



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 12:39 AM UTC

PDB ID : 7VHP / pdb_00007vhp
EMDB ID : EMD-32002
Title : Structural insights into the membrane microdomain organization by SPFH family proteins
Authors : Ma, C.Y.; Wang, C.K.; Luo, D.Y.; Yan, L.; Yang, W.X.; Li, N.N.; Gao, N.
Deposited on : 2021-09-22
Resolution : 3.27 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:

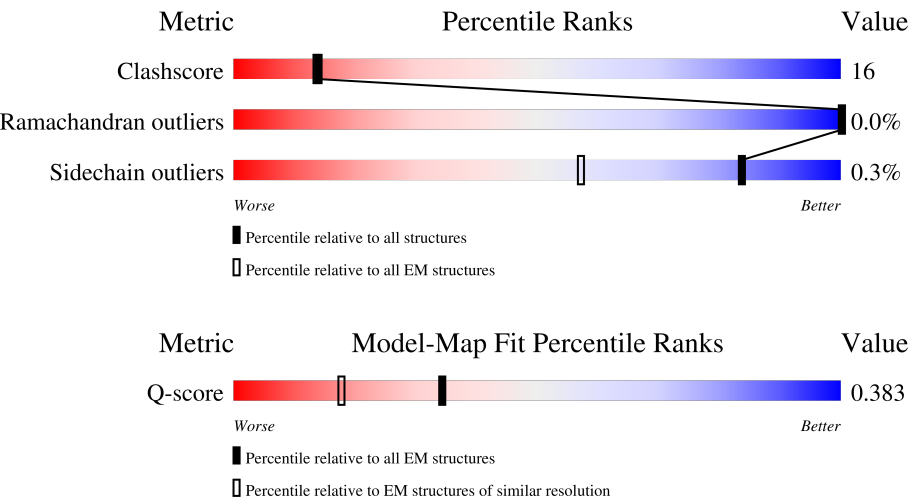
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.27 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14508 (2.77 - 3.77)

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	644	6% . 90%
1	B	644	6% . 90%
1	C	644	5% 5% 90%
1	D	644	7% . 90%

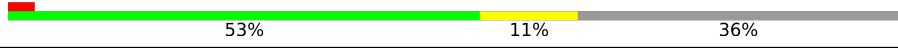
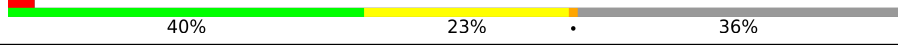
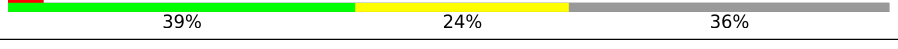
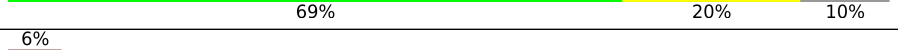
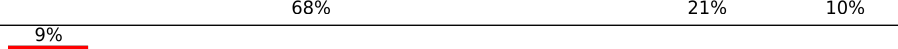
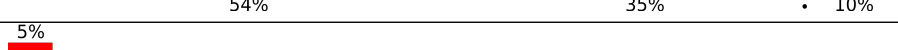
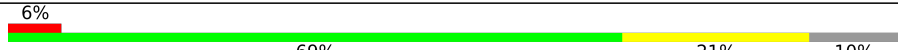
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Mol	Chain	Length	Quality of chain
1	J	644	6% 90%
1	K	644	6% 90%
1	L	644	5% 5% 90%
1	M	644	7% 90%
1	T	644	7% 90%
1	V	644	8% 90%
1	W	644	6% 90%
1	X	644	6% 90%
1	Y	644	6% 90%
1	Z	644	6% 90%
1	a	644	5% 5% 90%
1	b	644	5% 5% 90%
1	c	644	7% 90%
1	d	644	8% 90%
1	e	644	7% 90%
1	f	644	8% 90%
1	s	644	7% 90%
1	t	644	7% 90%
1	u	644	8% 90%
1	v	644	8% 90%
2	E	419	52% 12% 36%
2	F	419	44% 20% 36%
2	N	419	53% 11% 36%
2	O	419	40% 22% 36%
2	S	419	50% 14% 36%

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Mol	Chain	Length	Quality of chain
2	U	419	
2	g	419	
2	h	419	
2	i	419	
2	j	419	
2	q	419	
2	r	419	
3	G	334	
3	H	334	
3	I	334	
3	P	334	
3	Q	334	
3	R	334	
3	k	334	
3	l	334	
3	m	334	
3	n	334	
3	o	334	
3	p	334	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 66600 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 ATP-dependent zinc metalloprotease FtsH.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	63	Total	C	N	O	0	0
			516	321	94	101		
1	B	63	Total	C	N	O	0	0
			516	321	94	101		
1	C	63	Total	C	N	O	0	0
			516	321	94	101		
1	D	63	Total	C	N	O	0	0
			516	321	94	101		
1	e	63	Total	C	N	O	0	0
			516	321	94	101		
1	f	63	Total	C	N	O	0	0
			516	321	94	101		
1	W	63	Total	C	N	O	0	0
			516	321	94	101		
1	Y	63	Total	C	N	O	0	0
			516	321	94	101		
1	a	63	Total	C	N	O	0	0
			516	321	94	101		
1	c	63	Total	C	N	O	0	0
			516	321	94	101		
1	s	63	Total	C	N	O	0	0
			516	321	94	101		
1	u	63	Total	C	N	O	0	0
			516	321	94	101		
1	X	63	Total	C	N	O	0	0
			516	321	94	101		
1	Z	63	Total	C	N	O	0	0
			516	321	94	101		
1	b	63	Total	C	N	O	0	0
			516	321	94	101		
1	d	63	Total	C	N	O	0	0
			516	321	94	101		
1	t	63	Total	C	N	O	0	0
			516	321	94	101		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	v	63	Total	C	N	O	0	0
			516	321	94	101		
1	J	63	Total	C	N	O	0	0
			516	321	94	101		
1	K	63	Total	C	N	O	0	0
			516	321	94	101		
1	L	63	Total	C	N	O	0	0
			516	321	94	101		
1	M	63	Total	C	N	O	0	0
			516	321	94	101		
1	T	63	Total	C	N	O	0	0
			516	321	94	101		
1	V	63	Total	C	N	O	0	0
			516	321	94	101		

- Molecule 2 is a protein called Protein HflK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	F	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	U	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	g	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	i	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	q	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	h	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	j	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	r	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	N	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	O	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		
2	S	267	Total	C	N	O	S	0	0
			2121	1332	374	410	5		

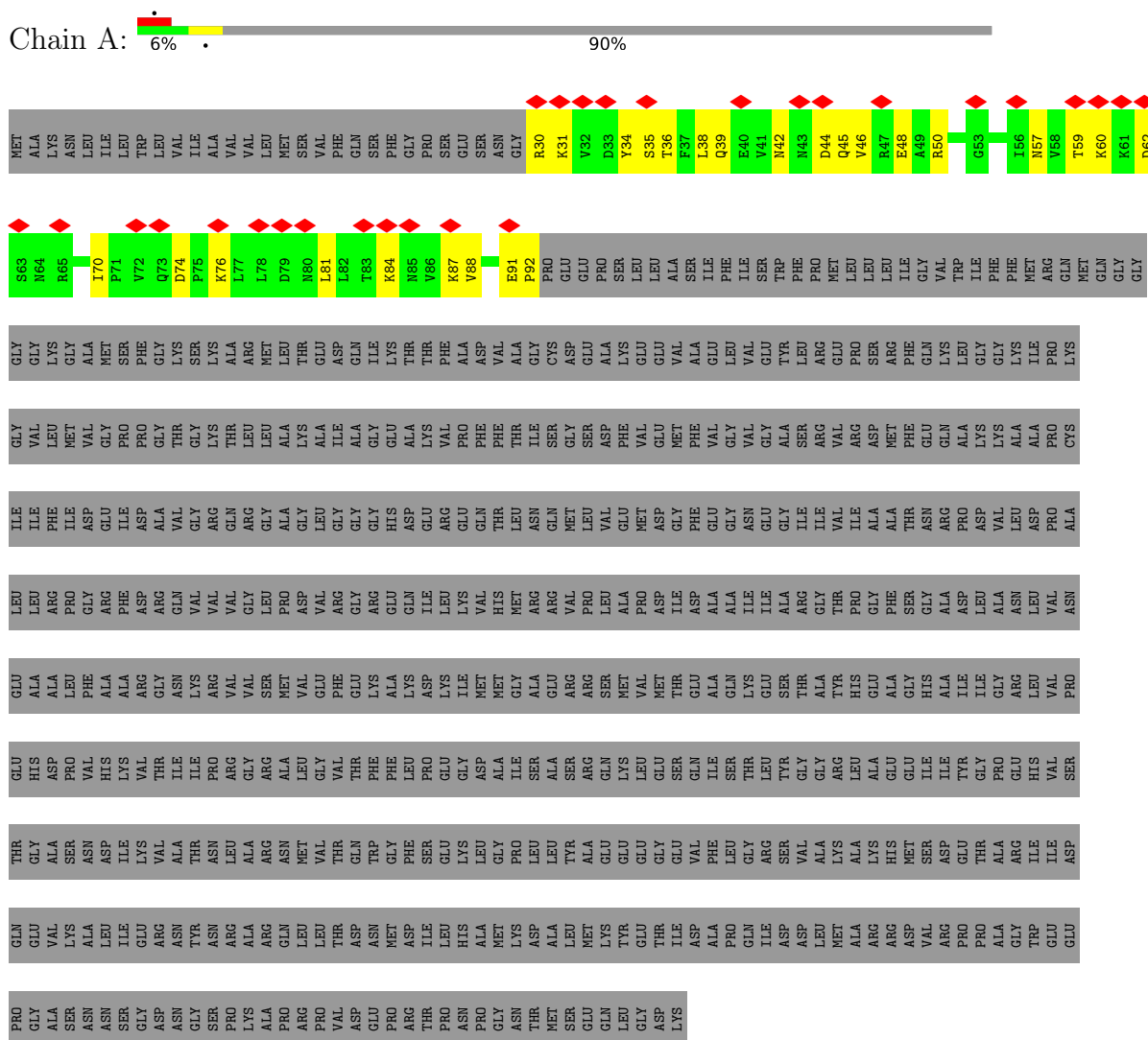
- Molecule 3 is a protein called Modulator of FtsH protease HflC.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	H	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	I	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	k	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	m	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	o	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	l	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	n	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	p	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	P	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	Q	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		
3	R	299	Total	C	N	O	S	0	0
			2397	1508	429	450	10		

