG11	1.92	0.52
1:X:248:LEU:HD23	1:Y:231:VAL:HG11	1.92	0.52
1:a:85:ARG:HH21	1:a:85:ARG:HG2	1.75	0.52
1:f:23:VAL:HG13	1:f:28:GLU:HB3	1.92	0.52
1:g:112:THR:O	1:g:116:ASN:ND2	2.43	0.52
1:h:112:THR:O	1:h:116:ASN:ND2	2.43	0.52
1:k:85:ARG:HH21	1:k:85:ARG:HG2	1.75	0.52
1:k:97:LEU:HA	1:l:62:GLN:HG2	1.92	0.52
1:k:248:LEU:HD23	1:l:231:VAL:HG11	1.92	0.52
1:m:248:LEU:HD23	1:n:231:VAL:HG11	1.92	0.52
1:q:23:VAL:HG13	1:q:28:GLU:HB3	1.92	0.52
1:r:112:THR:O	1:r:116:ASN:ND2	2.43	0.52
1:v:248:LEU:HD23	1:w:231:VAL:HG11	1.92	0.52
1:x:97:LEU:HA	1:y:62:GLN:HG2	1.92	0.52
1:y:112:THR:O	1:y:116:ASN:ND2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:ASP:OD1	1:B:5:ASP:N	2.40	0.52
1:E:23:VAL:HG13	1:E:28:GLU:HB3	1.92	0.52
1:E:97:LEU:HA	1:F:62:GLN:HG2	1.92	0.52
1:E:112:THR:O	1:E:116:ASN:ND2	2.43	0.52
1:L:23:VAL:HG13	1:L:28:GLU:HB3	1.92	0.52
1:M:85:ARG:HH21	1:M:85:ARG:HG2	1.75	0.52
1:M:97:LEU:HA	1:N:62:GLN:HG2	1.92	0.52
1:O:112:THR:O	1:O:116:ASN:ND2	2.43	0.52
1:Q:23:VAL:HG13	1:Q:28:GLU:HB3	1.92	0.52
1:S:23:VAL:HG13	1:S:28:GLU:HB3	1.92	0.52
1:e:23:VAL:HG13	1:e:28:GLU:HB3	1.92	0.52
1:g:23:VAL:HG13	1:g:28:GLU:HB3	1.92	0.52
1:i:23:VAL:HG13	1:i:28:GLU:HB3	1.92	0.52
1:k:69:PRO:O	1:l:70:ASN:ND2	2.43	0.52
1:l:5:ASP:N	1:l:5:ASP:OD1	2.40	0.52
1:o:112:THR:O	1:o:116:ASN:ND2	2.43	0.52
1:y:23:VAL:HG13	1:y:28:GLU:HB3	1.92	0.52
1:A:248:LEU:HD23	1:B:231:VAL:HG11	1.92	0.51
1:C:112:THR:O	1:C:116:ASN:ND2	2.43	0.51
1:I:23:VAL:HG13	1:I:28:GLU:HB3	1.92	0.51
1:K:69:PRO:O	1:L:70:ASN:ND2	2.43	0.51
1:M:248:LEU:HD23	1:N:231:VAL:HG11	1.92	0.51
1:R:112:THR:O	1:R:116:ASN:ND2	2.43	0.51
1:R:267:SER:OG	1:R:268:VAL:N	2.39	0.51
1:S:7:ASN:OD1	1:g:84:ASP:HB3	2.10	0.51
1:S:97:LEU:HA	1:T:62:GLN:HG2	1.92	0.51
1:V:23:VAL:HG13	1:V:28:GLU:HB3	1.92	0.51
1:c:97:LEU:HA	1:d:62:GLN:HG2	1.92	0.51
1:i:97:LEU:HA	1:j:62:GLN:HG2	1.92	0.51
1:o:5:ASP:N	1:o:5:ASP:OD1	2.40	0.51
1:o:85:ARG:CG	1:o:85:ARG:NH2	2.73	0.51
1:C:84:ASP:HB2	1:c:6:PHE:C	2.35	0.51
1:C:85:ARG:CG	1:C:85:ARG:NH2	2.73	0.51
1:G:112:THR:O	1:G:116:ASN:ND2	2.43	0.51
1:I:112:THR:O	1:I:116:ASN:ND2	2.43	0.51
1:K:97:LEU:HA	1:L:62:GLN:HG2	1.92	0.51
1:K:248:LEU:HD23	1:L:231:VAL:HG11	1.92	0.51
1:O:85:ARG:CG	1:O:85:ARG:NH2	2.73	0.51
1:S:84:ASP:HB2	1:s:6:PHE:C	2.35	0.51
1:V:112:THR:O	1:V:116:ASN:ND2	2.43	0.51
1:X:85:ARG:HH21	1:X:85:ARG:HG2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:5:ASP:N	1:Y:5:ASP:OD1	2.40	0.51
1:b:112:THR:O	1:b:116:ASN:ND2	2.43	0.51
1:c:85:ARG:CG	1:c:85:ARG:NH2	2.73	0.51
1:d:23:VAL:HG13	1:d:28:GLU:HB3	1.92	0.51
1:e:5:ASP:OD1	1:e:5:ASP:N	2.40	0.51
1:e:97:LEU:HA	1:f:62:GLN:HG2	1.92	0.51
1:l:23:VAL:HG13	1:l:28:GLU:HB3	1.92	0.51
1:q:5:ASP:N	1:q:5:ASP:OD1	2.40	0.51
1:q:69:PRO:O	1:r:70:ASN:ND2	2.43	0.51
1:q:97:LEU:HA	1:r:62:GLN:HG2	1.92	0.51
1:t:23:VAL:HG13	1:t:28:GLU:HB3	1.92	0.51
1:x:248:LEU:HD23	1:y:231:VAL:HG11	1.92	0.51
1:B:112:THR:O	1:B:116:ASN:ND2	2.43	0.51
1:C:97:LEU:HA	1:D:62:GLN:HG2	1.92	0.51
1:D:112:THR:O	1:D:116:ASN:ND2	2.43	0.51
1:I:248:LEU:HD23	1:J:231:VAL:HG11	1.92	0.51
1:O:248:LEU:HD23	1:P:231:VAL:HG11	1.92	0.51
1:Q:69:PRO:O	1:R:70:ASN:ND2	2.43	0.51
1:W:23:VAL:HG13	1:W:28:GLU:HB3	1.92	0.51
1:c:248:LEU:HD23	1:d:231:VAL:HG11	1.92	0.51
1:i:248:LEU:HD23	1:j:231:VAL:HG11	1.92	0.51
1:k:112:THR:O	1:k:116:ASN:ND2	2.43	0.51
1:m:85:ARG:HH21	1:m:85:ARG:HG2	1.75	0.51
1:w:23:VAL:HG13	1:w:28:GLU:HB3	1.92	0.51
1:C:85:ARG:HH21	1:C:85:ARG:HG2	1.75	0.51
1:E:5:ASP:OD1	1:E:5:ASP:N	2.40	0.51
1:E:85:ARG:CG	1:E:85:ARG:NH2	2.73	0.51
1:F:112:THR:O	1:F:116:ASN:ND2	2.43	0.51
1:O:5:ASP:N	1:O:5:ASP:OD1	2.40	0.51
1:Q:85:ARG:CG	1:Q:85:ARG:NH2	2.73	0.51
1:Q:97:LEU:HA	1:R:62:GLN:HG2	1.92	0.51
1:W:112:THR:O	1:W:116:ASN:ND2	2.43	0.51
1:Y:23:VAL:HG13	1:Y:28:GLU:HB3	1.92	0.51
1:e:85:ARG:CG	1:e:85:ARG:NH2	2.73	0.51
1:f:267:SER:OG	1:f:268:VAL:N	2.39	0.51
1:h:267:SER:OG	1:h:268:VAL:N	2.39	0.51
1:j:23:VAL:HG13	1:j:28:GLU:HB3	1.92	0.51
1:o:248:LEU:HD23	1:p:231:VAL:HG11	1.92	0.51
1:q:85:ARG:CG	1:q:85:ARG:NH2	2.73	0.51
1:v:23:VAL:HG13	1:v:28:GLU:HB3	1.92	0.51
1:x:85:ARG:HH21	1:x:85:ARG:HG2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:112:THR:O	1:x:116:ASN:ND2	2.43	0.51
1:G:69:PRO:O	1:H:70:ASN:ND2	2.43	0.51
1:K:112:THR:O	1:K:116:ASN:ND2	2.43	0.51
1:O:6:PHE:HD2	1:c:84:ASP:OD1	1.94	0.51
1:Y:112:THR:O	1:Y:116:ASN:ND2	2.43	0.51
1:a:248:LEU:HD23	1:b:231:VAL:HG11	1.92	0.51
1:e:69:PRO:O	1:f:70:ASN:ND2	2.43	0.51
1:v:69:PRO:O	1:w:70:ASN:ND2	2.43	0.51
1:v:112:THR:O	1:v:116:ASN:ND2	2.43	0.51
1:C:248:LEU:HD23	1:D:231:VAL:HG11	1.92	0.51
1:E:69:PRO:O	1:F:70:ASN:ND2	2.43	0.51
1:G:248:LEU:HD23	1:H:231:VAL:HG11	1.92	0.51
1:I:85:ARG:HH21	1:I:85:ARG:HG2	1.75	0.51
1:J:23:VAL:HG13	1:J:28:GLU:HB3	1.92	0.51
1:X:112:THR:O	1:X:116:ASN:ND2	2.43	0.51
1:d:112:THR:O	1:d:116:ASN:ND2	2.43	0.51
1:j:112:THR:O	1:j:116:ASN:ND2	2.43	0.51
1:l:112:THR:O	1:l:116:ASN:ND2	2.43	0.51
1:s:97:LEU:HA	1:t:62:GLN:HG2	1.92	0.51
1:s:112:THR:O	1:s:116:ASN:ND2	2.43	0.51
1:I:69:PRO:O	1:J:70:ASN:ND2	2.43	0.51
1:J:112:THR:O	1:J:116:ASN:ND2	2.43	0.51
1:Q:5:ASP:N	1:Q:5:ASP:OD1	2.40	0.51
1:V:69:PRO:O	1:W:70:ASN:ND2	2.43	0.51
1:X:84:ASP:HB2	1:x:6:PHE:C	2.36	0.51
1:c:85:ARG:HH21	1:c:85:ARG:HG2	1.75	0.51
1:f:112:THR:O	1:f:116:ASN:ND2	2.43	0.51
1:g:69:PRO:O	1:h:70:ASN:ND2	2.43	0.51
1:i:112:THR:O	1:i:116:ASN:ND2	2.43	0.51
1:q:112:THR:O	1:q:116:ASN:ND2	2.43	0.51
1:t:112:THR:O	1:t:116:ASN:ND2	2.43	0.51
1:E:267:SER:OG	1:E:268:VAL:N	2.39	0.51
1:H:112:THR:O	1:H:116:ASN:ND2	2.43	0.51
1:H:267:SER:OG	1:H:268:VAL:N	2.39	0.51
1:M:23:VAL:HG13	1:M:28:GLU:HB3	1.92	0.51
1:V:7:ASN:OD1	1:i:84:ASP:HB3	2.10	0.51
1:g:248:LEU:HD23	1:h:231:VAL:HG11	1.92	0.51
1:i:69:PRO:O	1:j:70:ASN:ND2	2.43	0.51
1:i:85:ARG:HH21	1:i:85:ARG:HG2	1.75	0.51
1:m:23:VAL:HG13	1:m:28:GLU:HB3	1.92	0.51
1:m:112:THR:O	1:m:116:ASN:ND2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:112:THR:O	1:p:116:ASN:ND2	2.43	0.51
1:s:69:PRO:O	1:t:70:ASN:ND2	2.43	0.51
1:s:85:ARG:HH21	1:s:85:ARG:HG2	1.75	0.51
1:C:23:VAL:HG13	1:C:28:GLU:HB3	1.92	0.51
1:E:248:LEU:HD23	1:F:231:VAL:HG11	1.92	0.51
1:I:84:ASP:O	1:i:10:LYS:CG	2.58	0.51
1:O:85:ARG:HH21	1:O:85:ARG:HG2	1.75	0.51
1:S:69:PRO:O	1:T:70:ASN:ND2	2.43	0.51
1:a:23:VAL:HG13	1:a:28:GLU:HB3	1.92	0.51
1:q:85:ARG:HH21	1:q:85:ARG:HG2	1.75	0.51
1:w:112:THR:O	1:w:116:ASN:ND2	2.43	0.51
1:S:85:ARG:HH21	1:S:85:ARG:HG2	1.75	0.51
1:V:6:PHE:HB3	1:i:83:LEU:CA	2.40	0.51
1:V:84:ASP:O	1:v:10:LYS:CG	2.59	0.51
1:c:23:VAL:HG13	1:c:28:GLU:HB3	1.92	0.51
1:q:248:LEU:HD23	1:r:231:VAL:HG11	1.92	0.51
1:x:23:VAL:HG13	1:x:28:GLU:HB3	1.92	0.51
1:Q:248:LEU:HD23	1:R:231:VAL:HG11	1.92	0.50
1:S:248:LEU:HD23	1:T:231:VAL:HG11	1.92	0.50
1:V:85:ARG:HH21	1:V:85:ARG:HG2	1.75	0.50
1:s:248:LEU:HD23	1:t:231:VAL:HG11	1.92	0.50
1:C:84:ASP:OD1	1:c:6:PHE:HD2	1.94	0.50
1:M:84:ASP:CB	1:m:6:PHE:HB2	2.41	0.50
1:O:23:VAL:HG13	1:O:28:GLU:HB3	1.92	0.50
1:Q:85:ARG:HH21	1:Q:85:ARG:HG2	1.75	0.50
1:X:23:VAL:HG13	1:X:28:GLU:HB3	1.92	0.50
1:c:5:ASP:OD1	1:c:5:ASP:N	2.40	0.50
1:o:85:ARG:HH21	1:o:85:ARG:HG2	1.75	0.50
1:A:23:VAL:HG13	1:A:28:GLU:HB3	1.92	0.50
1:E:85:ARG:HH21	1:E:85:ARG:HG2	1.75	0.50
1:G:85:ARG:CG	1:G:85:ARG:NH2	2.73	0.50
1:K:23:VAL:HG13	1:K:28:GLU:HB3	1.92	0.50
1:e:85:ARG:HH21	1:e:85:ARG:HG2	1.75	0.50
1:e:248:LEU:HD23	1:f:231:VAL:HG11	1.92	0.50
1:o:23:VAL:HG13	1:o:28:GLU:HB3	1.92	0.50
1:G:85:ARG:HH21	1:G:85:ARG:HG2	1.75	0.50
1:g:85:ARG:HH21	1:g:85:ARG:HG2	1.75	0.50
1:v:85:ARG:HH21	1:v:85:ARG:HG2	1.75	0.50
1:P:112:THR:O	1:P:116:ASN:ND2	2.43	0.50
1:k:23:VAL:HG13	1:k:28:GLU:HB3	1.92	0.50
1:V:6:PHE:O	1:i:83:LEU:CD1	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:6:PHE:CB	1:e:84:ASP:N	2.74	0.50
1:x:265:GLN:HE22	1:y:219:THR:HA	1.77	0.50
1:K:265:GLN:HE22	1:L:219:THR:HA	1.77	0.50
1:G:19:LEU:HG	1:H:91:ILE:HG12	1.94	0.50
1:P:29:LYS:HE3	1:P:58:LYS:HE2	1.94	0.50
1:X:84:ASP:HB2	1:x:7:ASN:N	2.27	0.50
1:X:265:GLN:HE22	1:Y:219:THR:HA	1.77	0.50
1:F:29:LYS:HE3	1:F:58:LYS:HE2	1.94	0.49
1:I:265:GLN:HE22	1:J:219:THR:HA	1.77	0.49
1:V:6:PHE:O	1:i:83:LEU:HD12	2.12	0.49
1:d:29:LYS:HE3	1:d:58:LYS:HE2	1.94	0.49
1:g:19:LEU:HG	1:h:91:ILE:HG12	1.94	0.49
1:k:265:GLN:HE22	1:l:219:THR:HA	1.77	0.49
1:E:29:LYS:HE3	1:E:58:LYS:HE2	1.95	0.49
1:M:6:PHE:O	1:a:83:LEU:CD1	2.60	0.49
1:V:29:LYS:HE3	1:V:58:LYS:HE2	1.94	0.49
1:q:19:LEU:HG	1:r:91:ILE:HG12	1.95	0.49
1:s:29:LYS:HE3	1:s:58:LYS:HE2	1.95	0.49
1:B:29:LYS:HE3	1:B:58:LYS:HE2	1.94	0.49
1:O:6:PHE:CB	1:c:84:ASP:N	2.73	0.49
1:i:29:LYS:HE3	1:i:58:LYS:HE2	1.95	0.49
1:p:29:LYS:HE3	1:p:58:LYS:HE2	1.94	0.49
1:v:19:LEU:HG	1:w:91:ILE:HG12	1.95	0.49
1:v:265:GLN:HE22	1:w:219:THR:HA	1.77	0.49
1:C:19:LEU:HG	1:D:91:ILE:HG12	1.95	0.49
1:S:19:LEU:HG	1:T:91:ILE:HG12	1.94	0.49
1:S:29:LYS:HE3	1:S:58:LYS:HE2	1.95	0.49
1:c:19:LEU:HG	1:d:91:ILE:HG12	1.95	0.49
1:n:29:LYS:HE3	1:n:58:LYS:HE2	1.94	0.49
1:A:84:ASP:OD1	1:a:6:PHE:HD2	1.95	0.49
1:M:265:GLN:HE22	1:N:219:THR:HA	1.77	0.49
1:X:6:PHE:HB2	1:k:84:ASP:CB	2.41	0.49
1:m:265:GLN:HE22	1:n:219:THR:HA	1.77	0.49
1:I:29:LYS:HE3	1:I:58:LYS:HE2	1.95	0.49
1:O:19:LEU:HG	1:P:91:ILE:HG12	1.94	0.49
1:r:29:LYS:HE3	1:r:58:LYS:HE2	1.94	0.49
1:O:29:LYS:HE3	1:O:58:LYS:HE2	1.94	0.49
1:Q:19:LEU:HG	1:R:91:ILE:HG12	1.95	0.49
1:V:84:ASP:HB2	1:v:6:PHE:C	2.38	0.49
1:e:29:LYS:HE3	1:e:58:LYS:HE2	1.95	0.49
1:f:29:LYS:HE3	1:f:58:LYS:HE2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:85:ARG:HH21	1:h:85:ARG:CG	2.21	0.49
1:q:29:LYS:HE3	1:q:58:LYS:HE2	1.94	0.49
1:D:29:LYS:HE3	1:D:58:LYS:HE2	1.94	0.49
1:S:84:ASP:HB2	1:s:6:PHE:HB2	1.95	0.49
1:V:19:LEU:HG	1:W:91:ILE:HG12	1.95	0.49
1:X:19:LEU:HG	1:Y:91:ILE:HG12	1.94	0.49
1:e:265:GLN:HE22	1:f:219:THR:HA	1.77	0.49
1:q:265:GLN:HE22	1:r:219:THR:HA	1.77	0.49
1:t:29:LYS:HE3	1:t:58:LYS:HE2	1.94	0.49
1:L:29:LYS:HE3	1:L:58:LYS:HE2	1.94	0.49
1:Q:265:GLN:HE22	1:R:219:THR:HA	1.77	0.49
1:a:265:GLN:HE22	1:b:219:THR:HA	1.77	0.49
1:c:29:LYS:HE3	1:c:58:LYS:HE2	1.95	0.49
1:i:265:GLN:HE22	1:j:219:THR:HA	1.77	0.49
1:k:19:LEU:HG	1:l:91:ILE:HG12	1.94	0.49
1:x:19:LEU:HG	1:y:91:ILE:HG12	1.94	0.49
1:A:265:GLN:HE22	1:B:219:THR:HA	1.77	0.49
1:L:86:LYS:HD3	1:L:86:LYS:HA	1.46	0.49
1:M:19:LEU:HG	1:N:91:ILE:HG12	1.95	0.49
1:T:29:LYS:HE3	1:T:58:LYS:HE2	1.95	0.49
1:b:29:LYS:HE3	1:b:58:LYS:HE2	1.94	0.49
1:y:29:LYS:HE3	1:y:58:LYS:HE2	1.94	0.49
1:G:265:GLN:HE22	1:H:219:THR:HA	1.77	0.48
1:K:29:LYS:HE3	1:K:58:LYS:HE2	1.94	0.48
1:T:85:ARG:HH21	1:T:85:ARG:CG	2.21	0.48
1:m:19:LEU:HG	1:n:91:ILE:HG12	1.95	0.48
1:v:29:LYS:HE3	1:v:58:LYS:HE2	1.94	0.48
1:x:29:LYS:HE3	1:x:58:LYS:HE2	1.95	0.48
1:I:19:LEU:HG	1:J:91:ILE:HG12	1.94	0.48
1:g:29:LYS:HE3	1:g:58:LYS:HE2	1.95	0.48
1:o:29:LYS:HE3	1:o:58:LYS:HE2	1.94	0.48
1:o:265:GLN:HE22	1:p:219:THR:HA	1.77	0.48
1:s:19:LEU:HG	1:t:91:ILE:HG12	1.95	0.48
1:E:19:LEU:HG	1:F:91:ILE:HG12	1.95	0.48
1:I:85:ARG:CG	1:I:85:ARG:NH2	2.73	0.48
1:O:265:GLN:HE22	1:P:219:THR:HA	1.77	0.48
1:V:85:ARG:CG	1:V:85:ARG:NH2	2.73	0.48
1:a:19:LEU:HG	1:b:91:ILE:HG12	1.95	0.48
1:g:265:GLN:HE22	1:h:219:THR:HA	1.77	0.48
1:i:19:LEU:HG	1:j:91:ILE:HG12	1.94	0.48
1:i:85:ARG:CG	1:i:85:ARG:NH2	2.73	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:29:LYS:HE3	1:j:58:LYS:HE2	1.94	0.48
1:n:86:LYS:HD3	1:n:86:LYS:HA	1.46	0.48
1:v:85:ARG:CG	1:v:85:ARG:NH2	2.73	0.48
1:C:29:LYS:HE3	1:C:58:LYS:HE2	1.94	0.48
1:G:29:LYS:HE3	1:G:58:LYS:HE2	1.95	0.48
1:G:84:ASP:O	1:g:10:LYS:CG	2.60	0.48
1:K:19:LEU:HG	1:L:91:ILE:HG12	1.95	0.48
1:N:29:LYS:HE3	1:N:58:LYS:HE2	1.94	0.48
1:h:29:LYS:HE3	1:h:58:LYS:HE2	1.95	0.48
1:E:265:GLN:HE22	1:F:219:THR:HA	1.77	0.48
1:J:29:LYS:HE3	1:J:58:LYS:HE2	1.94	0.48
1:V:265:GLN:HE22	1:W:219:THR:HA	1.77	0.48
1:X:85:ARG:CG	1:X:85:ARG:NH2	2.73	0.48
1:e:19:LEU:HG	1:f:91:ILE:HG12	1.95	0.48
1:k:85:ARG:CG	1:k:85:ARG:NH2	2.73	0.48
1:m:114:TYR:OH	1:n:220:HIS:O	2.32	0.48
1:o:19:LEU:HG	1:p:91:ILE:HG12	1.94	0.48
1:x:85:ARG:CG	1:x:85:ARG:NH2	2.73	0.48
1:K:85:ARG:CG	1:K:85:ARG:NH2	2.73	0.48
1:L:72:ASN:ND2	1:L:76:GLU:OE2	2.47	0.48
1:S:84:ASP:O	1:s:10:LYS:CG	2.60	0.48
1:W:29:LYS:HE3	1:W:58:LYS:HE2	1.94	0.48
1:m:29:LYS:HE3	1:m:58:LYS:HE2	1.95	0.48
1:A:86:LYS:HA	1:A:86:LYS:HD3	1.47	0.48
1:C:72:ASN:ND2	1:C:76:GLU:OE2	2.47	0.48
1:J:85:ARG:HH21	1:J:85:ARG:CG	2.21	0.48
1:N:72:ASN:ND2	1:N:76:GLU:OE2	2.47	0.48
1:Q:29:LYS:HE3	1:Q:58:LYS:HE2	1.94	0.48
1:l:72:ASN:ND2	1:l:76:GLU:OE2	2.47	0.48
1:t:85:ARG:HH21	1:t:85:ARG:CG	2.22	0.48
1:A:19:LEU:HG	1:B:91:ILE:HG12	1.95	0.48
1:A:29:LYS:HE3	1:A:58:LYS:HE2	1.95	0.48
1:Q:72:ASN:ND2	1:Q:76:GLU:OE2	2.47	0.48
1:R:29:LYS:HE3	1:R:58:LYS:HE2	1.94	0.48
1:c:72:ASN:ND2	1:c:76:GLU:OE2	2.47	0.48
1:f:72:ASN:ND2	1:f:76:GLU:OE2	2.47	0.48
1:l:29:LYS:HE3	1:l:58:LYS:HE2	1.94	0.48
1:s:265:GLN:HE22	1:t:219:THR:HA	1.77	0.48
1:J:72:ASN:ND2	1:J:76:GLU:OE2	2.47	0.48
1:M:85:ARG:CG	1:M:85:ARG:NH2	2.73	0.48
1:O:86:LYS:HD3	1:O:86:LYS:HA	1.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:72:ASN:ND2	1:T:76:GLU:OE2	2.47	0.48
1:X:72:ASN:ND2	1:X:76:GLU:OE2	2.47	0.48
1:Y:29:LYS:HE3	1:Y:58:LYS:HE2	1.94	0.48
1:m:72:ASN:ND2	1:m:76:GLU:OE2	2.47	0.48
1:m:85:ARG:CG	1:m:85:ARG:NH2	2.73	0.48
1:s:72:ASN:ND2	1:s:76:GLU:OE2	2.47	0.48
1:R:72:ASN:ND2	1:R:76:GLU:OE2	2.47	0.48
1:V:84:ASP:HB2	1:v:6:PHE:HB2	1.96	0.48
1:Y:86:LYS:HD3	1:Y:86:LYS:HA	1.46	0.48
1:b:72:ASN:ND2	1:b:76:GLU:OE2	2.47	0.48
1:e:72:ASN:ND2	1:e:76:GLU:OE2	2.47	0.48
1:k:29:LYS:HE3	1:k:58:LYS:HE2	1.95	0.48
1:k:72:ASN:ND2	1:k:76:GLU:OE2	2.47	0.48
1:n:72:ASN:ND2	1:n:76:GLU:OE2	2.47	0.48
1:P:72:ASN:ND2	1:P:76:GLU:OE2	2.47	0.47
1:X:29:LYS:HE3	1:X:58:LYS:HE2	1.95	0.47
1:c:265:GLN:HE22	1:d:219:THR:HA	1.77	0.47
1:h:86:LYS:HD3	1:h:86:LYS:HA	1.46	0.47
1:m:86:LYS:HD3	1:m:86:LYS:HA	1.47	0.47
1:q:72:ASN:ND2	1:q:76:GLU:OE2	2.47	0.47
1:F:72:ASN:ND2	1:F:76:GLU:OE2	2.47	0.47
1:Q:84:ASP:CB	1:q:6:PHE:HB2	2.44	0.47
1:X:84:ASP:O	1:x:10:LYS:CG	2.61	0.47
1:h:72:ASN:ND2	1:h:76:GLU:OE2	2.47	0.47
1:j:72:ASN:ND2	1:j:76:GLU:OE2	2.47	0.47
1:p:72:ASN:ND2	1:p:76:GLU:OE2	2.47	0.47
1:t:72:ASN:ND2	1:t:76:GLU:OE2	2.47	0.47
1:v:72:ASN:ND2	1:v:76:GLU:OE2	2.47	0.47
1:y:72:ASN:ND2	1:y:76:GLU:OE2	2.47	0.47
1:A:72:ASN:ND2	1:A:76:GLU:OE2	2.47	0.47
1:M:6:PHE:HB2	1:a:84:ASP:CB	2.42	0.47
1:M:29:LYS:HE3	1:M:58:LYS:HE2	1.95	0.47
1:O:72:ASN:ND2	1:O:76:GLU:OE2	2.47	0.47
1:Y:72:ASN:ND2	1:Y:76:GLU:OE2	2.47	0.47
1:j:85:ARG:HH21	1:j:85:ARG:CG	2.21	0.47
1:x:72:ASN:ND2	1:x:76:GLU:OE2	2.47	0.47
1:A:84:ASP:CB	1:a:6:PHE:HB2	2.44	0.47
1:G:72:ASN:ND2	1:G:76:GLU:OE2	2.47	0.47
1:K:84:ASP:OD1	1:k:6:PHE:HD2	1.96	0.47
1:K:114:TYR:OH	1:L:220:HIS:O	2.31	0.47
1:M:6:PHE:O	1:a:83:LEU:HD12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:72:ASN:ND2	1:M:76:GLU:OE2	2.47	0.47
1:O:114:TYR:OH	1:P:220:HIS:O	2.32	0.47
1:Q:84:ASP:OD1	1:q:6:PHE:HD2	1.97	0.47
1:S:72:ASN:ND2	1:S:76:GLU:OE2	2.47	0.47
1:i:72:ASN:ND2	1:i:76:GLU:OE2	2.47	0.47
1:D:72:ASN:ND2	1:D:76:GLU:OE2	2.47	0.47
1:E:72:ASN:ND2	1:E:76:GLU:OE2	2.47	0.47
1:H:29:LYS:HE3	1:H:58:LYS:HE2	1.94	0.47
1:I:72:ASN:ND2	1:I:76:GLU:OE2	2.47	0.47
1:K:72:ASN:ND2	1:K:76:GLU:OE2	2.47	0.47
1:M:114:TYR:OH	1:N:220:HIS:O	2.32	0.47
1:X:86:LYS:HD3	1:X:86:LYS:HA	1.47	0.47
1:S:265:GLN:HE22	1:T:219:THR:HA	1.77	0.47
1:V:72:ASN:ND2	1:V:76:GLU:OE2	2.47	0.47
1:X:84:ASP:OD1	1:x:6:PHE:HD2	1.97	0.47
1:w:29:LYS:HE3	1:w:58:LYS:HE2	1.94	0.47
1:A:144:LEU:O	1:A:148:ARG:HB2	2.15	0.47
1:B:72:ASN:ND2	1:B:76:GLU:OE2	2.47	0.47
1:D:144:LEU:O	1:D:148:ARG:HB2	2.15	0.47
1:H:72:ASN:ND2	1:H:76:GLU:OE2	2.47	0.47
1:H:144:LEU:O	1:H:148:ARG:HB2	2.15	0.47
1:K:84:ASP:O	1:k:10:LYS:CG	2.61	0.47
1:N:144:LEU:O	1:N:148:ARG:HB2	2.15	0.47
1:Q:7:ASN:HB3	1:f:8:VAL:HG12	1.97	0.47
1:R:144:LEU:O	1:R:148:ARG:HB2	2.15	0.47
1:S:48:LYS:O	1:S:52:THR:OG1	2.31	0.47
1:T:144:LEU:O	1:T:148:ARG:HB2	2.15	0.47
1:W:72:ASN:ND2	1:W:76:GLU:OE2	2.47	0.47
1:a:29:LYS:HE3	1:a:58:LYS:HE2	1.95	0.47
1:a:72:ASN:ND2	1:a:76:GLU:OE2	2.47	0.47
1:a:144:LEU:O	1:a:148:ARG:HB2	2.15	0.47
1:b:144:LEU:O	1:b:148:ARG:HB2	2.15	0.47
1:d:72:ASN:ND2	1:d:76:GLU:OE2	2.47	0.47
1:k:144:LEU:O	1:k:148:ARG:HB2	2.15	0.47
1:r:72:ASN:ND2	1:r:76:GLU:OE2	2.47	0.47
1:t:144:LEU:O	1:t:148:ARG:HB2	2.15	0.47
1:w:72:ASN:ND2	1:w:76:GLU:OE2	2.47	0.47
1:C:84:ASP:CB	1:c:6:PHE:HB2	2.44	0.47
1:C:265:GLN:HE22	1:D:219:THR:HA	1.77	0.47
1:M:6:PHE:HB3	1:a:83:LEU:CA	2.43	0.47
1:v:86:LYS:HD3	1:v:86:LYS:HA	1.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:84:ASP:OD1	1:e:6:PHE:HD2	1.97	0.47
1:W:144:LEU:O	1:W:148:ARG:HB2	2.15	0.47
1:f:144:LEU:O	1:f:148:ARG:HB2	2.15	0.47
1:h:144:LEU:O	1:h:148:ARG:HB2	2.15	0.47
1:o:72:ASN:ND2	1:o:76:GLU:OE2	2.47	0.47
1:x:144:LEU:O	1:x:148:ARG:HB2	2.15	0.47
1:F:144:LEU:O	1:F:148:ARG:HB2	2.15	0.47
1:I:144:LEU:O	1:I:148:ARG:HB2	2.15	0.47
1:K:144:LEU:O	1:K:148:ARG:HB2	2.15	0.47
1:L:144:LEU:O	1:L:148:ARG:HB2	2.15	0.47
1:M:144:LEU:O	1:M:148:ARG:HB2	2.15	0.47
1:V:144:LEU:O	1:V:148:ARG:HB2	2.15	0.47
1:W:85:ARG:HH21	1:W:85:ARG:CG	2.21	0.47
1:g:72:ASN:ND2	1:g:76:GLU:OE2	2.47	0.47
1:j:144:LEU:O	1:j:148:ARG:HB2	2.15	0.47
1:l:144:LEU:O	1:l:148:ARG:HB2	2.15	0.47
1:p:144:LEU:O	1:p:148:ARG:HB2	2.15	0.47
1:r:144:LEU:O	1:r:148:ARG:HB2	2.15	0.47
1:w:144:LEU:O	1:w:148:ARG:HB2	2.15	0.47
1:d:144:LEU:O	1:d:148:ARG:HB2	2.15	0.46
1:o:144:LEU:O	1:o:148:ARG:HB2	2.15	0.46
1:O:48:LYS:O	1:O:52:THR:OG1	2.31	0.46
1:i:144:LEU:O	1:i:148:ARG:HB2	2.15	0.46
1:r:86:LYS:HD3	1:r:86:LYS:HA	1.46	0.46
1:v:144:LEU:O	1:v:148:ARG:HB2	2.15	0.46
1:B:144:LEU:O	1:B:148:ARG:HB2	2.15	0.46
1:C:144:LEU:O	1:C:148:ARG:HB2	2.15	0.46
1:Q:114:TYR:OH	1:R:220:HIS:O	2.31	0.46
1:X:144:LEU:O	1:X:148:ARG:HB2	2.15	0.46
1:m:144:LEU:O	1:m:148:ARG:HB2	2.15	0.46
1:n:144:LEU:O	1:n:148:ARG:HB2	2.15	0.46
1:C:48:LYS:O	1:C:52:THR:OG1	2.31	0.46
1:O:6:PHE:O	1:c:83:LEU:HD12	2.16	0.46
1:J:144:LEU:O	1:J:148:ARG:HB2	2.15	0.46
1:Y:144:LEU:O	1:Y:148:ARG:HB2	2.15	0.46
1:s:114:TYR:OH	1:t:220:HIS:O	2.31	0.46
1:a:85:ARG:CG	1:a:85:ARG:NH2	2.73	0.46
1:A:85:ARG:CG	1:A:85:ARG:NH2	2.73	0.46
1:B:86:LYS:HA	1:B:86:LYS:HD3	1.46	0.46
1:a:114:TYR:OH	1:b:220:HIS:O	2.32	0.46
1:c:114:TYR:OH	1:d:220:HIS:O	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:83:LEU:HD13	1:f:83:LEU:HA	1.85	0.46
1:E:84:ASP:CB	1:e:6:PHE:HB2	2.46	0.46
1:G:144:LEU:O	1:G:148:ARG:HB2	2.15	0.46
1:N:86:LYS:HD3	1:N:86:LYS:HA	1.46	0.46
1:O:144:LEU:O	1:O:148:ARG:HB2	2.15	0.46
1:P:144:LEU:O	1:P:148:ARG:HB2	2.15	0.46
1:Q:144:LEU:O	1:Q:148:ARG:HB2	2.15	0.46
1:V:6:PHE:HB2	1:i:84:ASP:CA	2.46	0.46
1:g:144:LEU:O	1:g:148:ARG:HB2	2.15	0.46
1:w:85:ARG:HH21	1:w:85:ARG:CG	2.21	0.46
1:D:83:LEU:HD13	1:D:83:LEU:HA	1.85	0.46
1:N:83:LEU:HD13	1:N:83:LEU:HA	1.85	0.46
1:S:6:PHE:O	1:g:83:LEU:CD1	2.63	0.46
1:S:7:ASN:HB3	1:h:8:VAL:HG12	1.97	0.46
1:o:48:LYS:O	1:o:52:THR:OG1	2.31	0.46
1:q:144:LEU:O	1:q:148:ARG:HB2	2.15	0.46
1:t:83:LEU:HD13	1:t:83:LEU:HA	1.85	0.46
1:t:86:LYS:HD3	1:t:86:LYS:HA	1.46	0.46
1:S:85:ARG:CG	1:S:85:ARG:NH2	2.73	0.46
1:S:144:LEU:O	1:S:148:ARG:HB2	2.15	0.46
1:s:85:ARG:CG	1:s:85:ARG:NH2	2.73	0.46
1:g:85:ARG:CG	1:g:85:ARG:NH2	2.73	0.45
1:N:48:LYS:O	1:N:52:THR:OG1	2.31	0.45
1:i:86:LYS:HD3	1:i:86:LYS:HA	1.47	0.45
1:D:39:ASP:N	1:D:39:ASP:OD1	2.50	0.45
1:G:9:LYS:HA	1:G:12:ALA:HB3	1.99	0.45
1:I:9:LYS:HA	1:I:12:ALA:HB3	1.99	0.45
1:L:39:ASP:OD1	1:L:39:ASP:N	2.50	0.45
1:V:48:LYS:O	1:V:52:THR:OG1	2.31	0.45
1:X:6:PHE:HB2	1:k:84:ASP:CA	2.46	0.45
1:c:144:LEU:O	1:c:148:ARG:HB2	2.15	0.45
1:e:144:LEU:O	1:e:148:ARG:HB2	2.15	0.45
1:g:9:LYS:HA	1:g:12:ALA:HB3	1.99	0.45
1:n:39:ASP:OD1	1:n:39:ASP:N	2.50	0.45
1:p:48:LYS:O	1:p:52:THR:OG1	2.31	0.45
1:N:9:LYS:HA	1:N:12:ALA:HB3	1.99	0.45
1:S:6:PHE:O	1:g:83:LEU:HD12	2.17	0.45
1:S:9:LYS:HA	1:S:12:ALA:HB3	1.99	0.45
1:X:48:LYS:O	1:X:52:THR:OG1	2.31	0.45
1:c:48:LYS:O	1:c:52:THR:OG1	2.31	0.45
1:i:9:LYS:HA	1:i:12:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:y:144:LEU:O	1:y:148:ARG:HB2	2.15	0.45
1:B:9:LYS:HA	1:B:12:ALA:HB3	1.99	0.45
1:I:39:ASP:OD1	1:I:39:ASP:N	2.50	0.45
1:b:9:LYS:HA	1:b:12:ALA:HB3	1.99	0.45
1:b:85:ARG:CG	1:b:85:ARG:NH2	2.79	0.45
1:i:39:ASP:OD1	1:i:39:ASP:N	2.50	0.45
1:n:9:LYS:HA	1:n:12:ALA:HB3	1.99	0.45
1:s:144:LEU:O	1:s:148:ARG:HB2	2.15	0.45
1:v:114:TYR:OH	1:w:220:HIS:O	2.32	0.45
1:B:85:ARG:CG	1:B:85:ARG:NH2	2.79	0.45
1:D:86:LYS:HA	1:D:86:LYS:HD3	1.46	0.45
1:I:48:LYS:O	1:I:52:THR:OG1	2.31	0.45
1:N:39:ASP:OD1	1:N:39:ASP:N	2.50	0.45
1:V:9:LYS:HA	1:V:12:ALA:HB3	1.99	0.45
1:d:39:ASP:OD1	1:d:39:ASP:N	2.50	0.45
1:k:91:ILE:H	1:k:91:ILE:HG13	1.63	0.45
1:l:39:ASP:OD1	1:l:39:ASP:N	2.50	0.45
1:s:9:LYS:HA	1:s:12:ALA:HB3	1.99	0.45
1:A:9:LYS:HA	1:A:12:ALA:HB3	1.99	0.45
1:D:85:ARG:CG	1:D:85:ARG:NH2	2.79	0.45
1:K:9:LYS:HA	1:K:12:ALA:HB3	1.99	0.45
1:N:85:ARG:CG	1:N:85:ARG:NH2	2.79	0.45
1:Q:9:LYS:HA	1:Q:12:ALA:HB3	1.99	0.45
1:V:39:ASP:OD1	1:V:39:ASP:N	2.50	0.45
1:W:86:LYS:HD3	1:W:86:LYS:HA	1.46	0.45
1:e:9:LYS:HA	1:e:12:ALA:HB3	1.99	0.45
1:n:85:ARG:CG	1:n:85:ARG:NH2	2.79	0.45
1:r:85:ARG:CG	1:r:85:ARG:NH2	2.79	0.45
1:C:9:LYS:HA	1:C:12:ALA:HB3	1.99	0.45
1:E:9:LYS:HA	1:E:12:ALA:HB3	1.99	0.45
1:I:86:LYS:HA	1:I:86:LYS:HD3	1.47	0.45
1:O:6:PHE:HB3	1:c:83:LEU:CA	2.45	0.45
1:P:9:LYS:HA	1:P:12:ALA:HB3	1.99	0.45
1:Q:6:PHE:HB2	1:e:84:ASP:CB	2.44	0.45
1:p:9:LYS:HA	1:p:12:ALA:HB3	1.99	0.45
1:v:9:LYS:HA	1:v:12:ALA:HB3	1.99	0.45
1:w:39:ASP:N	1:w:39:ASP:OD1	2.50	0.45
1:L:9:LYS:HA	1:L:12:ALA:HB3	1.99	0.45
1:R:85:ARG:CG	1:R:85:ARG:NH2	2.79	0.45
1:V:114:TYR:OH	1:W:220:HIS:O	2.32	0.45
1:W:39:ASP:N	1:W:39:ASP:OD1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:9:LYS:HA	1:d:12:ALA:HB3	1.99	0.45
1:e:114:TYR:OH	1:f:220:HIS:O	2.32	0.45
1:x:114:TYR:OH	1:y:220:HIS:O	2.32	0.45
1:D:9:LYS:HA	1:D:12:ALA:HB3	1.99	0.45
1:N:68:GLN:NE2	1:N:77:GLU:OE1	2.50	0.45
1:R:39:ASP:N	1:R:39:ASP:OD1	2.50	0.45
1:a:9:LYS:HA	1:a:12:ALA:HB3	1.99	0.45
1:b:83:LEU:HD13	1:b:83:LEU:HA	1.85	0.45
1:c:9:LYS:HA	1:c:12:ALA:HB3	1.99	0.45
1:d:85:ARG:CG	1:d:85:ARG:NH2	2.79	0.45
1:k:9:LYS:HA	1:k:12:ALA:HB3	1.99	0.45
1:n:68:GLN:NE2	1:n:77:GLU:OE1	2.50	0.45
1:p:39:ASP:OD1	1:p:39:ASP:N	2.50	0.45
1:q:9:LYS:HA	1:q:12:ALA:HB3	1.99	0.45
1:q:48:LYS:O	1:q:52:THR:OG1	2.31	0.45
1:v:48:LYS:O	1:v:52:THR:OG1	2.31	0.45
1:y:83:LEU:HD13	1:y:83:LEU:HA	1.85	0.45
1:D:68:GLN:NE2	1:D:77:GLU:OE1	2.50	0.44
1:r:39:ASP:N	1:r:39:ASP:OD1	2.50	0.44
1:y:48:LYS:O	1:y:52:THR:OG1	2.31	0.44
1:F:85:ARG:CG	1:F:85:ARG:NH2	2.79	0.44
1:G:84:ASP:OD1	1:g:6:PHE:HD2	2.00	0.44
1:H:39:ASP:OD1	1:H:39:ASP:N	2.50	0.44
1:O:9:LYS:HA	1:O:12:ALA:HB3	1.99	0.44
1:P:39:ASP:OD1	1:P:39:ASP:N	2.50	0.44
1:P:85:ARG:CG	1:P:85:ARG:NH2	2.79	0.44
1:S:114:TYR:OH	1:T:220:HIS:O	2.32	0.44
1:Y:9:LYS:HA	1:Y:12:ALA:HB3	1.99	0.44
1:Y:68:GLN:NE2	1:Y:77:GLU:OE1	2.50	0.44
1:b:68:GLN:NE2	1:b:77:GLU:OE1	2.50	0.44
1:d:68:GLN:NE2	1:d:77:GLU:OE1	2.51	0.44
1:f:39:ASP:OD1	1:f:39:ASP:N	2.50	0.44
1:f:48:LYS:O	1:f:52:THR:OG1	2.31	0.44
1:f:85:ARG:CG	1:f:85:ARG:NH2	2.79	0.44
1:l:9:LYS:HA	1:l:12:ALA:HB3	1.99	0.44
1:y:68:GLN:NE2	1:y:77:GLU:OE1	2.50	0.44
1:E:144:LEU:O	1:E:148:ARG:HB2	2.15	0.44
1:F:83:LEU:HD13	1:F:83:LEU:HA	1.85	0.44
1:G:68:GLN:NE2	1:G:77:GLU:OE1	2.50	0.44
1:M:9:LYS:HA	1:M:12:ALA:HB3	1.99	0.44
1:P:68:GLN:NE2	1:P:77:GLU:OE1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:6:PHE:O	1:e:83:LEU:CD1	2.64	0.44
1:V:68:GLN:NE2	1:V:77:GLU:OE1	2.50	0.44
1:Y:39:ASP:OD1	1:Y:39:ASP:N	2.50	0.44
1:l:68:GLN:NE2	1:l:77:GLU:OE1	2.50	0.44
1:n:144:LEU:O	1:n:148:ARG:CB	2.66	0.44
1:o:68:GLN:NE2	1:o:77:GLU:OE1	2.50	0.44
1:y:39:ASP:OD1	1:y:39:ASP:N	2.50	0.44
1:G:144:LEU:O	1:G:148:ARG:CB	2.66	0.44
1:H:144:LEU:O	1:H:148:ARG:CB	2.66	0.44
1:L:68:GLN:NE2	1:L:77:GLU:OE1	2.50	0.44
1:M:68:GLN:NE2	1:M:77:GLU:OE1	2.50	0.44
1:Q:48:LYS:O	1:Q:52:THR:OG1	2.31	0.44
1:S:6:PHE:HB3	1:g:83:LEU:CA	2.44	0.44
1:T:83:LEU:HD13	1:T:83:LEU:HA	1.85	0.44
1:g:68:GLN:NE2	1:g:77:GLU:OE1	2.50	0.44
1:h:39:ASP:N	1:h:39:ASP:OD1	2.50	0.44
1:i:68:GLN:NE2	1:i:77:GLU:OE1	2.50	0.44
1:j:39:ASP:OD1	1:j:39:ASP:N	2.50	0.44
1:m:68:GLN:NE2	1:m:77:GLU:OE1	2.50	0.44
1:n:67:LEU:O	1:n:90:ARG:NH2	2.51	0.44
1:q:144:LEU:O	1:q:148:ARG:CB	2.66	0.44
1:s:67:LEU:O	1:s:90:ARG:NH2	2.51	0.44
1:t:144:LEU:O	1:t:148:ARG:CB	2.66	0.44
1:v:39:ASP:OD1	1:v:39:ASP:N	2.50	0.44
1:v:67:LEU:O	1:v:90:ARG:NH2	2.51	0.44
1:v:68:GLN:NE2	1:v:77:GLU:OE1	2.50	0.44
1:B:68:GLN:NE2	1:B:77:GLU:OE1	2.50	0.44
1:B:144:LEU:O	1:B:148:ARG:CB	2.66	0.44
1:C:68:GLN:NE2	1:C:77:GLU:OE1	2.50	0.44
1:H:85:ARG:NH2	1:H:85:ARG:CG	2.79	0.44
1:J:9:LYS:HA	1:J:12:ALA:HB3	1.99	0.44
1:O:68:GLN:NE2	1:O:77:GLU:OE1	2.50	0.44
1:O:144:LEU:O	1:O:148:ARG:CB	2.66	0.44
1:Q:144:LEU:O	1:Q:148:ARG:CB	2.66	0.44
1:S:67:LEU:O	1:S:90:ARG:NH2	2.51	0.44
1:S:68:GLN:NE2	1:S:77:GLU:OE1	2.50	0.44
1:V:67:LEU:O	1:V:90:ARG:NH2	2.51	0.44
1:X:9:LYS:HA	1:X:12:ALA:HB3	1.99	0.44
1:b:39:ASP:OD1	1:b:39:ASP:N	2.50	0.44
1:c:68:GLN:NE2	1:c:77:GLU:OE1	2.50	0.44
1:g:144:LEU:O	1:g:148:ARG:CB	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:67:LEU:O	1:i:90:ARG:NH2	2.51	0.44
1:i:144:LEU:O	1:i:148:ARG:CB	2.66	0.44
1:p:68:GLN:NE2	1:p:77:GLU:OE1	2.51	0.44
1:p:85:ARG:CG	1:p:85:ARG:NH2	2.79	0.44
1:w:91:ILE:H	1:w:91:ILE:HG13	1.63	0.44
1:y:9:LYS:HA	1:y:12:ALA:HB3	1.99	0.44
1:A:144:LEU:O	1:A:148:ARG:CB	2.66	0.44
1:G:67:LEU:O	1:G:90:ARG:NH2	2.51	0.44
1:H:67:LEU:O	1:H:90:ARG:NH2	2.51	0.44
1:I:68:GLN:NE2	1:I:77:GLU:OE1	2.50	0.44
1:J:39:ASP:OD1	1:J:39:ASP:N	2.50	0.44
1:K:67:LEU:O	1:K:90:ARG:NH2	2.51	0.44
1:K:84:ASP:CB	1:k:6:PHE:HB2	2.46	0.44
1:K:144:LEU:O	1:K:148:ARG:CB	2.66	0.44
1:L:144:LEU:O	1:L:148:ARG:CB	2.66	0.44
1:Q:84:ASP:HB3	1:q:7:ASN:CG	2.41	0.44
1:V:144:LEU:O	1:V:148:ARG:CB	2.66	0.44
1:a:68:GLN:NE2	1:a:77:GLU:OE1	2.50	0.44
1:d:86:LYS:HD3	1:d:86:LYS:HA	1.46	0.44
1:f:9:LYS:HA	1:f:12:ALA:HB3	1.99	0.44
1:h:67:LEU:O	1:h:90:ARG:NH2	2.51	0.44
1:p:67:LEU:O	1:p:90:ARG:NH2	2.51	0.44
1:q:86:LYS:HA	1:q:86:LYS:HD3	1.47	0.44
1:x:67:LEU:O	1:x:90:ARG:NH2	2.51	0.44
1:A:114:TYR:OH	1:B:220:HIS:O	2.32	0.44
1:C:114:TYR:OH	1:D:220:HIS:O	2.32	0.44
1:F:9:LYS:HA	1:F:12:ALA:HB3	1.99	0.44
1:R:9:LYS:HA	1:R:12:ALA:HB3	1.99	0.44
1:R:91:ILE:H	1:R:91:ILE:HG13	1.63	0.44
1:R:144:LEU:O	1:R:148:ARG:CB	2.66	0.44
1:S:6:PHE:HB2	1:g:84:ASP:CA	2.48	0.44
1:S:84:ASP:HB3	1:s:7:ASN:CG	2.39	0.44
1:b:96:LEU:HD12	1:b:96:LEU:HA	1.86	0.44
1:i:114:TYR:OH	1:j:220:HIS:O	2.32	0.44
1:j:144:LEU:O	1:j:148:ARG:CB	2.66	0.44
1:m:9:LYS:HA	1:m:12:ALA:HB3	1.99	0.44
1:o:39:ASP:N	1:o:39:ASP:OD1	2.50	0.44
1:q:224:LEU:O	1:q:228:ASN:ND2	2.50	0.44
1:r:9:LYS:HA	1:r:12:ALA:HB3	1.99	0.44
1:t:67:LEU:O	1:t:90:ARG:NH2	2.51	0.44
1:t:96:LEU:HD12	1:t:96:LEU:HA	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:144:LEU:O	1:v:148:ARG:CB	2.66	0.44
1:w:67:LEU:O	1:w:90:ARG:NH2	2.51	0.44
1:w:83:LEU:HD13	1:w:83:LEU:HA	1.85	0.44
1:x:144:LEU:O	1:x:148:ARG:CB	2.66	0.44
1:y:144:LEU:O	1:y:148:ARG:CB	2.66	0.44
1:B:67:LEU:O	1:B:90:ARG:NH2	2.51	0.44
1:F:68:GLN:NE2	1:F:77:GLU:OE1	2.50	0.44
1:G:48:LYS:O	1:G:52:THR:OG1	2.31	0.44
1:I:67:LEU:O	1:I:90:ARG:NH2	2.51	0.44
1:K:48:LYS:O	1:K:52:THR:OG1	2.31	0.44
1:K:67:LEU:HB3	1:K:136:ILE:HG22	2.00	0.44
1:P:144:LEU:O	1:P:148:ARG:CB	2.66	0.44
1:Q:224:LEU:O	1:Q:228:ASN:ND2	2.50	0.44
1:W:144:LEU:O	1:W:148:ARG:CB	2.66	0.44
1:Y:83:LEU:HD13	1:Y:83:LEU:HA	1.85	0.44
1:a:144:LEU:O	1:a:148:ARG:CB	2.66	0.44
1:c:67:LEU:HB3	1:c:136:ILE:HG22	2.00	0.44
1:c:144:LEU:O	1:c:148:ARG:CB	2.66	0.44
1:e:67:LEU:O	1:e:90:ARG:NH2	2.51	0.44
1:e:144:LEU:O	1:e:148:ARG:CB	2.66	0.44
1:f:68:GLN:NE2	1:f:77:GLU:OE1	2.50	0.44
1:f:224:LEU:O	1:f:228:ASN:ND2	2.50	0.44
1:i:91:ILE:H	1:i:91:ILE:HG13	1.63	0.44
1:j:9:LYS:HA	1:j:12:ALA:HB3	1.99	0.44
1:j:96:LEU:HD12	1:j:96:LEU:HA	1.86	0.44
1:m:67:LEU:HB3	1:m:136:ILE:HG22	2.00	0.44
1:m:144:LEU:O	1:m:148:ARG:CB	2.66	0.44
1:o:9:LYS:HA	1:o:12:ALA:HB3	1.99	0.44
1:r:144:LEU:O	1:r:148:ARG:CB	2.66	0.44
1:s:68:GLN:NE2	1:s:77:GLU:OE1	2.50	0.44
1:A:67:LEU:HB3	1:A:136:ILE:HG22	2.00	0.44
1:A:68:GLN:NE2	1:A:77:GLU:OE1	2.50	0.44
1:C:39:ASP:OD1	1:C:39:ASP:N	2.50	0.44
1:C:144:LEU:O	1:C:148:ARG:CB	2.66	0.44
1:E:67:LEU:O	1:E:90:ARG:NH2	2.51	0.44
1:E:144:LEU:O	1:E:148:ARG:CB	2.66	0.44
1:F:39:ASP:OD1	1:F:39:ASP:N	2.50	0.44
1:M:67:LEU:HB3	1:M:136:ILE:HG22	2.00	0.44
1:N:67:LEU:O	1:N:90:ARG:NH2	2.51	0.44
1:V:7:ASN:HB3	1:j:8:VAL:HG12	1.99	0.44
1:W:9:LYS:HA	1:W:12:ALA:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:144:LEU:O	1:d:148:ARG:CB	2.66	0.44
1:h:85:ARG:CG	1:h:85:ARG:NH2	2.79	0.44
1:o:144:LEU:O	1:o:148:ARG:CB	2.66	0.44
1:x:67:LEU:HB3	1:x:136:ILE:HG22	2.00	0.44
1:E:84:ASP:O	1:e:10:LYS:CG	2.65	0.43
1:E:97:LEU:HD13	1:F:62:GLN:HG2	2.00	0.43
1:E:114:TYR:OH	1:F:220:HIS:O	2.31	0.43
1:F:144:LEU:O	1:F:148:ARG:CB	2.66	0.43
1:G:91:ILE:H	1:G:91:ILE:HG13	1.63	0.43
1:H:9:LYS:HA	1:H:12:ALA:HB3	1.99	0.43
1:H:85:ARG:HH21	1:H:85:ARG:CG	2.21	0.43
1:P:67:LEU:O	1:P:90:ARG:NH2	2.51	0.43
1:S:86:LYS:HA	1:S:86:LYS:HD3	1.47	0.43
1:S:144:LEU:O	1:S:148:ARG:CB	2.66	0.43
1:T:67:LEU:O	1:T:90:ARG:NH2	2.51	0.43
1:W:67:LEU:O	1:W:90:ARG:NH2	2.51	0.43
1:X:67:LEU:HB3	1:X:136:ILE:HG22	2.00	0.43
1:Y:144:LEU:O	1:Y:148:ARG:CB	2.66	0.43
1:b:67:LEU:O	1:b:90:ARG:NH2	2.51	0.43
1:f:144:LEU:O	1:f:148:ARG:CB	2.66	0.43
1:h:144:LEU:O	1:h:148:ARG:CB	2.66	0.43
1:o:67:LEU:HB3	1:o:136:ILE:HG22	2.00	0.43
1:p:144:LEU:O	1:p:148:ARG:CB	2.66	0.43
1:s:144:LEU:O	1:s:148:ARG:CB	2.66	0.43
1:x:9:LYS:HA	1:x:12:ALA:HB3	1.99	0.43
1:B:83:LEU:HD13	1:B:83:LEU:HA	1.85	0.43
1:C:67:LEU:HB3	1:C:136:ILE:HG22	2.00	0.43
1:D:67:LEU:O	1:D:90:ARG:NH2	2.51	0.43
1:M:39:ASP:N	1:M:39:ASP:OD1	2.50	0.43
1:N:144:LEU:O	1:N:148:ARG:CB	2.66	0.43
1:Q:67:LEU:O	1:Q:90:ARG:NH2	2.51	0.43
1:R:68:GLN:NE2	1:R:77:GLU:OE1	2.50	0.43
1:S:97:LEU:HD13	1:T:62:GLN:HG2	2.01	0.43
1:T:39:ASP:N	1:T:39:ASP:OD1	2.50	0.43
1:T:144:LEU:O	1:T:148:ARG:CB	2.66	0.43
1:X:67:LEU:O	1:X:90:ARG:NH2	2.51	0.43
1:a:67:LEU:HB3	1:a:136:ILE:HG22	2.00	0.43
1:b:144:LEU:O	1:b:148:ARG:CB	2.66	0.43
1:g:97:LEU:HD13	1:h:62:GLN:HG2	2.00	0.43
1:j:91:ILE:H	1:j:91:ILE:HG13	1.63	0.43
1:k:144:LEU:O	1:k:148:ARG:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:173:ASP:HA	1:p:176:LYS:HE2	2.01	0.43
1:q:97:LEU:HD13	1:r:62:GLN:HG2	2.01	0.43
1:t:39:ASP:OD1	1:t:39:ASP:N	2.50	0.43
1:v:97:LEU:HD13	1:w:62:GLN:HG2	2.00	0.43
1:C:86:LYS:HA	1:C:86:LYS:HD3	1.47	0.43
1:D:144:LEU:O	1:D:148:ARG:CB	2.66	0.43
1:J:67:LEU:O	1:J:90:ARG:NH2	2.51	0.43
1:L:224:LEU:O	1:L:228:ASN:ND2	2.50	0.43
1:P:173:ASP:HA	1:P:176:LYS:HE2	2.01	0.43
1:T:9:LYS:HA	1:T:12:ALA:HB3	1.99	0.43
1:W:68:GLN:NE2	1:W:77:GLU:OE1	2.50	0.43
1:X:68:GLN:NE2	1:X:77:GLU:OE1	2.50	0.43
1:b:91:ILE:H	1:b:91:ILE:HG13	1.63	0.43
1:e:48:LYS:O	1:e:52:THR:OG1	2.31	0.43
1:h:9:LYS:HA	1:h:12:ALA:HB3	1.99	0.43
1:k:67:LEU:O	1:k:90:ARG:NH2	2.51	0.43
1:l:67:LEU:O	1:l:90:ARG:NH2	2.51	0.43
1:l:144:LEU:O	1:l:148:ARG:CB	2.66	0.43
1:m:39:ASP:OD1	1:m:39:ASP:N	2.50	0.43
1:w:9:LYS:HA	1:w:12:ALA:HB3	1.99	0.43
1:w:68:GLN:NE2	1:w:77:GLU:OE1	2.50	0.43
1:x:68:GLN:NE2	1:x:77:GLU:OE1	2.50	0.43
1:A:67:LEU:O	1:A:90:ARG:NH2	2.51	0.43
1:E:39:ASP:N	1:E:39:ASP:OD1	2.50	0.43
1:G:97:LEU:HD13	1:H:62:GLN:HG2	2.01	0.43
1:I:91:ILE:H	1:I:91:ILE:HG13	1.63	0.43
1:J:67:LEU:HB3	1:J:136:ILE:HG22	2.00	0.43
1:J:144:LEU:O	1:J:148:ARG:CB	2.66	0.43
1:O:39:ASP:N	1:O:39:ASP:OD1	2.50	0.43
1:O:67:LEU:HB3	1:O:136:ILE:HG22	2.01	0.43
1:Q:84:ASP:N	1:q:6:PHE:HB2	2.33	0.43
1:Q:97:LEU:HD13	1:R:62:GLN:HG2	2.01	0.43
1:R:67:LEU:O	1:R:90:ARG:NH2	2.51	0.43
1:T:173:ASP:HA	1:T:176:LYS:HE2	2.01	0.43
1:Y:67:LEU:O	1:Y:90:ARG:NH2	2.51	0.43
1:d:96:LEU:HD12	1:d:96:LEU:HA	1.86	0.43
1:d:173:ASP:HA	1:d:176:LYS:HE2	2.01	0.43
1:e:224:LEU:O	1:e:228:ASN:ND2	2.50	0.43
1:h:173:ASP:HA	1:h:176:LYS:HE2	2.01	0.43
1:j:67:LEU:HB3	1:j:136:ILE:HG22	2.00	0.43
1:j:68:GLN:NE2	1:j:77:GLU:OE1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:67:LEU:O	1:q:90:ARG:NH2	2.51	0.43
1:r:67:LEU:O	1:r:90:ARG:NH2	2.51	0.43
1:r:85:ARG:HH21	1:r:85:ARG:CG	2.22	0.43
1:t:173:ASP:HA	1:t:176:LYS:HE2	2.01	0.43
1:w:86:LYS:HA	1:w:86:LYS:HD3	1.46	0.43
1:C:224:LEU:O	1:C:228:ASN:ND2	2.50	0.43
1:E:48:LYS:O	1:E:52:THR:OG1	2.31	0.43
1:E:68:GLN:NE2	1:E:77:GLU:OE1	2.50	0.43
1:F:173:ASP:HA	1:F:176:LYS:HE2	2.01	0.43
1:G:224:LEU:O	1:G:228:ASN:ND2	2.50	0.43
1:H:68:GLN:NE2	1:H:77:GLU:OE1	2.50	0.43
1:I:97:LEU:HD13	1:J:62:GLN:HG2	2.01	0.43
1:J:173:ASP:HA	1:J:176:LYS:HE2	2.01	0.43
1:L:83:LEU:HD13	1:L:83:LEU:HA	1.85	0.43
1:O:67:LEU:O	1:O:90:ARG:NH2	2.51	0.43
1:Q:67:LEU:HB3	1:Q:136:ILE:HG22	2.00	0.43
1:T:85:ARG:CG	1:T:85:ARG:NH2	2.79	0.43
1:V:97:LEU:HD13	1:W:62:GLN:HG2	2.00	0.43
1:V:173:ASP:HA	1:V:176:LYS:HE2	2.01	0.43
1:X:173:ASP:HA	1:X:176:LYS:HE2	2.01	0.43
1:a:173:ASP:HA	1:a:176:LYS:HE2	2.01	0.43
1:c:67:LEU:O	1:c:90:ARG:NH2	2.51	0.43
1:c:97:LEU:HD13	1:d:62:GLN:HG2	2.01	0.43
1:e:97:LEU:HD13	1:f:62:GLN:HG2	2.01	0.43
1:g:67:LEU:O	1:g:90:ARG:NH2	2.51	0.43
1:g:224:LEU:O	1:g:228:ASN:ND2	2.50	0.43
1:h:68:GLN:NE2	1:h:77:GLU:OE1	2.50	0.43
1:k:67:LEU:HB3	1:k:136:ILE:HG22	2.00	0.43
1:k:68:GLN:NE2	1:k:77:GLU:OE1	2.50	0.43
1:o:67:LEU:O	1:o:90:ARG:NH2	2.51	0.43
1:t:9:LYS:HA	1:t:12:ALA:HB3	1.99	0.43
1:y:67:LEU:HB3	1:y:136:ILE:HG22	2.00	0.43
1:D:224:LEU:O	1:D:228:ASN:ND2	2.50	0.43
1:E:86:LYS:HD3	1:E:86:LYS:HA	1.47	0.43
1:I:144:LEU:O	1:I:148:ARG:CB	2.66	0.43
1:K:86:LYS:HA	1:K:86:LYS:HD3	1.47	0.43
1:O:97:LEU:HD13	1:P:62:GLN:HG2	2.01	0.43
1:V:67:LEU:HB3	1:V:136:ILE:HG22	2.00	0.43
1:a:39:ASP:OD1	1:a:39:ASP:N	2.50	0.43
1:e:39:ASP:OD1	1:e:39:ASP:N	2.50	0.43
1:e:67:LEU:HB3	1:e:136:ILE:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:97:LEU:HD13	1:j:62:GLN:HG2	2.01	0.43
1:i:173:ASP:HA	1:i:176:LYS:HE2	2.01	0.43
1:k:173:ASP:HA	1:k:176:LYS:HE2	2.01	0.43
1:l:224:LEU:O	1:l:228:ASN:ND2	2.50	0.43
1:m:67:LEU:O	1:m:90:ARG:NH2	2.51	0.43
1:r:68:GLN:NE2	1:r:77:GLU:OE1	2.51	0.43
1:s:97:LEU:HD13	1:t:62:GLN:HG2	2.01	0.43
1:w:144:LEU:O	1:w:148:ARG:CB	2.66	0.43
1:B:39:ASP:N	1:B:39:ASP:OD1	2.50	0.43
1:C:97:LEU:HD13	1:D:62:GLN:HG2	2.01	0.43
1:I:67:LEU:HB3	1:I:136:ILE:HG22	2.00	0.43
1:I:173:ASP:HA	1:I:176:LYS:HE2	2.01	0.43
1:J:68:GLN:NE2	1:J:77:GLU:OE1	2.50	0.43
1:K:68:GLN:NE2	1:K:77:GLU:OE1	2.50	0.43
1:K:173:ASP:HA	1:K:176:LYS:HE2	2.01	0.43
1:M:6:PHE:HB2	1:a:84:ASP:CA	2.49	0.43
1:R:85:ARG:HH21	1:R:85:ARG:CG	2.21	0.43
1:T:68:GLN:NE2	1:T:77:GLU:OE1	2.50	0.43
1:W:67:LEU:HB3	1:W:136:ILE:HG22	2.00	0.43
1:X:144:LEU:O	1:X:148:ARG:CB	2.66	0.43
1:a:67:LEU:O	1:a:90:ARG:NH2	2.51	0.43
1:c:39:ASP:OD1	1:c:39:ASP:N	2.50	0.43
1:e:68:GLN:NE2	1:e:77:GLU:OE1	2.50	0.43
1:g:86:LYS:HA	1:g:86:LYS:HD3	1.47	0.43
1:j:173:ASP:HA	1:j:176:LYS:HE2	2.01	0.43
1:q:67:LEU:HB3	1:q:136:ILE:HG22	2.00	0.43
1:x:173:ASP:HA	1:x:176:LYS:HE2	2.01	0.43
1:D:67:LEU:HB3	1:D:136:ILE:HG22	2.00	0.43
1:E:67:LEU:HB3	1:E:136:ILE:HG22	2.00	0.43
1:J:224:LEU:O	1:J:228:ASN:ND2	2.50	0.43
1:L:67:LEU:O	1:L:90:ARG:NH2	2.51	0.43
1:Q:68:GLN:NE2	1:Q:77:GLU:OE1	2.50	0.43
1:Q:84:ASP:O	1:q:10:LYS:CG	2.65	0.43
1:c:224:LEU:O	1:c:228:ASN:ND2	2.50	0.43
1:f:67:LEU:O	1:f:90:ARG:NH2	2.51	0.43
1:i:67:LEU:HB3	1:i:136:ILE:HG22	2.00	0.43
1:o:97:LEU:HD13	1:p:62:GLN:HG2	2.01	0.43
1:p:86:LYS:HD3	1:p:86:LYS:HA	1.46	0.43
1:s:48:LYS:O	1:s:52:THR:OG1	2.31	0.43
1:t:67:LEU:HB3	1:t:136:ILE:HG22	2.00	0.43
1:v:173:ASP:HA	1:v:176:LYS:HE2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ASP:HA	1:B:176:LYS:HE2	2.01	0.43
1:F:67:LEU:O	1:F:90:ARG:NH2	2.51	0.43
1:M:67:LEU:O	1:M:90:ARG:NH2	2.51	0.43
1:M:173:ASP:HA	1:M:176:LYS:HE2	2.01	0.43
1:S:67:LEU:HB3	1:S:136:ILE:HG22	2.00	0.43
1:Y:67:LEU:HB3	1:Y:136:ILE:HG22	2.00	0.43
1:d:67:LEU:O	1:d:90:ARG:NH2	2.51	0.43
1:d:67:LEU:HB3	1:d:136:ILE:HG22	2.00	0.43
1:m:173:ASP:HA	1:m:176:LYS:HE2	2.01	0.43
1:n:173:ASP:HA	1:n:176:LYS:HE2	2.01	0.43
1:p:67:LEU:HB3	1:p:136:ILE:HG22	2.00	0.43
1:v:67:LEU:HB3	1:v:136:ILE:HG22	2.00	0.43
1:y:173:ASP:HA	1:y:176:LYS:HE2	2.01	0.43
1:A:173:ASP:HA	1:A:176:LYS:HE2	2.01	0.43
1:C:67:LEU:O	1:C:90:ARG:NH2	2.51	0.43
1:F:86:LYS:HD3	1:F:86:LYS:HA	1.46	0.43
1:G:84:ASP:CB	1:g:6:PHE:HB2	2.49	0.43
1:H:173:ASP:HA	1:H:176:LYS:HE2	2.01	0.43
1:O:84:ASP:N	1:o:6:PHE:HB2	2.34	0.43
1:Q:39:ASP:OD1	1:Q:39:ASP:N	2.50	0.43
1:T:67:LEU:HB3	1:T:136:ILE:HG22	2.00	0.43
1:f:173:ASP:HA	1:f:176:LYS:HE2	2.01	0.43
1:g:67:LEU:HB3	1:g:136:ILE:HG22	2.00	0.43
1:h:83:LEU:HD13	1:h:83:LEU:HA	1.85	0.43
1:j:67:LEU:O	1:j:90:ARG:NH2	2.51	0.43
1:l:83:LEU:HD13	1:l:83:LEU:HA	1.85	0.43
1:t:68:GLN:NE2	1:t:77:GLU:OE1	2.50	0.43
1:y:97:LEU:HD13	1:y:97:LEU:HA	1.86	0.43
1:A:97:LEU:HD13	1:B:62:GLN:HG2	2.01	0.42