3 Residue-property plots

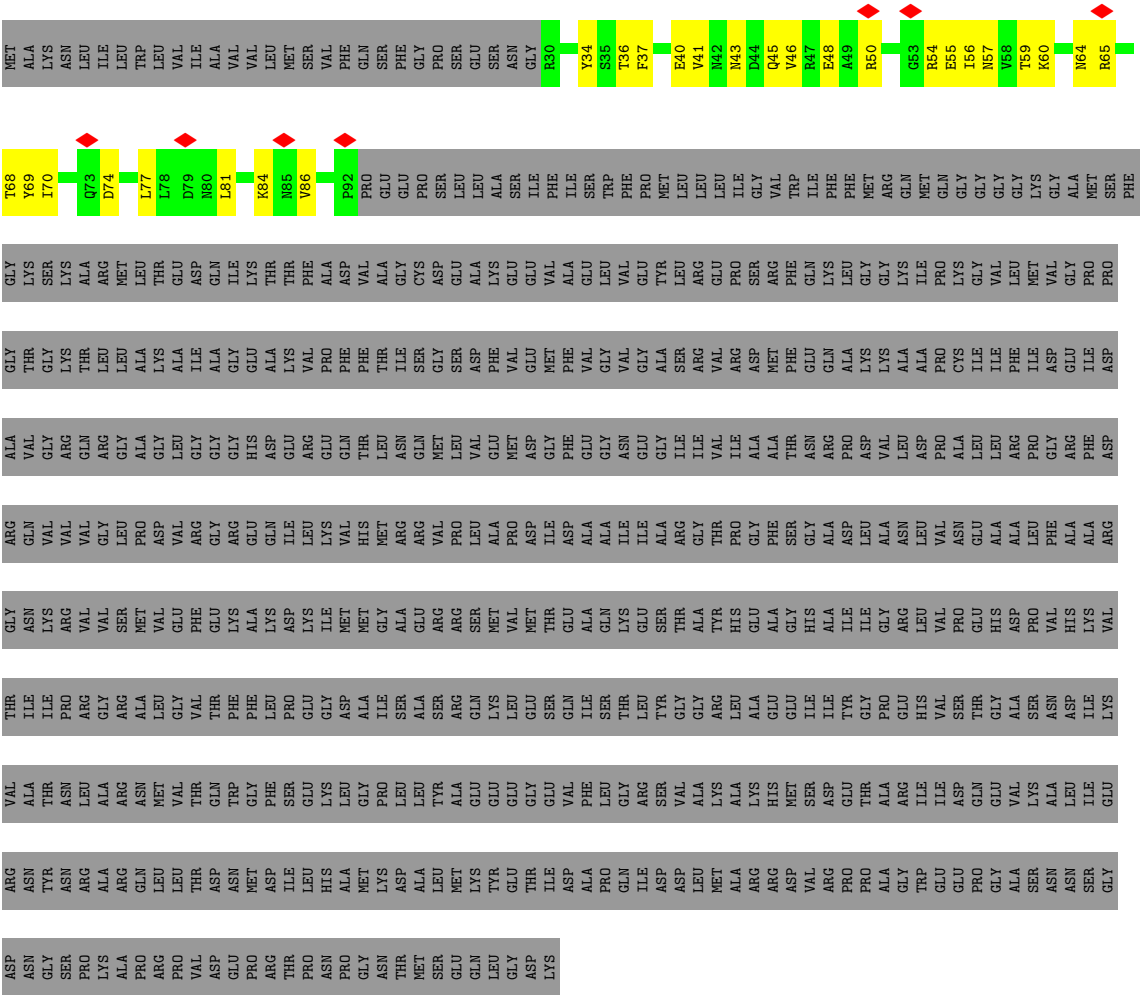
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: ATP-dependent zinc metalloprotease FtsH