1:C:94:PRO:HG2	1:C:129:GLY:HA2	2.01	0.42
1:D:173:ASP:HA	1:D:176:LYS:HE2	2.01	0.42
1:M:144:LEU:O	1:M:148:ARG:CB	2.66	0.42
1:R:224:LEU:O	1:R:228:ASN:ND2	2.50	0.42
1:S:224:LEU:O	1:S:228:ASN:ND2	2.50	0.42
1:X:84:ASP:CB	1:x:6:PHE:HB2	2.48	0.42
1:g:173:ASP:HA	1:g:176:LYS:HE2	2.01	0.42
1:j:224:LEU:O	1:j:228:ASN:ND2	2.50	0.42
1:t:85:ARG:CG	1:t:85:ARG:NH2	2.79	0.42
1:B:67:LEU:HB3	1:B:136:ILE:HG22	2.00	0.42
1:E:84:ASP:HB3	1:e:7:ASN:CG	2.44	0.42
1:I:114:TYR:OH	1:J:220:HIS:O	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:97:LEU:HD13	1:L:62:GLN:HG2	2.00	0.42
1:M:94:PRO:HG2	1:M:129:GLY:HA2	2.01	0.42
1:M:97:LEU:HD13	1:N:62:GLN:HG2	2.01	0.42
1:P:67:LEU:HB3	1:P:136:ILE:HG22	2.01	0.42
1:S:39:ASP:N	1:S:39:ASP:OD1	2.50	0.42
1:S:94:PRO:HG2	1:S:129:GLY:HA2	2.02	0.42
1:S:173:ASP:HA	1:S:176:LYS:HE2	2.01	0.42
1:W:83:LEU:HD13	1:W:83:LEU:HA	1.85	0.42
1:X:97:LEU:HD13	1:Y:62:GLN:HG2	2.01	0.42
1:X:114:TYR:OH	1:Y:220:HIS:O	2.32	0.42
1:Y:224:LEU:O	1:Y:228:ASN:ND2	2.50	0.42
1:a:94:PRO:HG2	1:a:129:GLY:HA2	2.01	0.42
1:c:86:LYS:HD3	1:c:86:LYS:HA	1.47	0.42
1:c:94:PRO:HG2	1:c:129:GLY:HA2	2.01	0.42
1:k:97:LEU:HD13	1:l:62:GLN:HG2	2.01	0.42
1:m:94:PRO:HG2	1:m:129:GLY:HA2	2.01	0.42
1:o:94:PRO:HG2	1:o:129:GLY:HA2	2.02	0.42
1:q:68:GLN:NE2	1:q:77:GLU:OE1	2.50	0.42
1:s:86:LYS:HD3	1:s:86:LYS:HA	1.47	0.42
1:E:94:PRO:HG2	1:E:129:GLY:HA2	2.02	0.42
1:G:67:LEU:HB3	1:G:136:ILE:HG22	2.00	0.42
1:H:86:LYS:HA	1:H:86:LYS:HD3	1.46	0.42
1:I:84:ASP:OD1	1:i:6:PHE:HD2	2.01	0.42
1:J:85:ARG:CG	1:J:85:ARG:NH2	2.79	0.42
1:T:248:LEU:HD12	1:T:248:LEU:HA	1.92	0.42
1:Y:94:PRO:HG2	1:Y:129:GLY:HA2	2.01	0.42
1:a:86:LYS:HA	1:a:86:LYS:HD3	1.47	0.42
1:e:94:PRO:HG2	1:e:129:GLY:HA2	2.02	0.42
1:g:94:PRO:HG2	1:g:129:GLY:HA2	2.01	0.42
1:h:91:ILE:H	1:h:91:ILE:HG13	1.63	0.42
1:r:248:LEU:HD12	1:r:248:LEU:HA	1.92	0.42
1:s:67:LEU:HB3	1:s:136:ILE:HG22	2.00	0.42
1:s:94:PRO:HG2	1:s:129:GLY:HA2	2.02	0.42
1:y:67:LEU:O	1:y:90:ARG:NH2	2.51	0.42
1:y:94:PRO:HG2	1:y:129:GLY:HA2	2.02	0.42
1:A:94:PRO:HG2	1:A:129:GLY:HA2	2.01	0.42
1:A:246:LEU:HD13	1:B:235:MET:HE1	2.02	0.42
1:E:224:LEU:O	1:E:228:ASN:ND2	2.50	0.42
1:L:67:LEU:HB3	1:L:136:ILE:HG22	2.00	0.42
1:L:96:LEU:HD12	1:L:96:LEU:HA	1.86	0.42
1:N:67:LEU:HB3	1:N:136:ILE:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:94:PRO:HG2	1:N:129:GLY:HA2	2.02	0.42
1:N:173:ASP:HA	1:N:176:LYS:HE2	2.01	0.42
1:O:94:PRO:HG2	1:O:129:GLY:HA2	2.02	0.42
1:W:173:ASP:HA	1:W:176:LYS:HE2	2.01	0.42
1:W:224:LEU:O	1:W:228:ASN:ND2	2.50	0.42
1:X:96:LEU:HD12	1:X:96:LEU:HA	1.91	0.42
1:Y:173:ASP:HA	1:Y:176:LYS:HE2	2.01	0.42
1:a:97:LEU:HD13	1:b:62:GLN:HG2	2.01	0.42
1:b:94:PRO:HG2	1:b:129:GLY:HA2	2.02	0.42
1:b:224:LEU:O	1:b:228:ASN:ND2	2.50	0.42
1:f:67:LEU:HB3	1:f:136:ILE:HG22	2.00	0.42
1:g:114:TYR:OH	1:h:220:HIS:O	2.32	0.42
1:s:173:ASP:HA	1:s:176:LYS:HE2	2.01	0.42
1:A:39:ASP:OD1	1:A:39:ASP:N	2.50	0.42
1:G:173:ASP:HA	1:G:176:LYS:HE2	2.01	0.42
1:H:67:LEU:HB3	1:H:136:ILE:HG22	2.00	0.42
1:I:97:LEU:HD12	1:I:97:LEU:C	2.45	0.42
1:K:246:LEU:HD13	1:L:235:MET:HE1	2.02	0.42
1:O:6:PHE:HB2	1:c:84:ASP:CB	2.49	0.42
1:O:224:LEU:O	1:O:228:ASN:ND2	2.50	0.42
1:Q:94:PRO:HG2	1:Q:129:GLY:HA2	2.02	0.42
1:V:97:LEU:HD12	1:V:97:LEU:C	2.45	0.42
1:X:246:LEU:HD13	1:Y:235:MET:HE1	2.02	0.42
1:b:67:LEU:HB3	1:b:136:ILE:HG22	2.00	0.42
1:h:67:LEU:HB3	1:h:136:ILE:HG22	2.00	0.42
1:i:97:LEU:HD12	1:i:97:LEU:C	2.45	0.42
1:l:86:LYS:HA	1:l:86:LYS:HD3	1.46	0.42
1:m:97:LEU:HD13	1:n:62:GLN:HG2	2.01	0.42
1:m:246:LEU:HD13	1:n:235:MET:HE1	2.02	0.42
1:n:97:LEU:HA	1:n:97:LEU:HD13	1.86	0.42
1:q:94:PRO:HG2	1:q:129:GLY:HA2	2.02	0.42
1:r:67:LEU:HB3	1:r:136:ILE:HG22	2.00	0.42
1:r:173:ASP:HA	1:r:176:LYS:HE2	2.01	0.42
1:w:173:ASP:HA	1:w:176:LYS:HE2	2.01	0.42
1:x:246:LEU:HD13	1:y:235:MET:HE1	2.02	0.42
1:y:86:LYS:HD3	1:y:86:LYS:HA	1.46	0.42
1:B:94:PRO:HG2	1:B:129:GLY:HA2	2.02	0.42
1:B:224:LEU:O	1:B:228:ASN:ND2	2.50	0.42
1:C:173:ASP:HA	1:C:176:LYS:HE2	2.01	0.42
1:G:94:PRO:HG2	1:G:129:GLY:HA2	2.01	0.42
1:L:173:ASP:HA	1:L:176:LYS:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:224:LEU:O	1:N:228:ASN:ND2	2.50	0.42
1:O:173:ASP:HA	1:O:176:LYS:HE2	2.01	0.42
1:P:91:ILE:H	1:P:91:ILE:HG13	1.63	0.42
1:R:67:LEU:HB3	1:R:136:ILE:HG22	2.00	0.42
1:a:246:LEU:HD13	1:b:235:MET:HE1	2.02	0.42
1:c:173:ASP:HA	1:c:176:LYS:HE2	2.01	0.42
1:n:67:LEU:HB3	1:n:136:ILE:HG22	2.00	0.42
1:n:94:PRO:HG2	1:n:129:GLY:HA2	2.01	0.42
1:s:224:LEU:O	1:s:228:ASN:ND2	2.50	0.42
1:w:67:LEU:HB3	1:w:136:ILE:HG22	2.00	0.42
1:x:97:LEU:HD13	1:y:62:GLN:HG2	2.01	0.42
1:D:97:LEU:HD13	1:D:97:LEU:HA	1.86	0.42
1:J:94:PRO:HG2	1:J:129:GLY:HA2	2.02	0.42
1:M:246:LEU:HD13	1:N:235:MET:HE1	2.02	0.42
1:b:173:ASP:HA	1:b:176:LYS:HE2	2.01	0.42
1:f:86:LYS:HA	1:f:86:LYS:HD3	1.46	0.42
1:i:94:PRO:HG2	1:i:129:GLY:HA2	2.02	0.42
1:i:246:LEU:HD13	1:j:235:MET:HE1	2.02	0.42
1:k:94:PRO:HG2	1:k:129:GLY:HA2	2.01	0.42
1:l:94:PRO:HG2	1:l:129:GLY:HA2	2.02	0.42
1:m:91:ILE:H	1:m:91:ILE:HG13	1.63	0.42
1:o:224:LEU:O	1:o:228:ASN:ND2	2.50	0.42
1:q:39:ASP:OD1	1:q:39:ASP:N	2.50	0.42
1:q:173:ASP:HA	1:q:176:LYS:HE2	2.01	0.42
1:E:173:ASP:HA	1:E:176:LYS:HE2	2.01	0.42
1:F:67:LEU:HB3	1:F:136:ILE:HG22	2.00	0.42
1:I:84:ASP:CB	1:i:6:PHE:HB2	2.50	0.42
1:I:94:PRO:HG2	1:I:129:GLY:HA2	2.02	0.42
1:K:94:PRO:HG2	1:K:129:GLY:HA2	2.02	0.42
1:M:86:LYS:HD3	1:M:86:LYS:HA	1.47	0.42
1:R:173:ASP:HA	1:R:176:LYS:HE2	2.01	0.42
1:e:96:LEU:HD12	1:e:96:LEU:HA	1.91	0.42
1:j:86:LYS:HA	1:j:86:LYS:HD3	1.46	0.42
1:t:91:ILE:H	1:t:91:ILE:HG13	1.63	0.42
1:x:86:LYS:HD3	1:x:86:LYS:HA	1.47	0.42
1:D:48:LYS:O	1:D:52:THR:OG1	2.31	0.42
1:L:85:ARG:HH21	1:L:85:ARG:CG	2.21	0.42
1:V:62:GLN:NE2	1:W:96:LEU:HB3	2.35	0.42
1:V:94:PRO:HG2	1:V:129:GLY:HA2	2.02	0.42
1:V:246:LEU:HD13	1:W:235:MET:HE1	2.02	0.42
1:X:94:PRO:HG2	1:X:129:GLY:HA2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:62:GLN:NE2	1:b:96:LEU:HB3	2.35	0.42
1:h:48:LYS:O	1:h:52:THR:OG1	2.31	0.42
1:j:85:ARG:CG	1:j:85:ARG:NH2	2.79	0.42
1:j:94:PRO:HG2	1:j:129:GLY:HA2	2.01	0.42
1:k:86:LYS:HD3	1:k:86:LYS:HA	1.47	0.42
1:v:62:GLN:NE2	1:w:96:LEU:HB3	2.35	0.42
1:v:94:PRO:HG2	1:v:129:GLY:HA2	2.02	0.42
1:v:224:LEU:O	1:v:228:ASN:ND2	2.50	0.42
1:x:94:PRO:HG2	1:x:129:GLY:HA2	2.02	0.42
1:A:62:GLN:NE2	1:B:96:LEU:HB3	2.35	0.42
1:E:219:THR:HA	1:F:265:GLN:HE22	1.85	0.42
1:I:62:GLN:NE2	1:J:96:LEU:HB3	2.35	0.42
1:O:120:LYS:O	1:O:124:THR:OG1	2.36	0.42
1:e:173:ASP:HA	1:e:176:LYS:HE2	2.01	0.42
1:i:62:GLN:NE2	1:j:96:LEU:HB3	2.35	0.42
1:k:246:LEU:HD13	1:l:235:MET:HE1	2.02	0.42
1:l:67:LEU:HB3	1:l:136:ILE:HG22	2.00	0.42
1:o:173:ASP:HA	1:o:176:LYS:HE2	2.01	0.42
1:o:246:LEU:HD13	1:p:235:MET:HE1	2.02	0.42
1:q:219:THR:HA	1:r:265:GLN:HE22	1.85	0.42
1:w:97:LEU:HD13	1:w:97:LEU:HA	1.86	0.42
1:G:84:ASP:HB3	1:g:7:ASN:CG	2.43	0.41
1:I:246:LEU:HD13	1:J:235:MET:HE1	2.02	0.41
1:K:224:LEU:O	1:K:228:ASN:ND2	2.50	0.41
1:M:7:ASN:HB3	1:b:8:VAL:HG12	2.02	0.41
1:P:248:LEU:HD12	1:P:248:LEU:HA	1.92	0.41
1:Q:173:ASP:HA	1:Q:176:LYS:HE2	2.01	0.41
1:R:86:LYS:HA	1:R:86:LYS:HD3	1.46	0.41
1:V:224:LEU:O	1:V:228:ASN:ND2	2.50	0.41
1:X:6:PHE:HB3	1:k:83:LEU:C	2.45	0.41
1:c:246:LEU:HD13	1:d:235:MET:HE1	2.02	0.41
1:d:224:LEU:O	1:d:228:ASN:ND2	2.50	0.41
1:e:219:THR:HA	1:f:265:GLN:HE22	1.85	0.41
1:l:173:ASP:HA	1:l:176:LYS:HE2	2.01	0.41
1:n:224:LEU:O	1:n:228:ASN:ND2	2.50	0.41
1:s:39:ASP:OD1	1:s:39:ASP:N	2.50	0.41
1:G:219:THR:HA	1:H:265:GLN:HE22	1.85	0.41
1:I:96:LEU:HD12	1:I:96:LEU:HA	1.91	0.41
1:K:39:ASP:OD1	1:K:39:ASP:N	2.50	0.41
1:M:62:GLN:NE2	1:N:96:LEU:HB3	2.35	0.41
1:M:224:LEU:O	1:M:228:ASN:ND2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:91:ILE:H	1:T:91:ILE:HG13	1.63	0.41
1:e:86:LYS:HD3	1:e:86:LYS:HA	1.47	0.41
1:m:62:GLN:NE2	1:n:96:LEU:HB3	2.35	0.41
1:y:224:LEU:O	1:y:228:ASN:ND2	2.50	0.41
1:C:246:LEU:HD13	1:D:235:MET:HE1	2.02	0.41
1:G:62:GLN:NE2	1:H:96:LEU:HB3	2.35	0.41
1:H:120:LYS:O	1:H:124:THR:OG1	2.36	0.41
1:L:85:ARG:CG	1:L:85:ARG:NH2	2.79	0.41
1:L:94:PRO:HG2	1:L:129:GLY:HA2	2.01	0.41
1:S:62:GLN:NE2	1:T:96:LEU:HB3	2.35	0.41
1:Y:98:GLY:HA3	1:Y:126:LYS:HG2	2.02	0.41
1:b:98:GLY:HA3	1:b:126:LYS:HG2	2.02	0.41
1:c:219:THR:HA	1:d:265:GLN:HE22	1.85	0.41
1:o:114:TYR:OH	1:p:220:HIS:O	2.32	0.41
1:o:219:THR:HA	1:p:265:GLN:HE22	1.85	0.41
1:s:62:GLN:NE2	1:t:96:LEU:HB3	2.35	0.41
1:v:246:LEU:HD13	1:w:235:MET:HE1	2.02	0.41
1:w:224:LEU:O	1:w:228:ASN:ND2	2.50	0.41
1:y:98:GLY:HA3	1:y:126:LYS:HG2	2.02	0.41
1:I:224:LEU:O	1:I:228:ASN:ND2	2.50	0.41
1:L:98:GLY:HA3	1:L:126:LYS:HG2	2.02	0.41
1:N:98:GLY:HA3	1:N:126:LYS:HG2	2.02	0.41
1:O:7:ASN:CG	1:c:84:ASP:HB3	2.45	0.41
1:O:219:THR:HA	1:P:265:GLN:HE22	1.85	0.41
1:O:246:LEU:HD13	1:P:235:MET:HE1	2.02	0.41
1:Q:6:PHE:O	1:e:83:LEU:HD12	2.21	0.41
1:Y:91:ILE:H	1:Y:91:ILE:HG13	1.63	0.41
1:c:120:LYS:O	1:c:124:THR:OG1	2.36	0.41
1:g:62:GLN:NE2	1:h:96:LEU:HB3	2.35	0.41
1:j:83:LEU:HD13	1:j:83:LEU:HA	1.85	0.41
1:k:96:LEU:HD12	1:k:96:LEU:HA	1.91	0.41
1:l:48:LYS:O	1:l:52:THR:OG1	2.31	0.41
1:p:91:ILE:H	1:p:91:ILE:HG13	1.63	0.41
1:D:94:PRO:HG2	1:D:129:GLY:HA2	2.02	0.41
1:F:94:PRO:HG2	1:F:129:GLY:HA2	2.02	0.41
1:G:39:ASP:N	1:G:39:ASP:OD1	2.50	0.41
1:J:248:LEU:HD12	1:J:248:LEU:HA	1.92	0.41
1:N:96:LEU:HD12	1:N:96:LEU:HA	1.86	0.41
1:V:86:LYS:HD3	1:V:86:LYS:HA	1.47	0.41
1:W:96:LEU:HD12	1:W:96:LEU:HA	1.86	0.41
1:n:98:GLY:HA3	1:n:126:LYS:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:94:PRO:HG2	1:p:129:GLY:HA2	2.02	0.41
1:q:62:GLN:NE2	1:r:96:LEU:HB3	2.35	0.41
1:s:219:THR:HA	1:t:265:GLN:HE22	1.85	0.41
1:x:62:GLN:NE2	1:y:96:LEU:HB3	2.35	0.41
1:B:98:GLY:HA3	1:B:126:LYS:HG2	2.02	0.41
1:H:83:LEU:HD13	1:H:83:LEU:HA	1.85	0.41
1:J:86:LYS:HD3	1:J:86:LYS:HA	1.46	0.41
1:Q:62:GLN:NE2	1:R:96:LEU:HB3	2.35	0.41
1:Q:219:THR:HA	1:R:265:GLN:HE22	1.85	0.41
1:R:120:LYS:O	1:R:124:THR:OG1	2.36	0.41
1:W:85:ARG:CG	1:W:85:ARG:NH2	2.79	0.41
1:X:7:ASN:HB3	1:l:8:VAL:HG12	2.02	0.41
1:X:62:GLN:NE2	1:Y:96:LEU:HB3	2.35	0.41
1:h:224:LEU:O	1:h:228:ASN:ND2	2.50	0.41
1:l:98:GLY:HA3	1:l:126:LYS:HG2	2.02	0.41
1:C:62:GLN:NE2	1:D:96:LEU:HB3	2.35	0.41
1:H:224:LEU:O	1:H:228:ASN:ND2	2.50	0.41
1:K:62:GLN:NE2	1:L:96:LEU:HB3	2.35	0.41
1:S:246:LEU:HD13	1:T:235:MET:HE1	2.02	0.41
1:T:224:LEU:O	1:T:228:ASN:ND2	2.50	0.41
1:W:94:PRO:HG2	1:W:129:GLY:HA2	2.02	0.41
1:f:94:PRO:HG2	1:f:129:GLY:HA2	2.02	0.41
1:g:246:LEU:HD13	1:h:235:MET:HE1	2.02	0.41
1:i:224:LEU:O	1:i:228:ASN:ND2	2.50	0.41
1:k:62:GLN:NE2	1:l:96:LEU:HB3	2.35	0.41
1:m:224:LEU:O	1:m:228:ASN:ND2	2.50	0.41
1:r:224:LEU:O	1:r:228:ASN:ND2	2.50	0.41
1:K:91:ILE:H	1:K:91:ILE:HG13	1.63	0.41
1:O:62:GLN:NE2	1:P:96:LEU:HB3	2.35	0.41
1:X:39:ASP:N	1:X:39:ASP:OD1	2.50	0.41
1:c:62:GLN:NE2	1:d:96:LEU:HB3	2.35	0.41
1:e:62:GLN:NE2	1:f:96:LEU:HB3	2.35	0.41
1:e:246:LEU:HD13	1:f:235:MET:HE1	2.02	0.41
1:g:39:ASP:N	1:g:39:ASP:OD1	2.50	0.41
1:h:98:GLY:HA3	1:h:126:LYS:HG2	2.02	0.41
1:l:85:ARG:NH2	1:l:85:ARG:CG	2.79	0.41
1:r:94:PRO:HG2	1:r:129:GLY:HA2	2.02	0.41
1:E:62:GLN:NE2	1:F:96:LEU:HB3	2.35	0.41
1:F:70:ASN:HB2	1:F:73:ALA:HB3	2.03	0.41
1:F:98:GLY:HA3	1:F:126:LYS:HG2	2.02	0.41
1:G:246:LEU:HD13	1:H:235:MET:HE1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:98:GLY:HA3	1:H:126:LYS:HG2	2.02	0.41
1:K:219:THR:HA	1:L:265:GLN:HE22	1.85	0.41
1:L:85:ARG:HG2	1:L:85:ARG:NH2	2.28	0.41
1:O:51:CYS:O	1:O:55:TRP:HB2	2.21	0.41
1:Q:246:LEU:HD13	1:R:235:MET:HE1	2.02	0.41
1:R:94:PRO:HG2	1:R:129:GLY:HA2	2.02	0.41
1:T:94:PRO:HG2	1:T:129:GLY:HA2	2.02	0.41
1:T:98:GLY:HA3	1:T:126:LYS:HG2	2.02	0.41
1:X:51:CYS:O	1:X:55:TRP:HB2	2.21	0.41
1:X:219:THR:HA	1:Y:265:GLN:HE22	1.85	0.41
1:b:86:LYS:HA	1:b:86:LYS:HD3	1.46	0.41
1:d:94:PRO:HG2	1:d:129:GLY:HA2	2.02	0.41
1:f:98:GLY:HA3	1:f:126:LYS:HG2	2.02	0.41
1:h:94:PRO:HG2	1:h:129:GLY:HA2	2.02	0.41
1:h:97:LEU:HA	1:h:97:LEU:HD13	1.86	0.41
1:l:85:ARG:HH21	1:l:85:ARG:CG	2.21	0.41
1:m:70:ASN:HB2	1:m:73:ALA:HB3	2.03	0.41
1:m:96:LEU:HB3	1:n:62:GLN:NE2	2.36	0.41
1:o:62:GLN:NE2	1:p:96:LEU:HB3	2.35	0.41
1:p:248:LEU:HD12	1:p:248:LEU:HA	1.92	0.41
1:q:97:LEU:HD12	1:q:97:LEU:C	2.45	0.41
1:q:246:LEU:HD13	1:r:235:MET:HE1	2.02	0.41
1:r:48:LYS:O	1:r:52:THR:OG1	2.31	0.41
1:s:246:LEU:HD13	1:t:235:MET:HE1	2.02	0.41
1:t:94:PRO:HG2	1:t:129:GLY:HA2	2.02	0.41
1:t:97:LEU:HD13	1:t:97:LEU:HA	1.86	0.41
1:t:98:GLY:HA3	1:t:126:LYS:HG2	2.02	0.41
1:w:70:ASN:HB2	1:w:73:ALA:HB3	2.03	0.41
1:A:51:CYS:O	1:A:55:TRP:HB2	2.21	0.41
1:A:70:ASN:HB2	1:A:73:ALA:HB3	2.03	0.41
1:C:70:ASN:HB2	1:C:73:ALA:HB3	2.03	0.41
1:H:70:ASN:HB2	1:H:73:ALA:HB3	2.03	0.41
1:H:94:PRO:HG2	1:H:129:GLY:HA2	2.02	0.41
1:J:70:ASN:HB2	1:J:73:ALA:HB3	2.03	0.41
1:M:84:ASP:O	1:m:10:LYS:CG	2.66	0.41
1:O:54:ILE:HD12	1:O:54:ILE:HA	1.99	0.41
1:T:86:LYS:HD3	1:T:86:LYS:HA	1.46	0.41
1:V:6:PHE:HB3	1:i:83:LEU:C	2.46	0.41
1:c:70:ASN:HB2	1:c:73:ALA:HB3	2.03	0.41
1:f:70:ASN:HB2	1:f:73:ALA:HB3	2.03	0.41
1:g:219:THR:HA	1:h:265:GLN:HE22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:85:ARG:HG2	1:l:85:ARG:NH2	2.28	0.41
1:p:98:GLY:HA3	1:p:126:LYS:HG2	2.02	0.41
1:q:96:LEU:HB3	1:r:62:GLN:NE2	2.36	0.41
1:v:96:LEU:HD12	1:v:96:LEU:HA	1.91	0.41
1:w:94:PRO:HG2	1:w:129:GLY:HA2	2.02	0.41
1:x:51:CYS:O	1:x:55:TRP:HB2	2.21	0.41
1:y:54:ILE:HD12	1:y:54:ILE:HA	1.99	0.41
1:B:54:ILE:HD12	1:B:54:ILE:HA	1.99	0.40
1:B:85:ARG:HG2	1:B:85:ARG:NH2	2.28	0.40
1:C:84:ASP:N	1:c:6:PHE:HB2	2.36	0.40
1:C:219:THR:HA	1:D:265:GLN:HE22	1.85	0.40
1:D:98:GLY:HA3	1:D:126:LYS:HG2	2.02	0.40
1:E:246:LEU:HD13	1:F:235:MET:HE1	2.02	0.40
1:H:48:LYS:O	1:H:52:THR:OG1	2.31	0.40
1:M:96:LEU:HB3	1:N:62:GLN:NE2	2.36	0.40
1:Q:70:ASN:HB2	1:Q:73:ALA:HB3	2.03	0.40
1:Q:96:LEU:HB3	1:R:62:GLN:NE2	2.36	0.40
1:R:98:GLY:HA3	1:R:126:LYS:HG2	2.02	0.40
1:S:219:THR:HA	1:T:265:GLN:HE22	1.85	0.40
1:W:70:ASN:HB2	1:W:73:ALA:HB3	2.04	0.40
1:W:98:GLY:HA3	1:W:126:LYS:HG2	2.02	0.40
1:b:85:ARG:HG2	1:b:85:ARG:NH2	2.28	0.40
1:j:98:GLY:HA3	1:j:126:LYS:HG2	2.02	0.40
1:m:51:CYS:O	1:m:55:TRP:HB2	2.21	0.40
1:r:70:ASN:HB2	1:r:73:ALA:HB3	2.04	0.40
1:t:70:ASN:HB2	1:t:73:ALA:HB3	2.04	0.40
1:t:224:LEU:O	1:t:228:ASN:ND2	2.50	0.40
1:t:248:LEU:HD12	1:t:248:LEU:HA	1.92	0.40
1:x:219:THR:HA	1:y:265:GLN:HE22	1.85	0.40
1:E:248:LEU:HD12	1:E:248:LEU:HA	1.92	0.40
1:J:98:GLY:HA3	1:J:126:LYS:HG2	2.02	0.40
1:K:51:CYS:O	1:K:55:TRP:HB2	2.22	0.40
1:K:93:ASN:HB3	1:L:65:VAL:HG13	2.04	0.40
1:M:219:THR:HA	1:N:265:GLN:HE22	1.85	0.40
1:O:7:ASN:HB3	1:d:8:VAL:HG12	2.03	0.40
1:O:70:ASN:HB2	1:O:73:ALA:HB3	2.03	0.40
1:P:70:ASN:HB2	1:P:73:ALA:HB3	2.03	0.40
1:T:70:ASN:HB2	1:T:73:ALA:HB3	2.03	0.40
1:W:91:ILE:H	1:W:91:ILE:HG13	1.63	0.40
1:a:224:LEU:O	1:a:228:ASN:ND2	2.50	0.40
1:c:51:CYS:O	1:c:55:TRP:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:98:GLY:HA3	1:d:126:LYS:HG2	2.02	0.40
1:e:70:ASN:HB2	1:e:73:ALA:HB3	2.03	0.40
1:g:48:LYS:O	1:g:52:THR:OG1	2.31	0.40
1:h:70:ASN:HB2	1:h:73:ALA:HB3	2.03	0.40
1:j:51:CYS:O	1:j:55:TRP:HB2	2.21	0.40
1:j:70:ASN:HB2	1:j:73:ALA:HB3	2.03	0.40
1:k:39:ASP:OD1	1:k:39:ASP:N	2.50	0.40
1:k:219:THR:HA	1:l:265:GLN:HE22	1.85	0.40
1:l:70:ASN:HB2	1:l:73:ALA:HB3	2.03	0.40
1:m:219:THR:HA	1:n:265:GLN:HE22	1.85	0.40
1:o:70:ASN:HB2	1:o:73:ALA:HB3	2.03	0.40
1:q:70:ASN:HB2	1:q:73:ALA:HB3	2.03	0.40
1:v:219:THR:HA	1:w:265:GLN:HE22	1.85	0.40
1:w:85:ARG:CG	1:w:85:ARG:NH2	2.79	0.40
1:x:93:ASN:HB3	1:y:65:VAL:HG13	2.04	0.40
1:E:51:CYS:O	1:E:55:TRP:HB2	2.21	0.40
1:L:70:ASN:HB2	1:L:73:ALA:HB3	2.03	0.40
1:M:51:CYS:O	1:M:55:TRP:HB2	2.21	0.40
1:M:70:ASN:HB2	1:M:73:ALA:HB3	2.03	0.40
1:P:94:PRO:HG2	1:P:129:GLY:HA2	2.02	0.40
1:P:98:GLY:HA3	1:P:126:LYS:HG2	2.02	0.40
1:Q:6:PHE:HB3	1:e:83:LEU:CA	2.49	0.40
1:Q:97:LEU:HD12	1:Q:97:LEU:C	2.45	0.40
1:R:70:ASN:HB2	1:R:73:ALA:HB3	2.03	0.40
1:W:51:CYS:O	1:W:55:TRP:HB2	2.22	0.40
1:Y:85:ARG:HG2	1:Y:85:ARG:NH2	2.28	0.40
1:Y:85:ARG:NH2	1:Y:85:ARG:CG	2.79	0.40
1:Y:97:LEU:HD13	1:Y:97:LEU:HA	1.86	0.40
1:c:248:LEU:HD12	1:c:248:LEU:HA	1.92	0.40
1:d:70:ASN:HB2	1:d:73:ALA:HB3	2.03	0.40
1:e:51:CYS:O	1:e:55:TRP:HB2	2.21	0.40
1:e:54:ILE:HD12	1:e:54:ILE:HA	1.99	0.40
1:e:96:LEU:HB3	1:f:62:GLN:NE2	2.36	0.40
1:i:93:ASN:HB3	1:j:65:VAL:HG13	2.04	0.40
1:k:93:ASN:HB3	1:l:65:VAL:HG13	2.04	0.40
1:m:96:LEU:HD12	1:m:96:LEU:HA	1.91	0.40
1:o:51:CYS:O	1:o:55:TRP:HB2	2.21	0.40
1:x:96:LEU:HB3	1:y:62:GLN:NE2	2.36	0.40
1:A:224:LEU:O	1:A:228:ASN:ND2	2.50	0.40
1:E:96:LEU:HB3	1:F:62:GLN:NE2	2.36	0.40
1:G:86:LYS:HA	1:G:86:LYS:HD3	1.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:93:ASN:HB3	1:J:65:VAL:HG13	2.04	0.40
1:J:54:ILE:HD12	1:J:54:ILE:HA	1.99	0.40
1:O:96:LEU:HB3	1:P:62:GLN:NE2	2.36	0.40
1:P:51:CYS:O	1:P:55:TRP:HB2	2.22	0.40
1:P:96:LEU:HD12	1:P:96:LEU:HA	1.86	0.40
1:S:84:ASP:OD1	1:s:6:PHE:HD2	2.04	0.40
1:V:47:SER:O	1:V:51:CYS:HB3	2.22	0.40
1:V:93:ASN:HB3	1:W:65:VAL:HG13	2.04	0.40
1:Y:70:ASN:HB2	1:Y:73:ALA:HB3	2.03	0.40
1:a:70:ASN:HB2	1:a:73:ALA:HB3	2.03	0.40
1:i:51:CYS:O	1:i:55:TRP:HB2	2.21	0.40
1:j:97:LEU:HA	1:j:97:LEU:HD13	1.86	0.40
1:p:70:ASN:HB2	1:p:73:ALA:HB3	2.03	0.40
1:v:51:CYS:O	1:v:55:TRP:HB2	2.22	0.40
1:w:98:GLY:HA3	1:w:126:LYS:HG2	2.02	0.40
1:E:70:ASN:HB2	1:E:73:ALA:HB3	2.03	0.40
1:G:47:SER:O	1:G:51:CYS:HB3	2.22	0.40
1:G:51:CYS:O	1:G:55:TRP:HB2	2.21	0.40
1:G:238:TYR:HD2	1:H:238:TYR:HD2	1.70	0.40
1:I:219:THR:HA	1:J:265:GLN:HE22	1.85	0.40
1:K:70:ASN:HB2	1:K:73:ALA:HB3	2.03	0.40
1:N:85:ARG:HG2	1:N:85:ARG:NH2	2.28	0.40
1:Q:54:ILE:HD12	1:Q:54:ILE:HA	1.99	0.40
1:T:47:SER:O	1:T:51:CYS:HB3	2.22	0.40
1:X:93:ASN:HB3	1:Y:65:VAL:HG13	2.04	0.40
1:X:96:LEU:HB3	1:Y:62:GLN:NE2	2.36	0.40
1:a:96:LEU:HB3	1:b:62:GLN:NE2	2.36	0.40
1:i:47:SER:O	1:i:51:CYS:HB3	2.22	0.40
1:i:54:ILE:HD12	1:i:54:ILE:HA	1.99	0.40
1:k:51:CYS:O	1:k:55:TRP:HB2	2.22	0.40
1:l:120:LYS:O	1:l:124:THR:OG1	2.36	0.40
1:o:96:LEU:HB3	1:p:62:GLN:NE2	2.37	0.40
1:r:120:LYS:O	1:r:124:THR:OG1	2.36	0.40
1:s:47:SER:O	1:s:51:CYS:HB3	2.22	0.40
1:s:96:LEU:HB3	1:t:62:GLN:NE2	2.36	0.40
1:s:97:LEU:HD12	1:s:97:LEU:C	2.45	0.40
1:v:47:SER:O	1:v:51:CYS:HB3	2.22	0.40
1:v:238:TYR:HD2	1:w:238:TYR:HD2	1.70	0.40
1:x:47:SER:O	1:x:51:CYS:HB3	2.22	0.40
1:x:70:ASN:HB2	1:x:73:ALA:HB3	2.03	0.40
1:y:85:ARG:HG2	1:y:85:ARG:NH2	2.28	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 PDB entries followed by that with respect to all EM entries.

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	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	B	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	C	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	D	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	E	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	F	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	G	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	H	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	I	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	J	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	K	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	L	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	M	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	N	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	O	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	P	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	Q	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	R	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	S	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	T	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	V	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	W	241/365 (66%)	213 (88%)	28 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	X	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	Y	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	a	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	b	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	c	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	d	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	e	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	f	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	g	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	h	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	i	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	j	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	k	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	l	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	m	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	n	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	o	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	p	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	q	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	r	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	s	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	t	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	v	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	w	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	x	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	y	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
All	All	11568/17520 (66%)	10272 (89%)	1296 (11%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	B	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	C	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	D	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	E	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	F	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	G	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	H	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	I	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	J	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	K	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	L	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	M	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	N	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	O	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	P	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	Q	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	R	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	S	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	T	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	V	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	W	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	X	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	Y	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	a	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	b	212/315 (67%)	199 (94%)	13 (6%)	17	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	c	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	d	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	e	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	f	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	g	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	h	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	i	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	j	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	k	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	l	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	m	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	n	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	o	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	p	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	q	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	r	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	s	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	t	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	v	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	w	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	x	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	y	212/315 (67%)	199 (94%)	13 (6%)	17	38
All	All	10176/15120 (67%)	9604 (94%)	572 (6%)	21	40