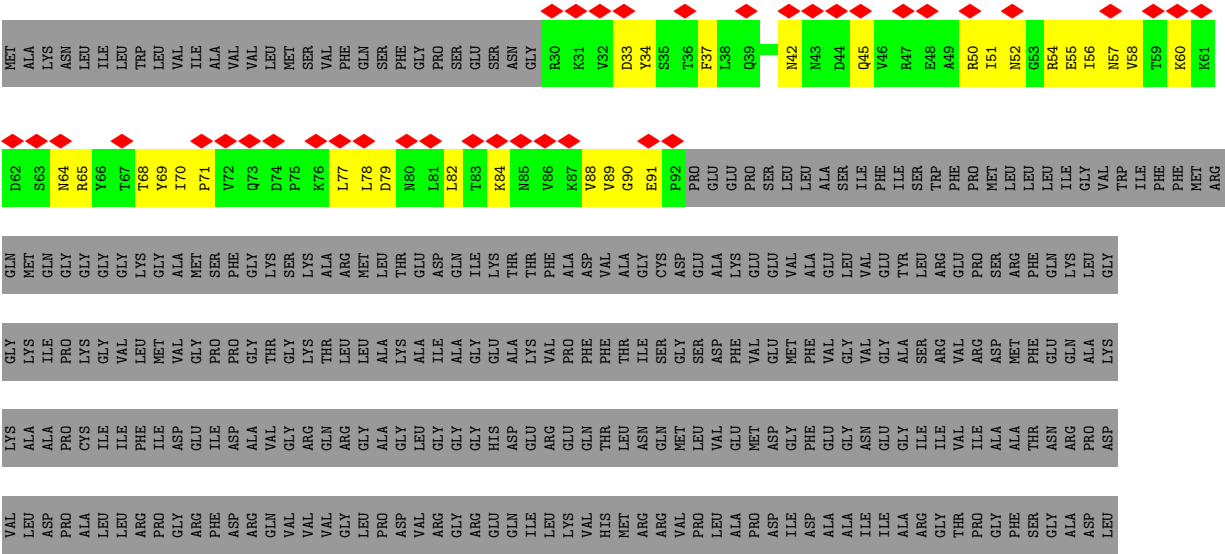


- Molecule 1: ATP-dependent zinc metalloprotease FtsH

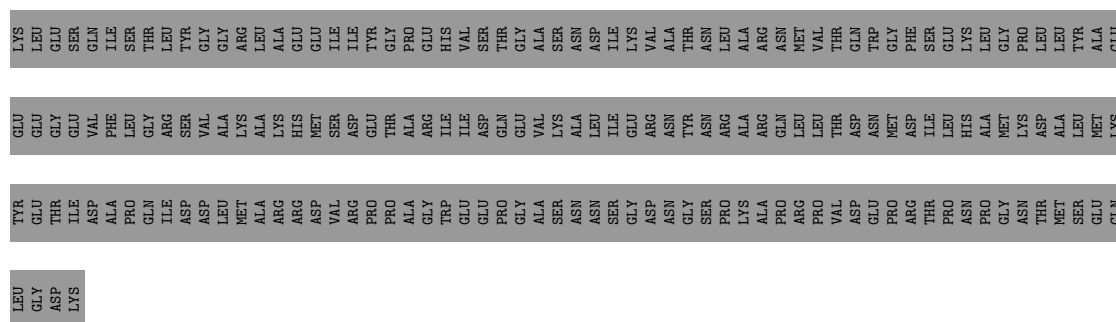




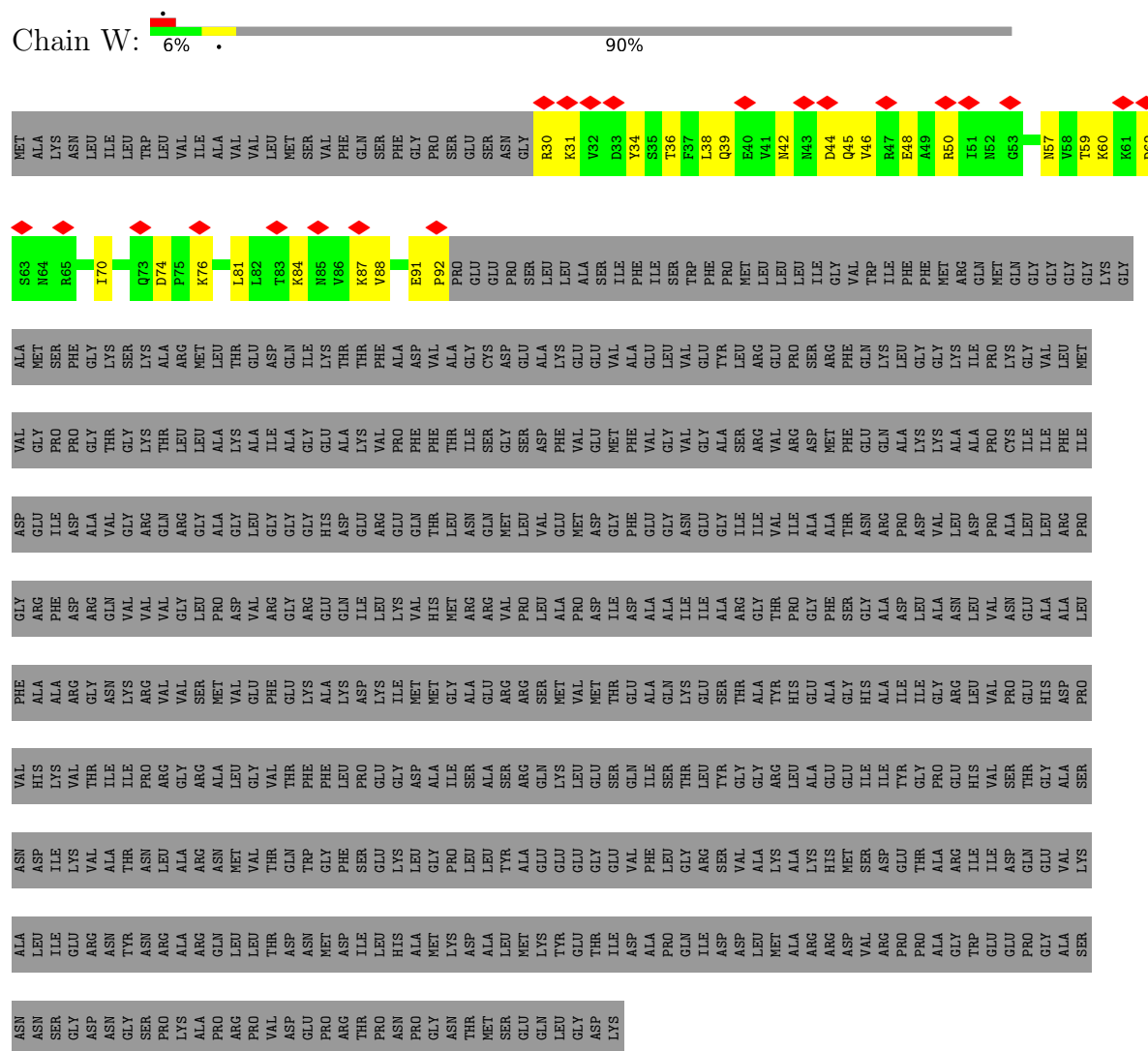
● Molecule 1: ATP-dependent zinc metalloprotease FtsH



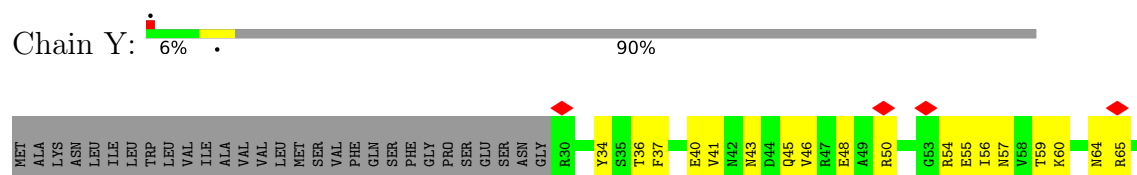




- Molecule 1: ATP-dependent zinc metalloprotease FtsH



- Molecule 1: ATP-dependent zinc metalloprotease FtsH



[illegible]

- Molecule 1: ATP-dependent zinc metalloprotease FtsH



SER	ARG	VAL	MET	GLY	ASP	LEU	MET
ARG	ARG	PRO	LEU	SER	GLU	LEU	LEU
GLN	SER	PRO	VAL	ASP	ALA	ALA	ALA
LEU	MET	ALA	GLU	PHE	LYS	SER	ASN
GLU	MET	PRO	MET	VAL	GLU	ILE	LEU
SER	THR	ASP	ASP	GIJ	GLU	PHE	ILE
GLN	GLU	ILE	PHE	MET	VAL	SER	LEU
ILE	ALA	ALA	GLY	VAL	GLU	TRP	TRP
SER	GLN	ALA	GLU	GLY	LEU	PHE	VAL
THR	LYS	ILE	ASN	VAL	VAL	PRO	ILE
LEU	GLU	ILE	GLI	GLY	GLU	MET	ALA
TYR	SER	ALA	GLY	ALA	TYR	LEU	VAL
GLY	THR	ARG	ILE	SER	LEU	LEU	VAL
GLY	ALA	GLY	ILE	ARG	ARG	LEU	VAL
ARG	TYR	THR	VAL	VAL	GLU	ILE	MET
LEU	HIS	PRO	ILE	ASP	PRO	GLY	SER
ALA	GLU	GLY	ALA	ASP	SER	VAL	VAL
GLU	ALA	PHE	MET	ASP	ARG	TRP	PHE
GLU	GLY	SER	THR	PHE	ARG	TRP	GLN
ILE	HIS	GLY	ASN	GLN	GLN	PHE	SER
ILE	ALA	ALA	ARG	GLN	LYS	PHE	PHE
TYR	ILE	ASP	PRO	ALA	LEU	MET	GLY
GLY	ILE	LEU	ASP	LYS	GLY	ARG	PRO
PRO	GLY	ALA	VAL	LYS	GLY	GLN	SER
GLU	ARG	ASN	LEU	ALA	LYS	MET	GLU
HIS	LEU	LEU	ASP	ALA	ILE	GLN	SER
VAL	VAL	VAL	PRO	PRO	GLY	GLY	ASN
SER	PRO	ASN	ALA	CYS	LYS	GLY	GLY
THR	GLU	GLU	LEU	ILE	GLY	GLY	R90
GLY	HIS	ALA	LEU	PHE	VAL	GLY	D33
ALA	ASP	ALA	ARG	ILE	LEU	LYS	L38
SER	PRO	LEU	PRO	ILE	MET	GLY	G99
ASN	VAL	PHE	GLY	ASP	VAL	ALA	E40
ASP	HIS	ALA	ARG	GIJ	GLY	SER	V41
ILE	LYS	ALA	PHE	ILE	PRO	SER	V46
LYS	VAL	ARG	ASP	ILE	PRO	PHE	R47
VAL	THR	GLY	ARG	ALA	PRO	GLY	E48
ALA	ILE	ASN	GLN	VAL	GLY	LYS	A49
THR	ILE	LYS	VAL	GLY	THR	LYS	R50
ASN	PRO	ARG	VAL	VAL	THR	ALA	T59
LEU	ARG	VAL	VAL	GLM	ALA	ARG	K60
ALA	GLY	VAL	GLY	GLN	LEU	MET	Y66
ARG	ARG	SER	LEU	GLY	LEU	THR	G73
ASN	ALA	MET	PRO	ALA	ALA	LEU	Y89
VAL	GLY	GLU	ASP	GLY	LYS	GLU	G90
THR	VAL	PHE	VAL	LEU	ALA	ASP	E91
GLN	THR	GLU	ARG	GLY	ILE	ASP	P92
THR	VAL	GLU	GLY	GLY	LYS	THR	PRO
ASN	THR	GLY	GLY	GLY	VAL	PHE	GLU
GLN	THR	GLU	GLY	GLY	VAL	ALA	GLY
THR	PHE	LYS	ARG	HIS	PRO	VAL	PRO
GLY	GLY	ALA	GLU	GLY	THR	GLU	GLY
PHE	LEU	LYS	GLN	ASP	LYS	THR	PRO
SER	PRO	ASP	ILE	GIJ	VAL	PHE	GLY
GLU	GLU	LYS	LEU	ARG	VAL	ALA	PRO
LYS	GLY	ILE	LYS	GLN	PRO	ALA	GLU
LEU	THR	THR	GLY	HIS	PHE	VAL	GLY
THR	VAL	THR	GLY	GLY	THR	GLY	PRO
GLN	THR	GLU	GLY	GLY	ILE	ASP	GLY
THR	THR	GLU	GLY	GLY	ALA	ASP	PRO
GLN	THR	GLU	GLY	GLY	ALA	ASP	GLY
THR	THR	GLU	GLY	GLY	ALA	ASP	PRO
ASN	THR	GLU	GLY	GLY	ALA	ASP	GLY
LEU	THR	GLU	GLY	GLY	ALA	ASP	PRO
ALA	ARG	VAL	GLY	GLY	ALA	ASP	GLY
ARG	ARG	SER	LEU	GLY	LEU	VAL	GLY
ASN	ALA	MET	PRO	GLY	ALA	ASP	PRO
VAL	LEU	VAL	VAL	VAL	LYS	THR	GLY
ASN	VAL	ARG	VAL	GLY	THR	GLY	PRO
THR	PRO	THR	VAL	GLY	LYS	GLY	GLY
LEU	ASN	VAL	VAL	GLY	LYS	GLY	GLY
ALA	GLY	VAL	VAL	GLM	THR	ALA	GLY
ARG	GLY	VAL	GLY	GLY	LEU	ASP	GLY
ASN	ALA	SER	LEU	GLY	LEU	THR	GLY