All (572) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	PHE
1	A	51	CYS
1	A	61	LYS
1	A	82	LYS
1	A	85	ARG
1	A	86	LYS
1	A	97	LEU

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Mol	Chain	Res	Type
1	A	241	CYS
1	A	266	THR
1	A	267	SER
1	A	268	VAL
1	B	51	CYS
1	B	61	LYS
1	B	82	LYS
1	B	83	LEU
1	B	84	ASP
1	B	85	ARG
1	B	86	LYS
1	B	97	LEU
1	B	241	CYS
1	B	266	THR
1	B	267	SER
1	B	268	VAL
1	C	6	PHE
1	C	51	CYS
1	C	61	LYS
1	C	82	LYS
1	C	85	ARG
1	C	86	LYS
1	C	97	LEU
1	C	241	CYS
1	C	266	THR
1	C	267	SER
1	C	268	VAL
1	D	6	PHE
1	D	51	CYS
1	D	61	LYS
1	D	82	LYS
1	D	83	LEU
1	D	84	ASP
1	D	85	ARG
1	D	86	LYS
1	D	97	LEU
1	D	241	CYS
1	D	266	THR
1	D	267	SER
1	D	268	VAL
1	E	6	PHE
1	E	51	CYS

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Mol	Chain	Res	Type
1	E	61	LYS
1	E	82	LYS
1	E	85	ARG
1	E	86	LYS
1	E	97	LEU
1	E	241	CYS
1	E	266	THR
1	E	267	SER
1	E	268	VAL
1	F	6	PHE
1	F	51	CYS
1	F	61	LYS
1	F	82	LYS
1	F	83	LEU
1	F	84	ASP
1	F	85	ARG
1	F	86	LYS
1	F	97	LEU
1	F	241	CYS
1	F	266	THR
1	F	267	SER
1	F	268	VAL
1	G	6	PHE
1	G	51	CYS
1	G	61	LYS
1	G	82	LYS
1	G	85	ARG
1	G	86	LYS
1	G	97	LEU
1	G	241	CYS
1	G	266	THR
1	G	267	SER
1	G	268	VAL
1	H	6	PHE
1	H	51	CYS
1	H	61	LYS
1	H	82	LYS
1	H	83	LEU
1	H	84	ASP
1	H	85	ARG
1	H	86	LYS
1	H	97	LEU