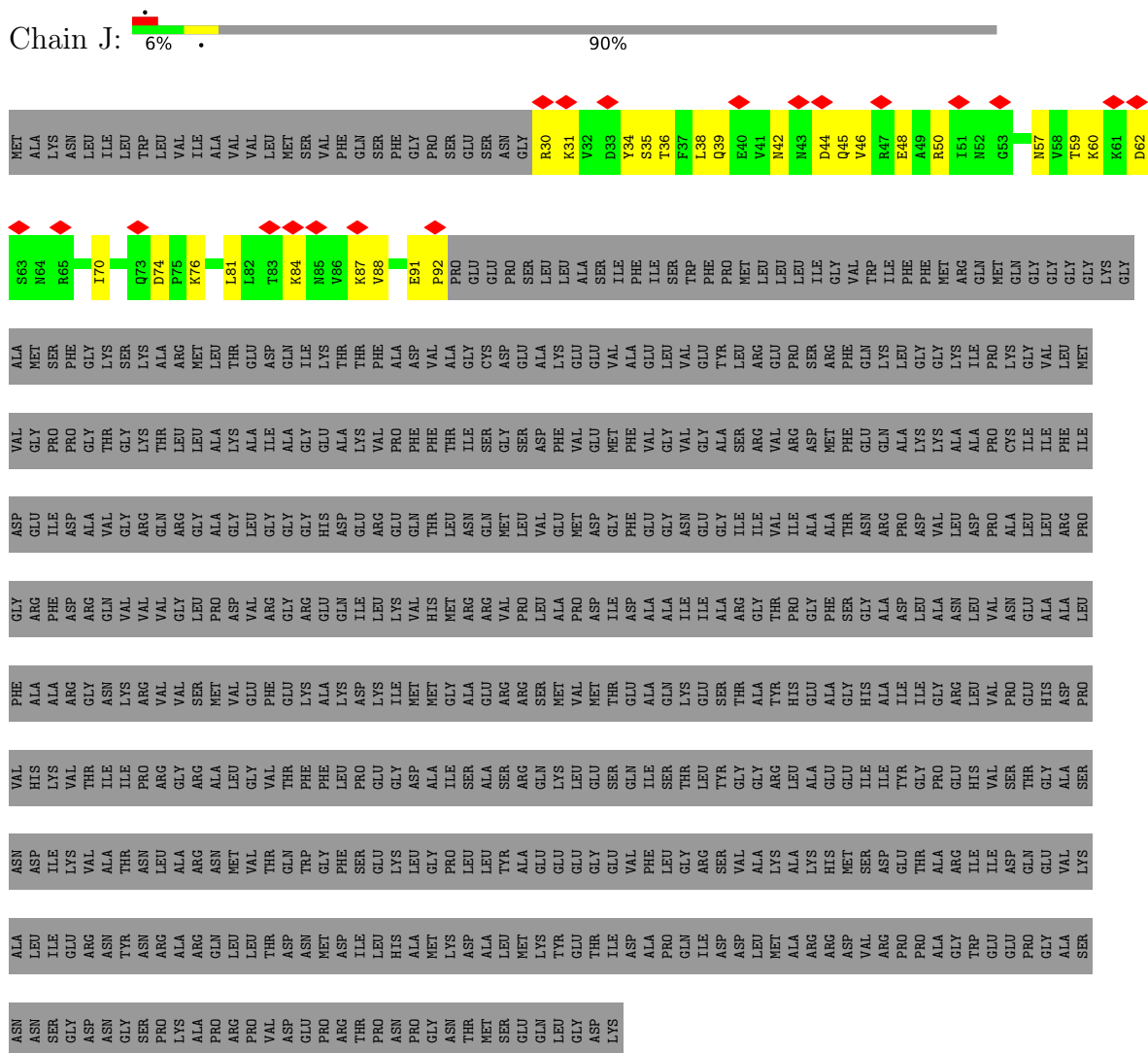
[illegible]

- Molecule 1: ATP-dependent zinc metalloprotease FtsH

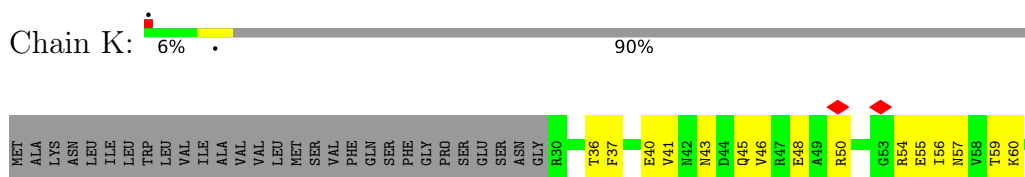


LYS	LEU	VAL	MET	ALA	GLU	PHE	LYS	SER	MET
LEU	GLU	VAL	VAL	PRO	MET	VAL	LYS	ILE	ALA
SER	GLU	MET	THR	ILE	ASP	GLU	GLU	ILE	LYS
GLN	GLU	ASP	GLU	ASP	PHE	GLU	ALA	SER	ASN
ILE	ALA	ALA	ALA	ALA	GLU	VAL	VAL	TRP	ILE
SER	GLN	ALA	GLN	ALA	GLY	GLY	LEU	PHE	LEU
THR	LYS	ILE	LYS	ILE	ASN	VAL	VAL	PRO	TRP
LEU	LEU	ILE	GLU	ILE	GLU	GLY	TYR	MET	VAL
TYR	SER	ALA	GLY	GLY	GLY	ALA	ARG	LEU	ILE
GLY	GLY	ARG	THR	GLY	ILE	SER	LEU	LEU	ILE
GLY	ALA	GLY	ILE	THR	VAL	VAL	ARG	LEU	ALA
ARG	THR	THR	THR	THR	VAL	ARG	GLU	ILE	VAL
LEU	HIS	ALA	GLY	GLY	ASN	GLN	LYS	PHE	VAL
ILE	ALA	ALA	ILE	ALA	ARG	GLN	LYS	PHE	PHE
TYR	ILE	ASP	ILE	ASP	PRO	ALA	LEU	MET	GLN
PRO	GLY	LEU	ILE	LEU	ASP	LYS	GLY	ARG	SER
GLU	GLY	ALA	GLY	ALA	VAL	LYS	LYS	GLN	PHE
HIS	GLU	ASN	ARG	ASN	LEU	ALA	LYS	MET	GLY
VAL	VAL	LEU	LEU	LEU	ASP	ALA	ILE	GLN	PRO
VAL	VAL	VAL	VAL	VAL	PRO	PRO	ILE	GLY	SER
SER	PRO	ASN	GLU	ALA	ALA	LYS	GLY	GLY	GLU
THR	THR	GLU	HIS	GLU	LEU	ILE	VAL	LYS	ASN
ALA	ALA	ALA	ASP	ALA	ARG	PHE	LEU	GLY	GLY
GLY	ASP	LEU	PRO	LEU	PRO	ILE	MET	GLY	R30
SER	VAL	PHE	VAL	PHE	GLY	ASP	VAL	ALA	
ASN	ASP	ALA	HIS	ALA	ARG	GLU	GLY	MET	D33
ILE	LYS	ALA	LYS	ALA	PHE	ILE	PRO	SER	
VAL	VAL	ARG	VAL	ARG	ASP	ASP	PRO	PHE	L38
ALA	GLY	GLY	THR	GLY	ARG	ALA	GLY	GLY	
ALA	ILE	ASN	ILE	ASN	GLN	VAL	THR	LYS	V41
THR	THR	LYS	ILE	LYS	VAL	GLY	GLY	SER	
ASN	ASN	ARG	PRO	ARG	VAL	ARG	LYS	LYS	V46
LEU	LEU	VAL	ARG	VAL	VAL	GLN	THR	ALA	R47
ALA	ALA	VAL	GLY	VAL	GLY	LEU	LEU	MET	E48
ARG	ARG	SER	ALA	SER	LEU	GLY	LEU	ARG	A49
ASN	ASN	MET	ALA	MET	PRO	ALA	ALA	LEU	R50
MET	MET	VAL	VAL	VAL	ASP	GLY	LYS	THR	
THR	THR	GLU	VAL	ASP	ARG	GLY	ILE	ASP	T59
GLN	GLN	GLU	THR	GLU	GLY	GLY	ALA	GLN	K60
TRP	TRP	PHE	PHE	LYS	ARG	GLY	GLY	ILE	
GLY	PHE	PHE	PHE	ALA	GLU	HIS	GLU	LYS	Q73
THR	THR	LEU	LEU	LYS	GLN	ASP	ALA	THR	
SER	GLU	ASP	PRO	ASP	ILE	GLU	LYS	THR	V89
GLU	SER	LYS	GLU	LYS	LEU	GLU	VAL	PHE	G90
LYS	LYS	ILE	GLY	ILE	LYS	GLN	PRO	ALA	E91
LEU	LEU	MET	ASP	MET	VAL	GLN	PHE	ASP	P92
GLY	GLY	ALA	ALA	MET	VAL	THR	VAL	VAL	PRO
PRO	PRO	ILE	GLY	MET	HIS	THR	GLY	GLY	GLU
LEU	LEU	GLY	SER	ALA	ARG	LEU	ILE	ALA	GLU
THR	THR	ALA	ALA	GLU	ARG	GLN	GLY	CYS	PRO
ALA	ALA	ARG	SER	ARG	VAL	MET	GLY	ASP	SER
			ARG	ARG	PRO	LEU	SER	GLU	LEU