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Mol	Chain	Res	Type
1	H	241	CYS
1	H	266	THR
1	H	267	SER
1	H	268	VAL
1	I	6	PHE
1	I	51	CYS
1	I	61	LYS
1	I	82	LYS
1	I	85	ARG
1	I	86	LYS
1	I	97	LEU
1	I	241	CYS
1	I	266	THR
1	I	267	SER
1	I	268	VAL
1	J	6	PHE
1	J	51	CYS
1	J	61	LYS
1	J	82	LYS
1	J	83	LEU
1	J	84	ASP
1	J	85	ARG
1	J	86	LYS
1	J	97	LEU
1	J	241	CYS
1	J	266	THR
1	J	267	SER
1	J	268	VAL
1	K	6	PHE
1	K	51	CYS
1	K	61	LYS
1	K	82	LYS
1	K	85	ARG
1	K	86	LYS
1	K	97	LEU
1	K	241	CYS
1	K	266	THR
1	K	267	SER
1	K	268	VAL
1	L	6	PHE
1	L	51	CYS
1	L	61	LYS

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Mol	Chain	Res	Type
1	L	82	LYS
1	L	83	LEU
1	L	84	ASP
1	L	85	ARG
1	L	86	LYS
1	L	97	LEU
1	L	241	CYS
1	L	266	THR
1	L	267	SER
1	L	268	VAL
1	M	6	PHE
1	M	51	CYS
1	M	61	LYS
1	M	82	LYS
1	M	85	ARG
1	M	86	LYS
1	M	97	LEU
1	M	241	CYS
1	M	266	THR
1	M	267	SER
1	M	268	VAL
1	N	6	PHE
1	N	51	CYS
1	N	61	LYS
1	N	82	LYS
1	N	83	LEU
1	N	84	ASP
1	N	85	ARG
1	N	86	LYS
1	N	97	LEU
1	N	241	CYS
1	N	266	THR
1	N	267	SER
1	N	268	VAL
1	O	6	PHE
1	O	51	CYS
1	O	61	LYS
1	O	82	LYS
1	O	85	ARG
1	O	86	LYS
1	O	97	LEU
1	O	241	CYS

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Mol	Chain	Res	Type
1	O	266	THR
1	O	267	SER
1	O	268	VAL
1	P	51	CYS
1	P	61	LYS
1	P	82	LYS
1	P	83	LEU
1	P	84	ASP
1	P	85	ARG
1	P	86	LYS
1	P	97	LEU
1	P	241	CYS
1	P	266	THR
1	P	267	SER
1	P	268	VAL
1	Q	6	PHE
1	Q	51	CYS
1	Q	61	LYS
1	Q	82	LYS
1	Q	85	ARG
1	Q	86	LYS
1	Q	97	LEU
1	Q	241	CYS
1	Q	266	THR
1	Q	267	SER
1	Q	268	VAL
1	R	6	PHE
1	R	51	CYS
1	R	61	LYS
1	R	82	LYS
1	R	83	LEU
1	R	84	ASP
1	R	85	ARG
1	R	86	LYS
1	R	97	LEU
1	R	241	CYS
1	R	266	THR
1	R	267	SER
1	R	268	VAL
1	S	6	PHE
1	S	51	CYS
1	S	61	LYS

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Mol	Chain	Res	Type
1	S	82	LYS
1	S	85	ARG
1	S	86	LYS
1	S	97	LEU
1	S	241	CYS
1	S	266	THR
1	S	267	SER
1	S	268	VAL
1	T	6	PHE
1	T	51	CYS
1	T	61	LYS
1	T	82	LYS
1	T	83	LEU
1	T	84	ASP
1	T	85	ARG
1	T	86	LYS
1	T	97	LEU
1	T	241	CYS
1	T	266	THR
1	T	267	SER
1	T	268	VAL
1	V	6	PHE
1	V	51	CYS
1	V	61	LYS
1	V	82	LYS
1	V	85	ARG
1	V	86	LYS
1	V	97	LEU
1	V	241	CYS
1	V	266	THR
1	V	267	SER
1	V	268	VAL
1	W	6	PHE
1	W	51	CYS
1	W	61	LYS
1	W	82	LYS
1	W	83	LEU
1	W	84	ASP
1	W	85	ARG
1	W	86	LYS
1	W	97	LEU
1	W	241	CYS

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Mol	Chain	Res	Type
1	W	266	THR
1	W	267	SER
1	W	268	VAL
1	X	6	PHE
1	X	51	CYS
1	X	61	LYS
1	X	82	LYS
1	X	85	ARG
1	X	86	LYS
1	X	97	LEU
1	X	241	CYS
1	X	266	THR
1	X	267	SER
1	X	268	VAL
1	Y	6	PHE
1	Y	51	CYS
1	Y	61	LYS
1	Y	82	LYS
1	Y	83	LEU
1	Y	84	ASP
1	Y	85	ARG
1	Y	86	LYS
1	Y	97	LEU
1	Y	241	CYS
1	Y	266	THR
1	Y	267	SER
1	Y	268	VAL
1	a	6	PHE
1	a	51	CYS
1	a	61	LYS
1	a	82	LYS
1	a	85	ARG
1	a	86	LYS
1	a	97	LEU
1	a	241	CYS
1	a	266	THR
1	a	267	SER
1	a	268	VAL
1	b	6	PHE
1	b	51	CYS
1	b	61	LYS
1	b	82	LYS

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Mol	Chain	Res	Type
1	b	83	LEU
1	b	84	ASP
1	b	85	ARG
1	b	86	LYS
1	b	97	LEU
1	b	241	CYS
1	b	266	THR
1	b	267	SER
1	b	268	VAL
1	c	6	PHE
1	c	51	CYS
1	c	61	LYS
1	c	82	LYS
1	c	85	ARG
1	c	86	LYS
1	c	97	LEU
1	c	241	CYS
1	c	266	THR
1	c	267	SER
1	c	268	VAL
1	d	6	PHE
1	d	51	CYS
1	d	61	LYS
1	d	82	LYS
1	d	83	LEU
1	d	84	ASP
1	d	85	ARG
1	d	86	LYS
1	d	97	LEU
1	d	241	CYS
1	d	266	THR
1	d	267	SER
1	d	268	VAL
1	e	6	PHE
1	e	51	CYS
1	e	61	LYS
1	e	82	LYS
1	e	85	ARG
1	e	86	LYS
1	e	97	LEU
1	e	241	CYS
1	e	266	THR

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Mol	Chain	Res	Type
1	e	267	SER
1	e	268	VAL
1	f	51	CYS
1	f	61	LYS
1	f	82	LYS
1	f	83	LEU
1	f	84	ASP
1	f	85	ARG
1	f	86	LYS
1	f	97	LEU
1	f	241	CYS
1	f	266	THR
1	f	267	SER
1	f	268	VAL
1	g	6	PHE
1	g	51	CYS
1	g	61	LYS
1	g	82	LYS
1	g	85	ARG
1	g	86	LYS
1	g	97	LEU
1	g	241	CYS
1	g	266	THR
1	g	267	SER
1	g	268	VAL
1	h	6	PHE
1	h	51	CYS
1	h	61	LYS
1	h	82	LYS
1	h	83	LEU
1	h	84	ASP
1	h	85	ARG
1	h	86	LYS
1	h	97	LEU
1	h	241	CYS
1	h	266	THR
1	h	267	SER
1	h	268	VAL
1	i	6	PHE
1	i	51	CYS
1	i	61	LYS
1	i	82	LYS

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Mol	Chain	Res	Type
1	i	85	ARG
1	i	86	LYS
1	i	97	LEU
1	i	241	CYS
1	i	266	THR
1	i	267	SER
1	i	268	VAL
1	j	6	PHE
1	j	51	CYS
1	j	61	LYS
1	j	82	LYS
1	j	83	LEU
1	j	84	ASP
1	j	85	ARG
1	j	86	LYS
1	j	97	LEU
1	j	241	CYS
1	j	266	THR
1	j	267	SER
1	j	268	VAL
1	k	6	PHE
1	k	51	CYS
1	k	61	LYS
1	k	82	LYS
1	k	85	ARG
1	k	86	LYS
1	k	97	LEU
1	k	241	CYS
1	k	266	THR
1	k	267	SER
1	k	268	VAL
1	l	51	CYS
1	l	61	LYS
1	l	82	LYS
1	l	83	LEU
1	l	84	ASP
1	l	85	ARG
1	l	86	LYS
1	l	97	LEU
1	l	241	CYS
1	l	266	THR
1	l	267	SER

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Mol	Chain	Res	Type
1	l	268	VAL
1	m	6	PHE
1	m	51	CYS
1	m	61	LYS
1	m	82	LYS
1	m	85	ARG
1	m	86	LYS
1	m	97	LEU
1	m	241	CYS
1	m	266	THR
1	m	267	SER
1	m	268	VAL
1	n	6	PHE
1	n	51	CYS
1	n	61	LYS
1	n	82	LYS
1	n	83	LEU
1	n	84	ASP
1	n	85	ARG
1	n	86	LYS
1	n	97	LEU
1	n	241	CYS
1	n	266	THR
1	n	267	SER
1	n	268	VAL
1	o	6	PHE
1	o	51	CYS
1	o	61	LYS
1	o	82	LYS
1	o	85	ARG
1	o	86	LYS
1	o	97	LEU
1	o	241	CYS
1	o	266	THR
1	o	267	SER
1	o	268	VAL
1	p	6	PHE
1	p	51	CYS
1	p	61	LYS
1	p	82	LYS
1	p	83	LEU
1	p	84	ASP

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Mol	Chain	Res	Type
1	p	85	ARG
1	p	86	LYS
1	p	97	LEU
1	p	241	CYS
1	p	266	THR
1	p	267	SER
1	p	268	VAL
1	q	6	PHE
1	q	51	CYS
1	q	61	LYS
1	q	82	LYS
1	q	85	ARG
1	q	86	LYS
1	q	97	LEU
1	q	241	CYS
1	q	266	THR
1	q	267	SER
1	q	268	VAL
1	r	6	PHE
1	r	51	CYS
1	r	61	LYS
1	r	82	LYS
1	r	83	LEU
1	r	84	ASP
1	r	85	ARG
1	r	86	LYS
1	r	97	LEU
1	r	241	CYS
1	r	266	THR
1	r	267	SER
1	r	268	VAL
1	s	6	PHE
1	s	51	CYS
1	s	61	LYS
1	s	82	LYS
1	s	85	ARG
1	s	86	LYS
1	s	97	LEU
1	s	241	CYS
1	s	266	THR
1	s	267	SER
1	s	268	VAL

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Mol	Chain	Res	Type
1	t	6	PHE
1	t	51	CYS
1	t	61	LYS
1	t	82	LYS
1	t	83	LEU
1	t	84	ASP
1	t	85	ARG
1	t	86	LYS
1	t	97	LEU
1	t	241	CYS
1	t	266	THR
1	t	267	SER
1	t	268	VAL
1	v	6	PHE
1	v	51	CYS
1	v	61	LYS
1	v	82	LYS
1	v	85	ARG
1	v	86	LYS
1	v	97	LEU
1	v	241	CYS
1	v	266	THR
1	v	267	SER
1	v	268	VAL
1	w	6	PHE
1	w	51	CYS
1	w	61	LYS
1	w	82	LYS
1	w	83	LEU
1	w	84	ASP
1	w	85	ARG
1	w	86	LYS
1	w	97	LEU
1	w	241	CYS
1	w	266	THR
1	w	267	SER
1	w	268	VAL
1	x	6	PHE
1	x	51	CYS
1	x	61	LYS
1	x	82	LYS
1	x	85	ARG

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Mol	Chain	Res	Type
1	x	86	LYS
1	x	97	LEU
1	x	241	CYS
1	x	266	THR
1	x	267	SER
1	x	268	VAL
1	y	6	PHE
1	y	51	CYS
1	y	61	LYS
1	y	82	LYS
1	y	83	LEU
1	y	84	ASP
1	y	85	ARG
1	y	86	LYS
1	y	97	LEU
1	y	241	CYS
1	y	266	THR
1	y	267	SER
1	y	268	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (156) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	72	ASN
1	A	258	ASN
1	A	265	GLN
1	B	72	ASN
1	B	258	ASN
1	B	265	GLN
1	C	72	ASN
1	C	258	ASN
1	C	265	GLN
1	D	72	ASN
1	D	258	ASN
1	D	265	GLN
1	E	32	GLN
1	E	72	ASN
1	E	258	ASN
1	E	265	GLN
1	F	72	ASN
1	F	258	ASN

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Mol	Chain	Res	Type
1	F	265	GLN
1	G	72	ASN
1	G	116	ASN
1	G	265	GLN
1	H	258	ASN
1	H	265	GLN
1	I	72	ASN
1	I	258	ASN
1	I	265	GLN
1	J	72	ASN
1	J	228	ASN
1	J	258	ASN
1	J	265	GLN
1	K	72	ASN
1	K	258	ASN
1	K	265	GLN
1	L	228	ASN
1	L	258	ASN
1	L	265	GLN
1	M	72	ASN
1	M	258	ASN
1	M	265	GLN
1	N	72	ASN
1	N	258	ASN
1	N	265	GLN
1	O	72	ASN
1	O	258	ASN
1	O	265	GLN
1	P	72	ASN
1	P	116	ASN
1	P	258	ASN
1	P	265	GLN
1	Q	72	ASN
1	Q	258	ASN
1	Q	265	GLN
1	R	258	ASN
1	R	265	GLN
1	S	72	ASN
1	S	93	ASN
1	S	258	ASN
1	S	265	GLN
1	T	72	ASN

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Mol	Chain	Res	Type
1	T	258	ASN
1	T	265	GLN
1	V	72	ASN
1	V	93	ASN
1	V	116	ASN
1	V	258	ASN
1	V	265	GLN
1	W	72	ASN
1	W	258	ASN
1	W	265	GLN
1	X	72	ASN
1	X	93	ASN
1	X	258	ASN
1	X	265	GLN
1	Y	72	ASN
1	Y	258	ASN
1	Y	265	GLN
1	a	72	ASN
1	a	258	ASN
1	a	265	GLN
1	b	72	ASN
1	b	116	ASN
1	b	258	ASN
1	b	265	GLN
1	c	72	ASN
1	c	93	ASN
1	c	258	ASN
1	c	265	GLN
1	d	72	ASN
1	d	258	ASN
1	d	265	GLN
1	e	72	ASN
1	e	258	ASN
1	e	265	GLN
1	f	72	ASN
1	f	258	ASN
1	f	265	GLN
1	g	72	ASN
1	g	265	GLN
1	h	72	ASN
1	h	258	ASN
1	h	265	GLN

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Mol	Chain	Res	Type
1	i	72	ASN
1	i	258	ASN
1	i	265	GLN
1	j	72	ASN
1	j	258	ASN
1	j	265	GLN
1	k	72	ASN
1	k	258	ASN
1	k	265	GLN
1	l	72	ASN
1	l	258	ASN
1	l	265	GLN
1	m	32	GLN
1	m	72	ASN
1	m	258	ASN
1	m	265	GLN
1	n	72	ASN
1	n	258	ASN
1	n	265	GLN
1	o	32	GLN
1	o	72	ASN
1	o	258	ASN
1	o	265	GLN
1	p	72	ASN
1	p	258	ASN
1	p	265	GLN
1	q	32	GLN
1	q	72	ASN
1	q	258	ASN
1	q	265	GLN
1	r	72	ASN
1	r	258	ASN
1	r	265	GLN
1	s	72	ASN
1	s	258	ASN
1	s	265	GLN
1	t	72	ASN
1	t	251	GLN
1	t	258	ASN
1	t	265	GLN
1	v	72	ASN
1	v	258	ASN

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Mol	Chain	Res	Type
1	v	265	GLN
1	w	72	ASN
1	w	258	ASN
1	w	265	GLN
1	x	72	ASN
1	x	251	GLN
1	x	258	ASN
1	x	265	GLN
1	y	72	ASN
1	y	258	ASN
1	y	265	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

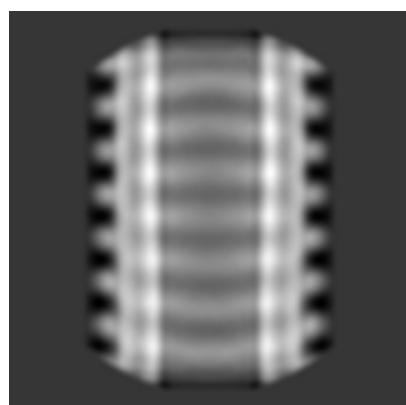
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20842. These allow visual inspection of the internal detail of the map and identification of artifacts.

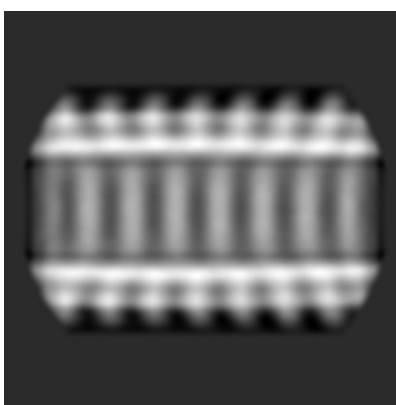
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

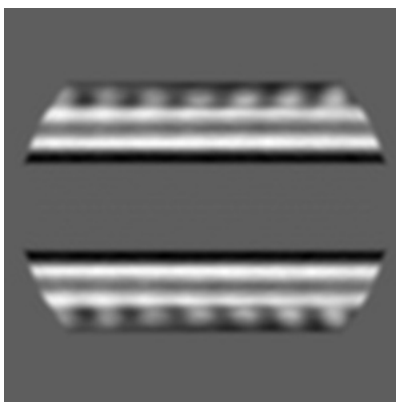
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

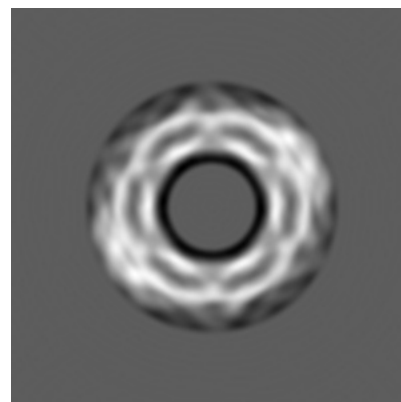
6.2.1 Primary map



X Index: 107



Y Index: 107



Z Index: 107

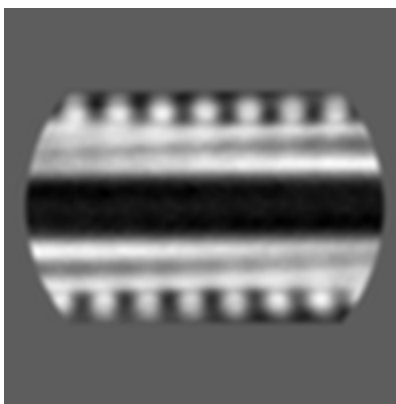
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

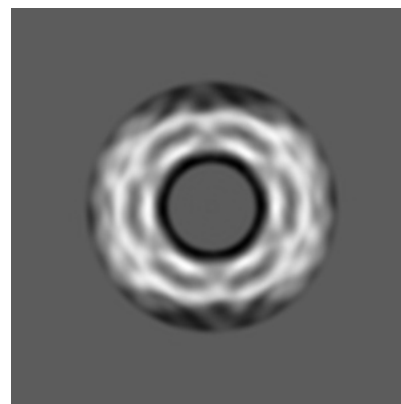
6.3.1 Primary map



X Index: 73



Y Index: 132

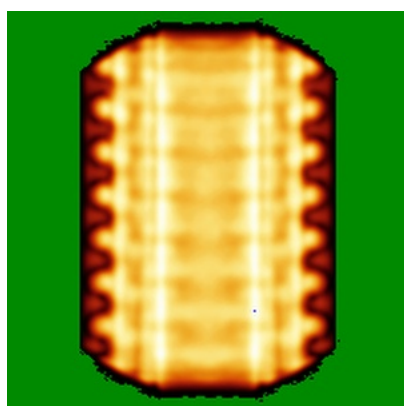


Z Index: 80

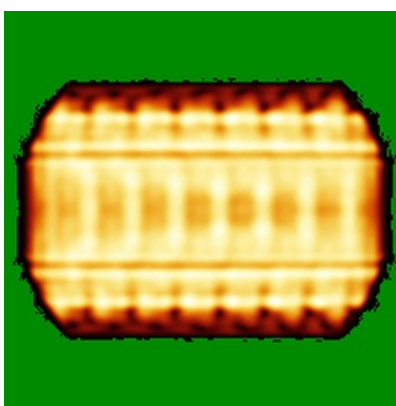
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

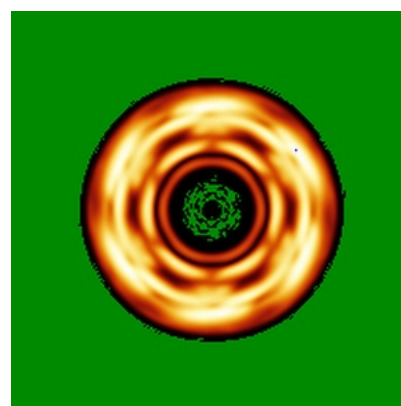
6.4.1 Primary map



X



Y

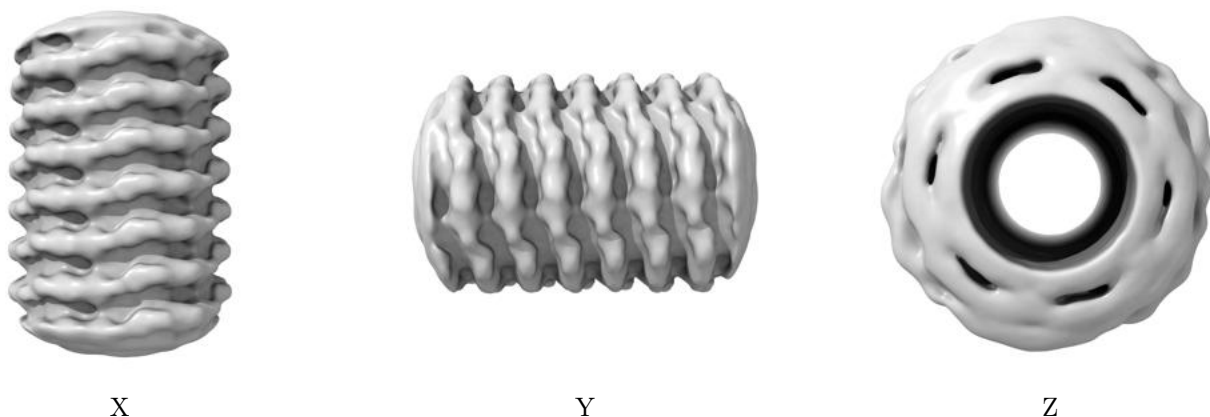


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

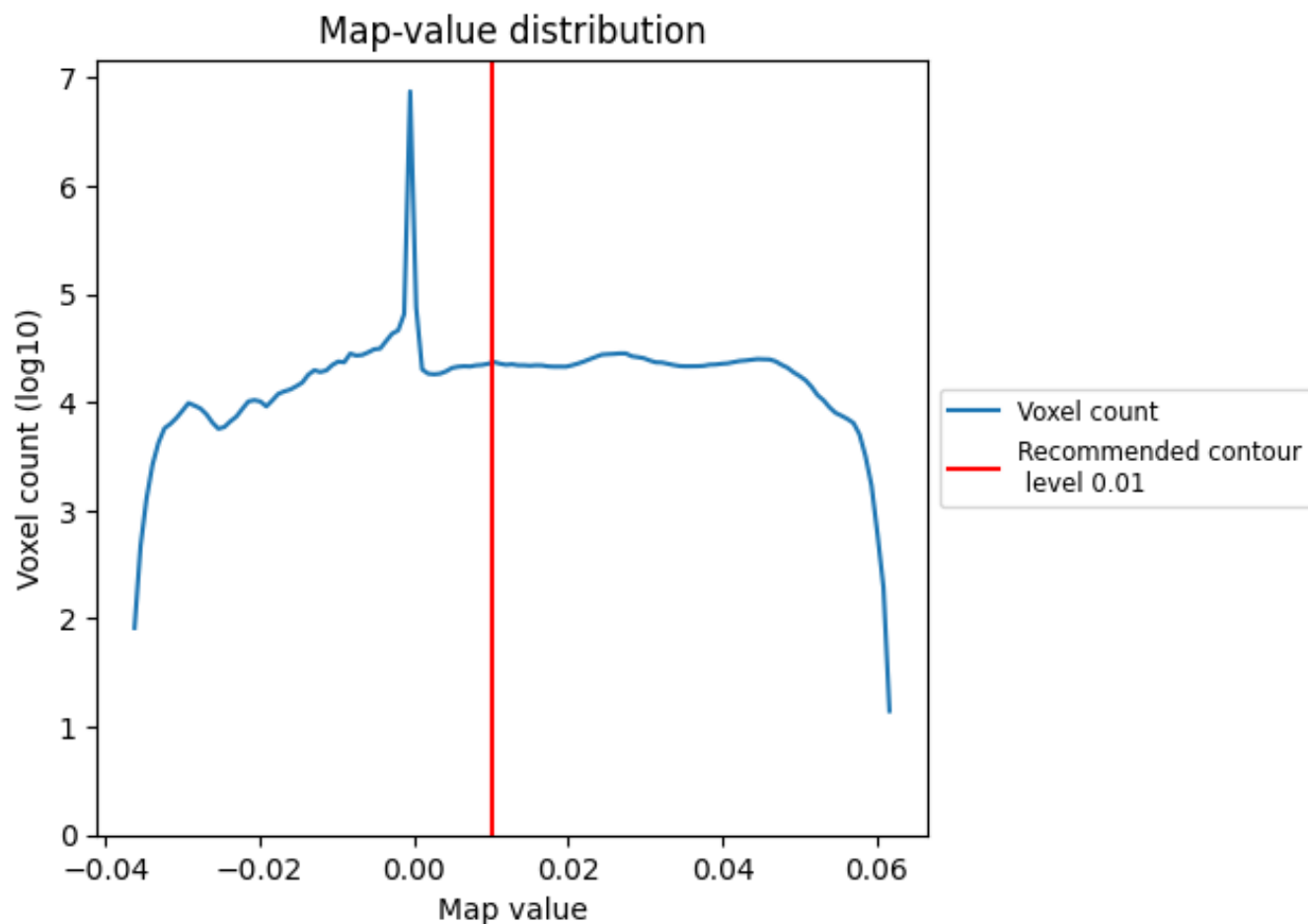
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