- Molecule 1: ATP-dependent zinc metalloprotease FtsH



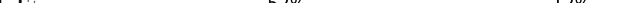
- Molecule 1: ATP-dependent zinc metalloprotease FtsH





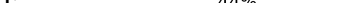
GLN	LYS	GLU
LEU	TYR	GLU
GLY	GLU	GLY
ASP	THR	GLU
LYS	ILE	VAL
	ASP	PHE
	ALA	LEU
	PRO	GLY
	GLN	ARG
	ILE	SER
	ASP	VAL
	ASP	ALA
	LEU	LYS
	MET	ALA
	ALA	LYS
	ARG	GLU
	ARG	THR
	ASP	THR
	VAL	THR
	ASP	GLU
	GLY	GLY
	TRP	VAL
	GLU	LYS
	GLU	ALA
	PRO	LEU
	GLY	GLU
	ALA	ARG
	SER	ASN
	ASN	ASN
	SER	ILE
	GLY	GLU
	ASP	ARG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

- Molecule 2: Protein HflK

Chain E:  52% 12% 36%

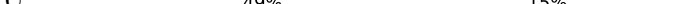
[illegible]

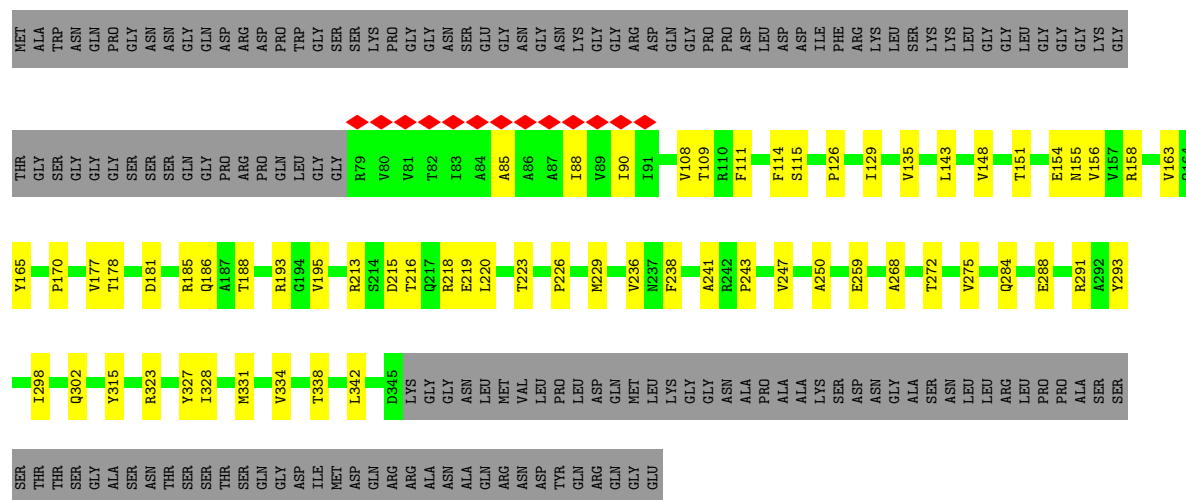
- Molecule 2: Protein HflK

Chain F:  44% 20% 36%

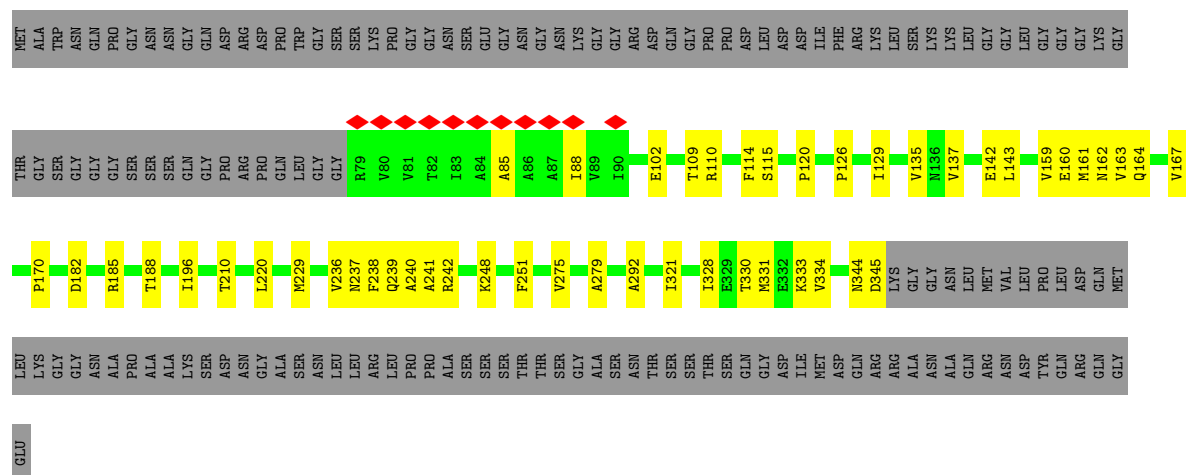
[illegible]

- Molecule 2: Protein HflK

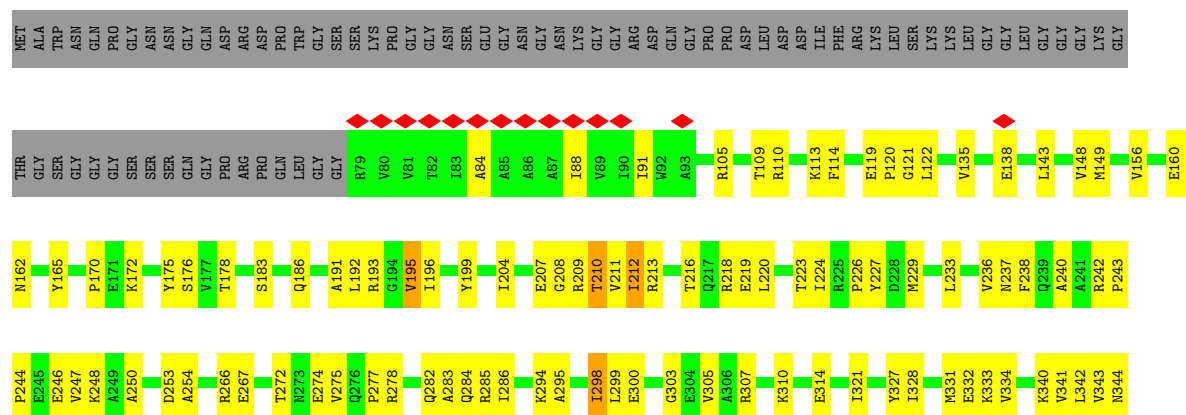
Chain U: 



• Molecule 2: Protein HflK



• Molecule 2: Protein HflK



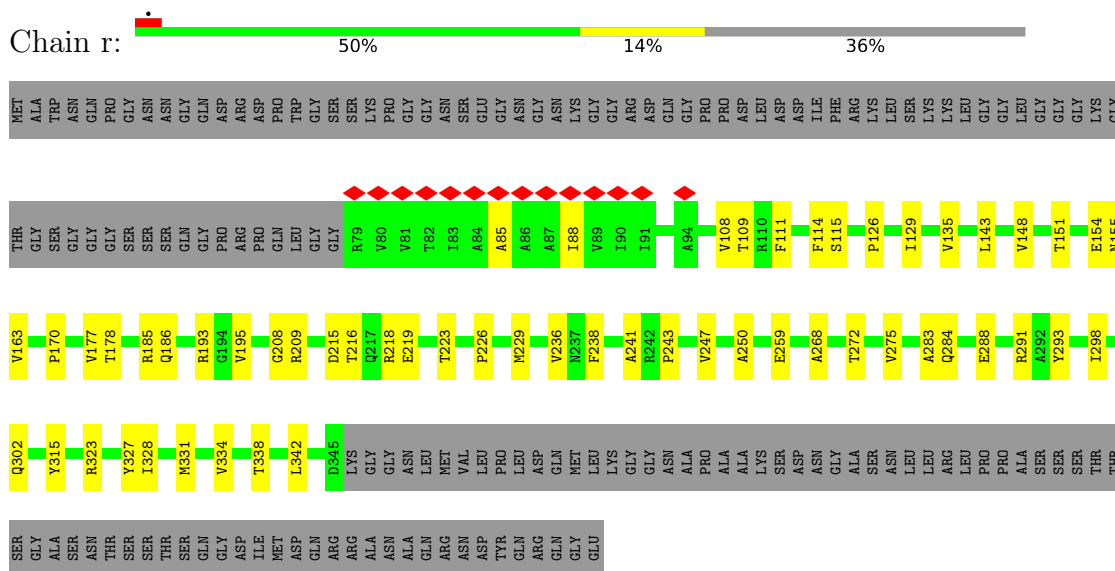
- Molecule 2: Protein HflK

- Molecule 2: Protein HflK

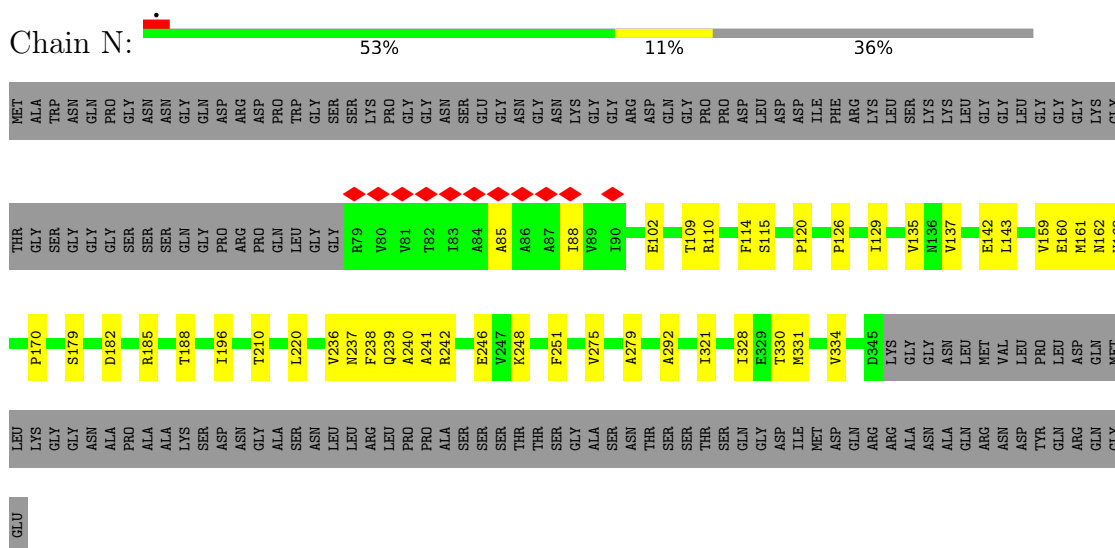
- Molecule 2: Protein HflK

THR	GLY	SER	GLY	GLY	GLY	SER	SER	SER	GLN	GLY	PRO	ARG	PRO	GLN	LEU	GLY	GLY
R79	V80	V81	T82	I83	A84	A85	A86	A87	I88	V89	I90	A93	A94	A103	E104	R105	T109
														K113	F114	E119	P120
														G121	L122	V135	E138
														L143	V148	M149	V156

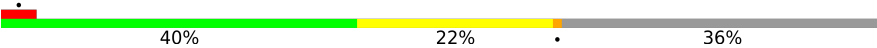
- Molecule 2: Protein HflK

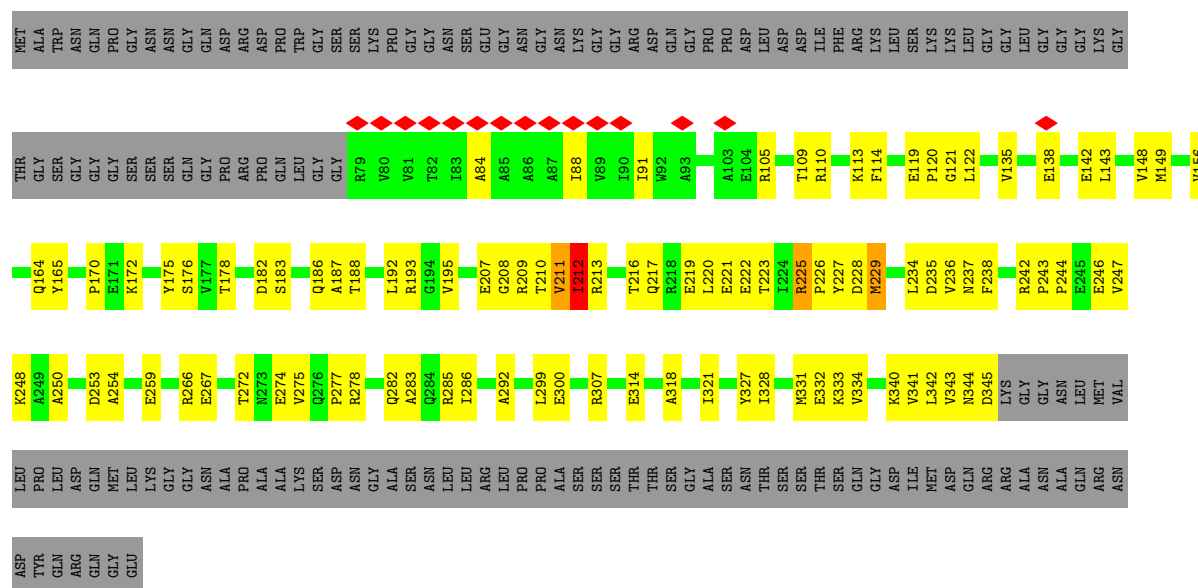


- Molecule 2: Protein HflK



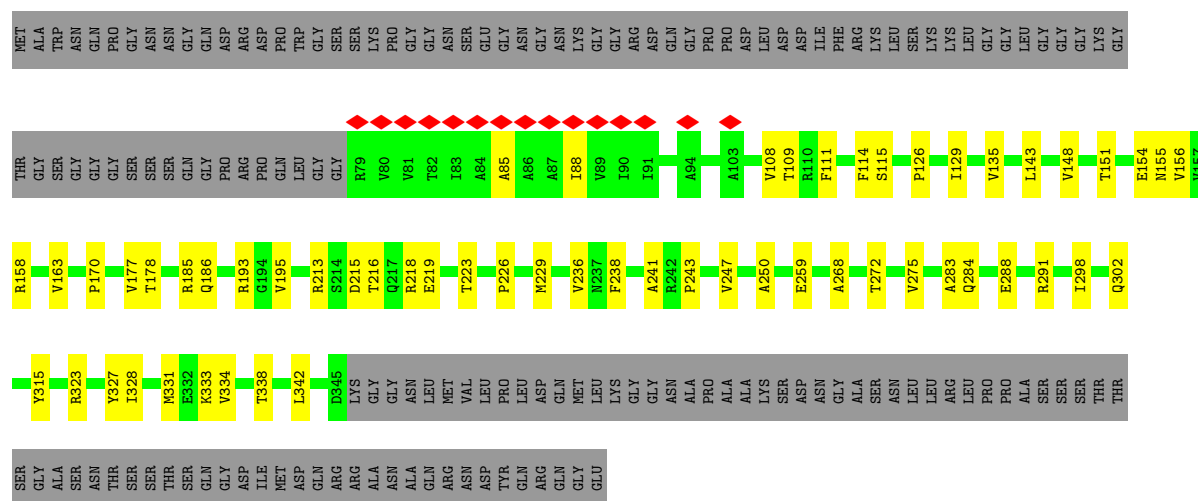
- Molecule 2: Protein HflK

Chain O: 



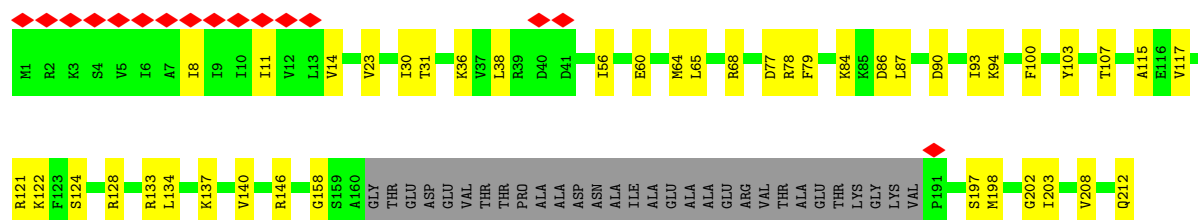
• Molecule 2: Protein HflK

Chain S: 



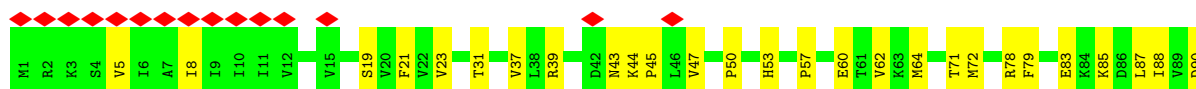
• Molecule 3: Modulator of FtsH protease HflC

Chain G: 