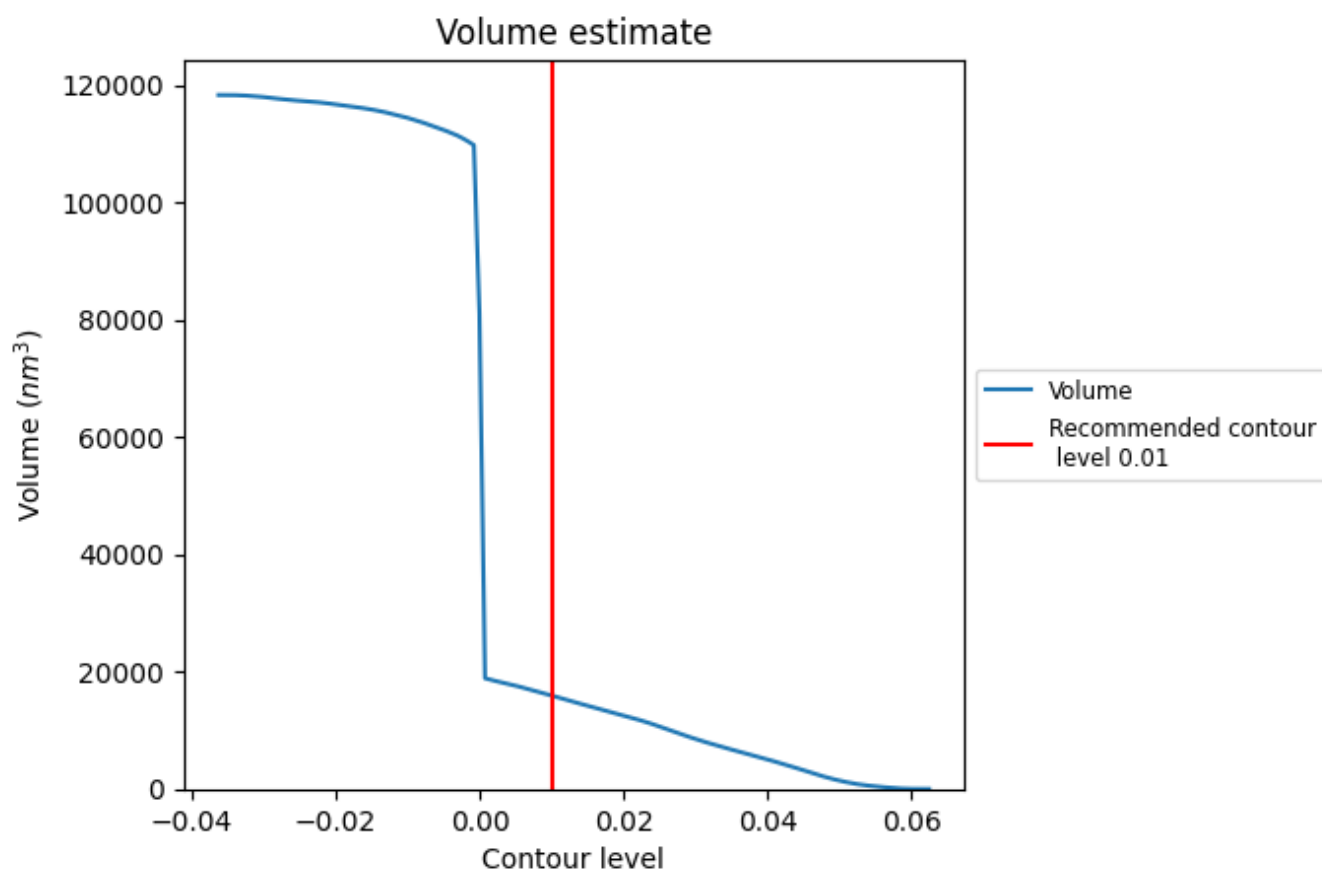
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

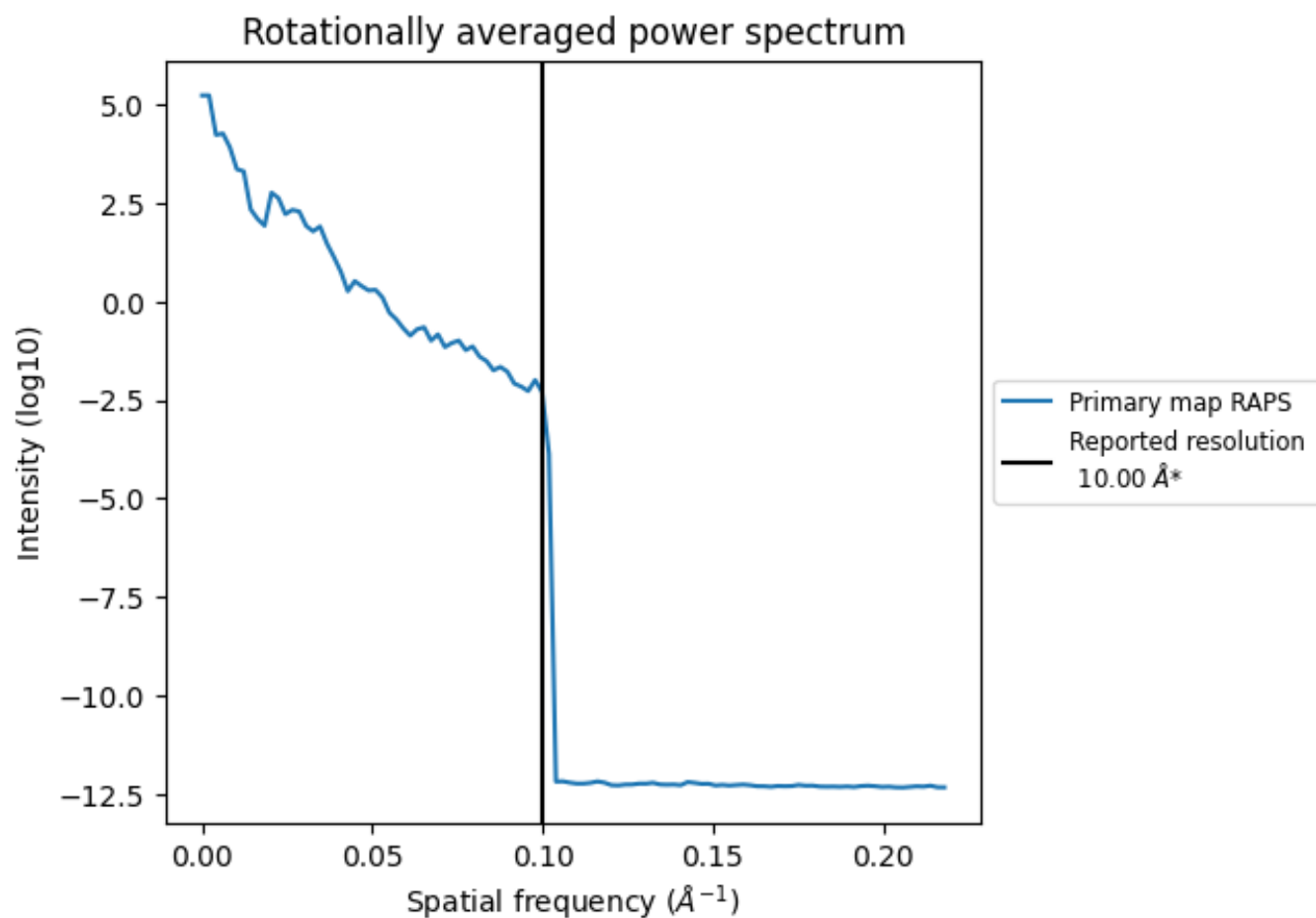
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15935 nm³; this corresponds to an approximate mass of 14395 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.100 Å⁻¹

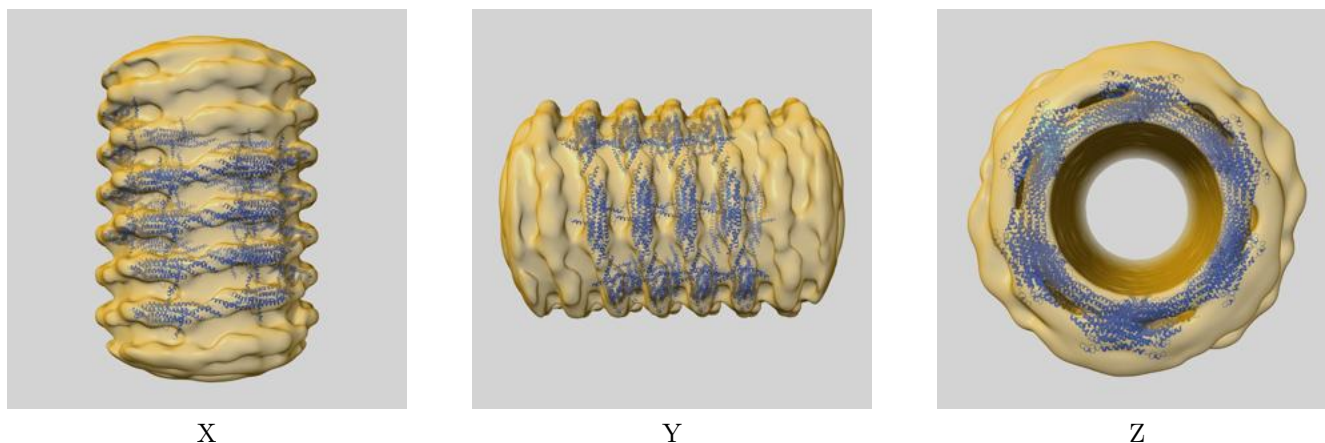
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

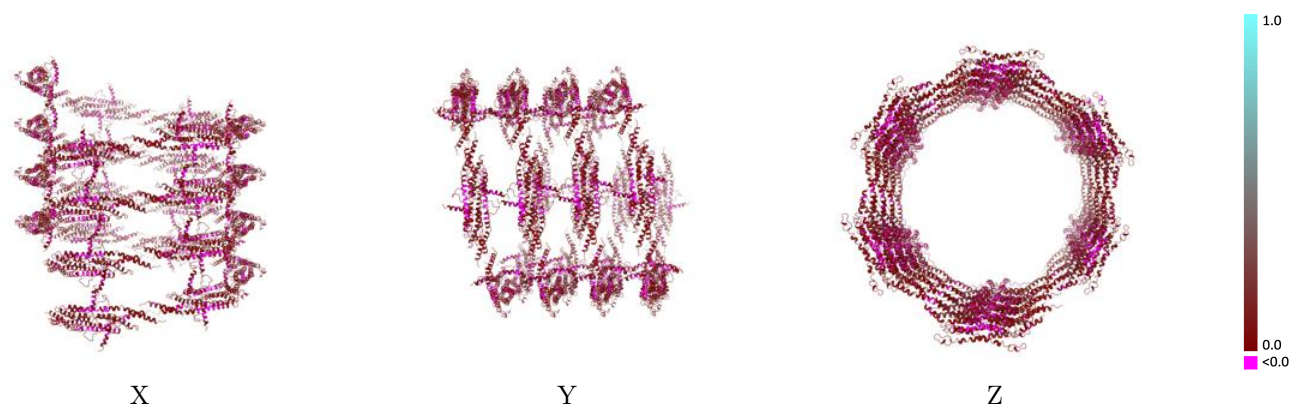
This section contains information regarding the fit between EMDB map EMD-20842 and PDB model 6UPN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



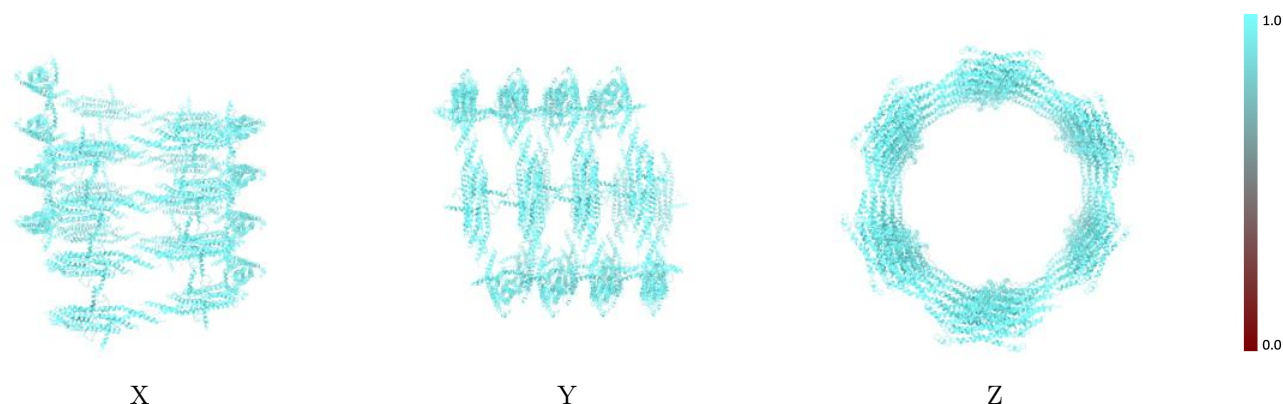
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



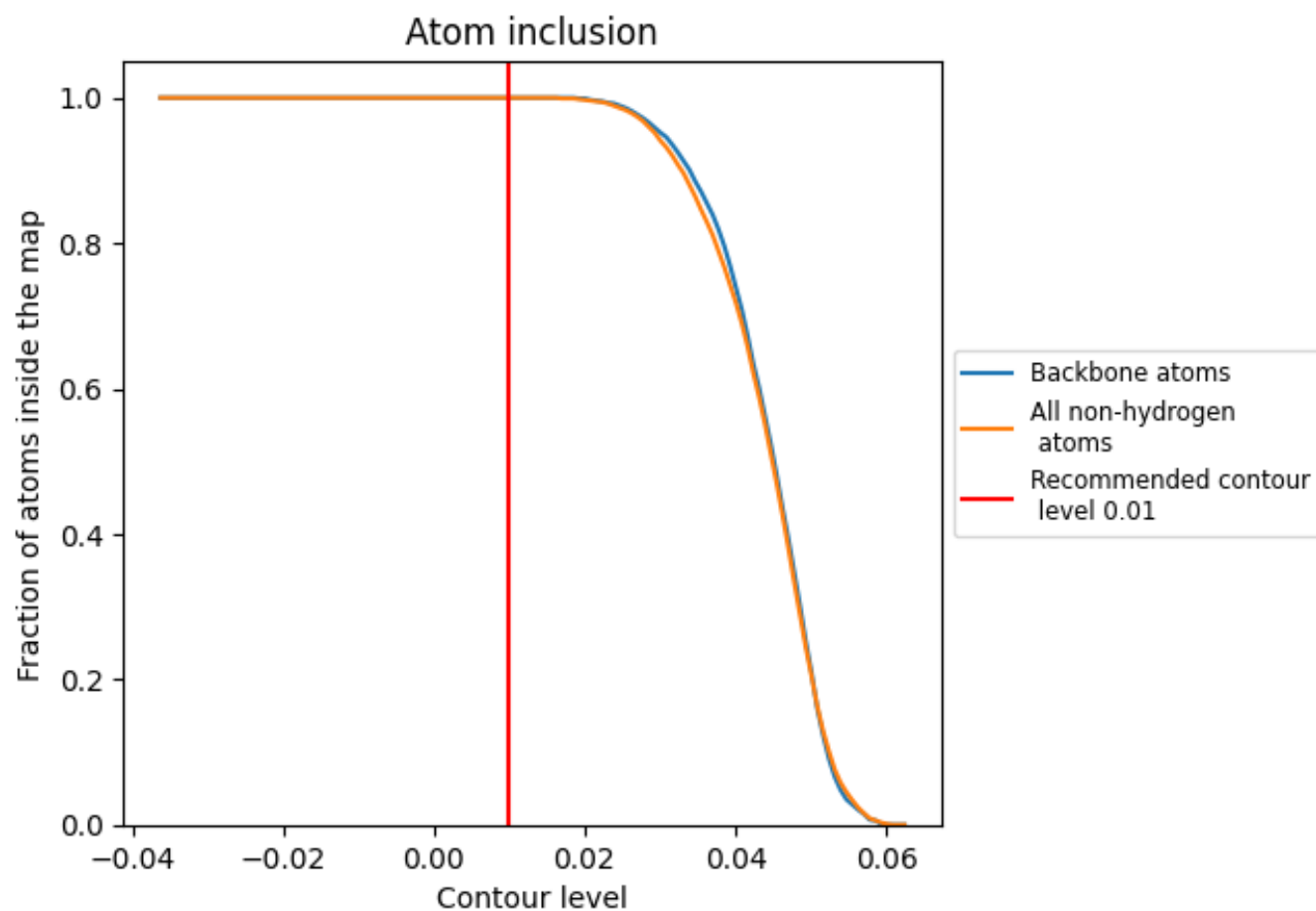
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 1.0000	 0.0790
A	 1.0000	 0.0880
B	 1.0000	 0.0710
C	 1.0000	 0.0890
D	 1.0000	 0.0710
E	 1.0000	 0.0870
F	 1.0000	 0.0700
G	 1.0000	 0.0850
H	 1.0000	 0.0730
I	 1.0000	 0.0850
J	 1.0000	 0.0730
K	 1.0000	 0.0850
L	 1.0000	 0.0710
M	 1.0000	 0.0870
N	 1.0000	 0.0710
O	 1.0000	 0.0890
P	 1.0000	 0.0690
Q	 1.0000	 0.0880
R	 1.0000	 0.0700
S	 1.0000	 0.0870
T	 1.0000	 0.0720
V	 1.0000	 0.0850
W	 1.0000	 0.0730
X	 1.0000	 0.0860
Y	 1.0000	 0.0730
a	 1.0000	 0.0890
b	 1.0000	 0.0710
c	 1.0000	 0.0890
d	 1.0000	 0.0720
e	 1.0000	 0.0870
f	 1.0000	 0.0680
g	 1.0000	 0.0860
h	 1.0000	 0.0730
i	 1.0000	 0.0870
j	 1.0000	 0.0710



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Chain	Atom inclusion	Q-score
k	 1.0000	 0.0860
l	 1.0000	 0.0720
m	 1.0000	 0.0880
n	 1.0000	 0.0690
o	 1.0000	 0.0890
p	 1.0000	 0.0710
q	 1.0000	 0.0890
r	 1.0000	 0.0720
s	 1.0000	 0.0880
t	 1.0000	 0.0730
v	 1.0000	 0.0860
w	 1.0000	 0.0690
x	 1.0000	 0.0860
y	 1.0000	 0.0720