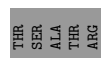
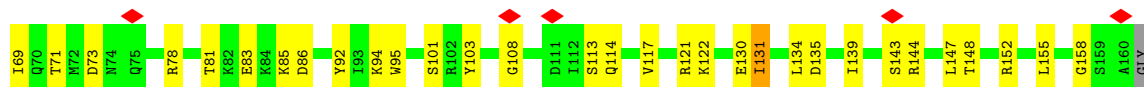
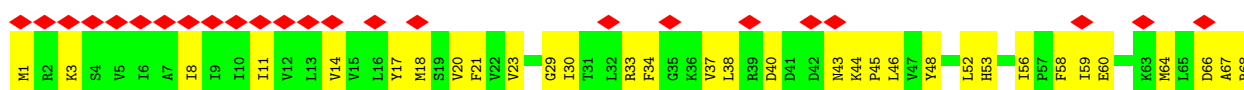




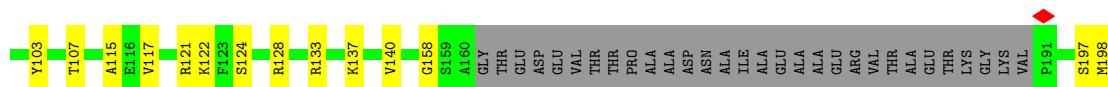
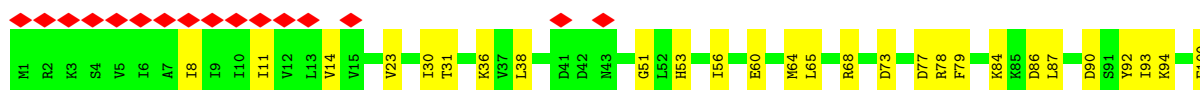
• Molecule 3: Modulator of FtsH protease HflC



• Molecule 3: Modulator of FtsH protease HflC

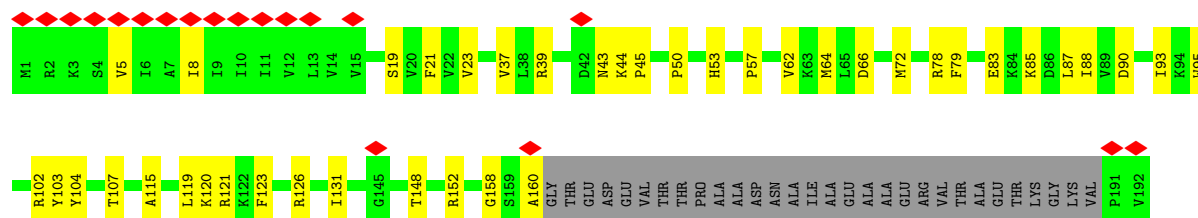


• Molecule 3: Modulator of FtsH protease HflC

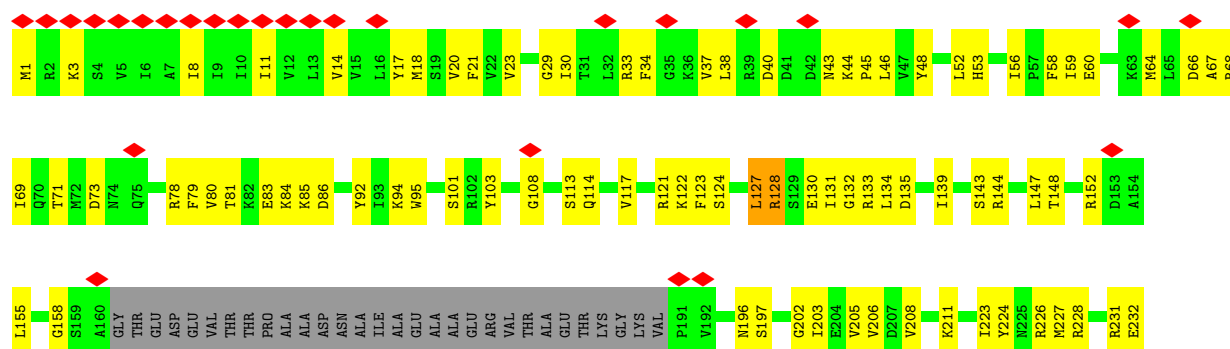




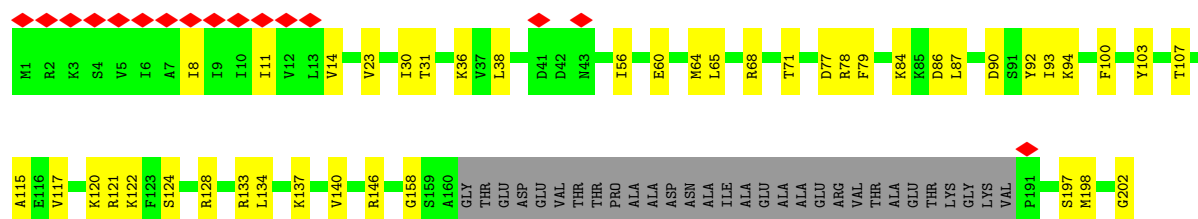
• Molecule 3: Modulator of FtsH protease HflC



• Molecule 3: Modulator of FtsH protease HflC

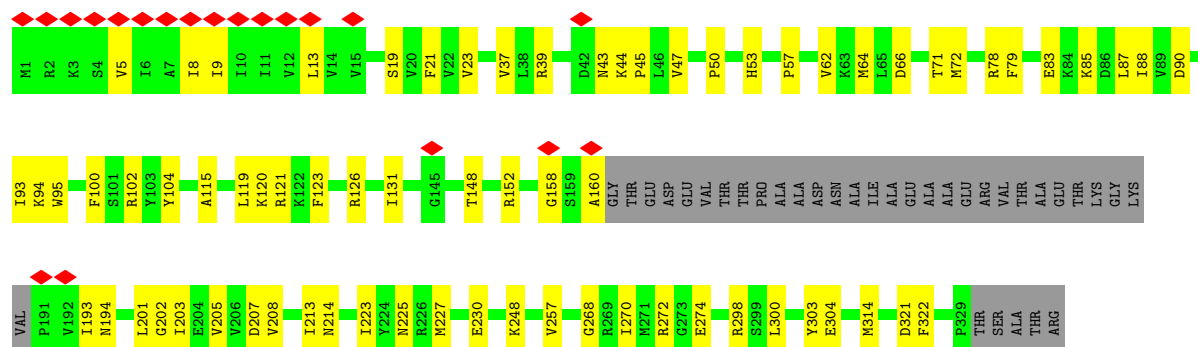


• Molecule 3: Modulator of FtsH protease HflC

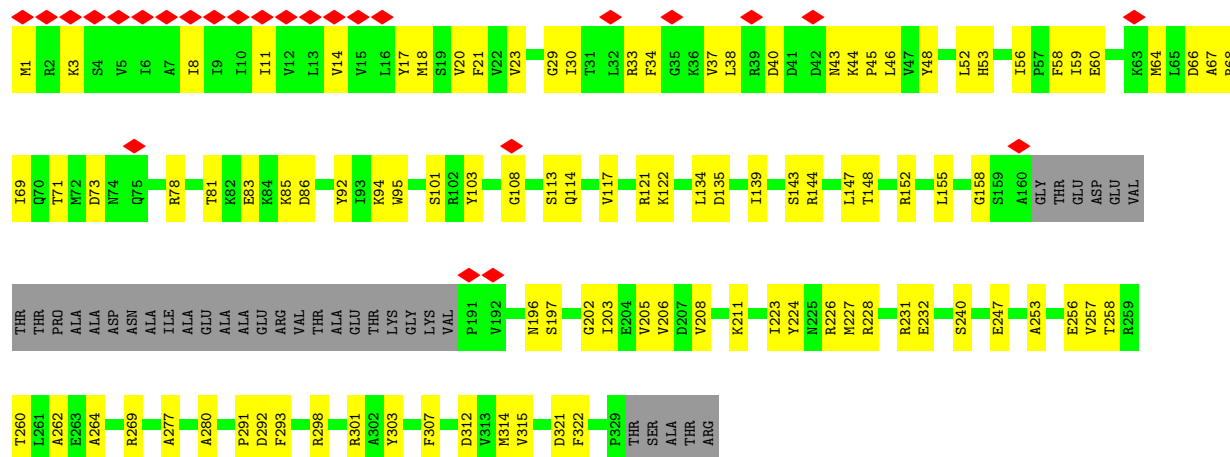


Chain n:





• Molecule 3: Modulator of FtsH protease HflC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84693	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0146	Depositor
Map size ($\text{\AA}$)	422.80002, 422.80002, 422.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.057, 1.057, 1.057	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	0.17	0/522	0.50	0/706
1	B	0.14	0/522	0.37	0/706
1	C	0.18	0/522	0.52	0/706
1	D	0.17	0/522	0.45	0/706
1	J	0.17	0/522	0.50	0/706
1	K	0.14	0/522	0.37	0/706
1	L	0.19	0/522	0.52	0/706
1	M	0.17	0/522	0.45	0/706
1	T	0.18	0/522	0.54	0/706
1	V	0.14	0/522	0.29	0/706
1	W	0.17	0/522	0.50	0/706
1	X	0.17	0/522	0.50	0/706
1	Y	0.14	0/522	0.37	0/706
1	Z	0.14	0/522	0.37	0/706
1	a	0.19	0/522	0.52	0/706
1	b	0.19	0/522	0.52	0/706
1	c	0.17	0/522	0.45	0/706
1	d	0.17	0/522	0.45	0/706
1	e	0.18	0/522	0.54	0/706
1	f	0.14	0/522	0.29	0/706
1	s	0.18	0/522	0.54	0/706
1	t	0.18	0/522	0.54	0/706
1	u	0.14	0/522	0.29	0/706
1	v	0.14	0/522	0.29	0/706
2	E	0.15	0/2154	0.33	0/2921
2	F	0.23	0/2154	0.38	0/2921
2	N	0.15	0/2154	0.33	0/2921
2	O	0.18	0/2154	0.43	1/2921 (0.0%)
2	S	0.15	0/2154	0.34	0/2921
2	U	0.15	0/2154	0.34	0/2921
2	g	0.15	0/2154	0.33	0/2921
2	h	0.15	0/2154	0.33	0/2921
2	i	0.21	0/2154	0.48	1/2921 (0.0%)
2	j	0.21	0/2154	0.51	0/2921

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	q	0.15	0/2154	0.34	0/2921
2	r	0.15	0/2154	0.34	0/2921
3	G	0.15	0/2432	0.32	0/3268
3	H	0.14	0/2432	0.33	0/3268
3	I	0.20	0/2432	0.42	1/3268 (0.0%)
3	P	0.16	0/2432	0.33	0/3268
3	Q	0.14	0/2432	0.33	0/3268
3	R	0.15	0/2432	0.36	0/3268
3	k	0.16	0/2432	0.35	0/3268
3	l	0.15	0/2432	0.33	0/3268
3	m	0.14	0/2432	0.33	0/3268
3	n	0.14	0/2432	0.33	0/3268
3	o	0.19	0/2432	0.46	1/3268 (0.0%)
3	p	0.18	0/2432	0.46	1/3268 (0.0%)
All	All	0.16	0/67560	0.39	5/91212 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	212	ILE	N-CA-C	7.12	117.22	110.53
3	p	112	ILE	N-CA-C	6.88	117.64	110.62
3	o	264	ALA	N-CA-C	-5.54	98.99	110.80
2	i	224	ILE	N-CA-C	5.43	116.21	110.72
3	I	131	ILE	N-CA-C	5.09	115.86	110.72

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	516	0	525	19	0
1	B	516	0	525	17	0
1	C	516	0	525	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	516	0	525	18	0
1	J	516	0	525	19	0
1	K	516	0	525	16	0
1	L	516	0	525	24	0
1	M	516	0	525	17	0
1	T	516	0	525	15	0
1	V	516	0	525	9	0
1	W	516	0	525	18	0
1	X	516	0	525	20	0
1	Y	516	0	525	18	0
1	Z	516	0	525	16	0
1	a	516	0	525	24	0
1	b	516	0	525	25	0
1	c	516	0	525	18	0
1	d	516	0	525	17	0
1	e	516	0	525	13	0
1	f	516	0	525	8	0
1	s	516	0	525	12	0
1	t	516	0	525	15	0
1	u	516	0	525	9	0
1	v	516	0	525	9	0
2	E	2121	0	2129	42	0
2	F	2121	0	2127	118	0
2	N	2121	0	2129	37	0
2	O	2121	0	2126	201	0
2	S	2121	0	2129	44	0
2	U	2121	0	2129	53	0
2	g	2121	0	2129	38	0
2	h	2121	0	2129	37	0
2	i	2121	0	2127	216	0
2	j	2121	0	2128	187	0
2	q	2121	0	2129	75	0
2	r	2121	0	2129	72	0
3	G	2397	0	2431	84	0
3	H	2397	0	2431	51	0
3	I	2397	0	2431	188	0
3	P	2397	0	2431	93	0
3	Q	2397	0	2431	48	0
3	R	2397	0	2429	112	0
3	k	2397	0	2431	112	0
3	l	2397	0	2431	74	0
3	m	2397	0	2431	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	n	2397	0	2431	44	0
3	o	2397	0	2431	177	0
3	p	2397	0	2428	229	0
All	All	66600	0	67307	2103	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 16.

All (2103) 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)
3:G:328:THR:HG22	2:q:327:TYR:CE2	1.20	1.67
2:i:149:MET:HE3	2:i:196:ILE:CD1	1.25	1.60
2:j:161:MET:HE3	2:j:212:ILE:CG2	1.29	1.57
2:i:149:MET:CE	2:i:196:ILE:CD1	1.87	1.50
2:F:310:LYS:NZ	3:o:274:GLU:CG	1.72	1.50
2:i:216:THR:CG2	2:i:236:VAL:HG11	1.38	1.50
3:k:324:ARG:HH22	3:m:328:THR:CB	1.25	1.48
3:p:272:ARG:HG3	2:r:293:TYR:CD1	1.48	1.48
3:k:324:ARG:HH22	3:m:328:THR:CG2	1.28	1.47
2:F:234:LEU:HD22	3:o:121:ARG:NH1	1.20	1.47
3:I:121:ARG:HH12	2:O:234:LEU:CD2	1.27	1.46
2:j:234:LEU:HD22	3:R:121:ARG:NH1	1.20	1.45
3:I:121:ARG:NH1	2:O:234:LEU:HD22	1.22	1.44
2:j:161:MET:CE	2:j:212:ILE:HG21	1.46	1.43
2:i:191:ALA:HB1	2:i:219:GLU:CG	1.48	1.41
2:i:149:MET:CE	2:i:196:ILE:HD11	1.45	1.40
2:O:217:GLN:OE1	2:O:236:VAL:CG1	1.69	1.40
3:G:328:THR:CG2	2:q:327:TYR:CE2	2.04	1.40
3:o:271:MET:SD	2:q:290:ALA:C	2.05	1.39
2:i:310:LYS:NZ	3:p:274:GLU:HG2	1.15	1.39
2:O:208:GLY:CA	2:O:212:ILE:HG12	1.54	1.38
3:G:328:THR:CG2	2:q:327:TYR:HE2	1.35	1.37
3:p:272:ARG:CG	2:r:293:TYR:CD1	2.06	1.37
3:o:271:MET:SD	2:q:291:ARG:N	1.97	1.36
3:p:119:LEU:HD13	3:p:198:MET:CE	1.56	1.36
2:O:208:GLY:HA2	2:O:212:ILE:CG1	1.55	1.34
3:I:108:GLY:HA3	2:O:138:GLU:OE1	1.18	1.34
2:i:138:GLU:OE2	3:p:114:GLN:NE2	1.60	1.33
3:I:108:GLY:CA	2:O:138:GLU:OE1	1.76	1.32
3:I:114:GLN:CG	2:O:138:GLU:OE2	1.76	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:310:LYS:NZ	3:o:274:GLU:HG3	1.35	1.31
2:j:234:LEU:CD2	3:R:121:ARG:HH12	1.44	1.31
2:i:138:GLU:OE2	3:p:114:GLN:CD	1.74	1.30
2:i:310:LYS:NZ	3:p:274:GLU:CG	1.94	1.30
3:k:324:ARG:CZ	3:m:328:THR:HG21	1.62	1.30
2:F:234:LEU:CD2	3:o:121:ARG:HH12	1.44	1.29
2:O:217:GLN:CD	2:O:236:VAL:HG12	1.56	1.29
2:i:314:GLU:CD	3:p:277:ALA:O	1.76	1.28
3:k:324:ARG:NH2	3:m:328:THR:CB	1.94	1.27
3:I:296:PHE:HA	3:P:325:TYR:CD1	1.67	1.27
3:k:326:MET:O	2:r:327:TYR:HE1	1.14	1.26
3:I:114:GLN:HG2	2:O:138:GLU:OE2	1.12	1.26
3:k:324:ARG:NH2	3:m:328:THR:HG21	1.49	1.25
3:p:272:ARG:CG	2:r:293:TYR:CE1	2.18	1.25
2:i:138:GLU:OE1	3:p:108:GLY:HA3	1.32	1.25
2:U:327:TYR:HE1	3:P:326:MET:O	1.20	1.25
3:k:324:ARG:NH1	3:m:328:THR:HG21	1.50	1.25
3:p:265:GLU:O	3:p:269:ARG:HG3	1.34	1.25
2:j:296:GLN:O	2:j:300:GLU:HG2	1.11	1.25
3:I:296:PHE:HA	3:P:325:TYR:CE1	1.71	1.25
2:j:138:GLU:OE1	3:R:108:GLY:HA3	1.32	1.25
2:i:138:GLU:CD	3:p:108:GLY:HA3	1.62	1.24
3:o:271:MET:CE	2:q:291:ARG:HB2	1.67	1.23
2:F:138:GLU:OE1	3:o:108:GLY:HA3	1.32	1.21
2:i:294:LYS:O	2:i:298:ILE:HG13	1.35	1.21
3:I:108:GLY:HA3	2:O:138:GLU:CD	1.65	1.21
2:O:207:GLU:O	2:O:211:VAL:CG2	1.89	1.20
2:j:191:ALA:CB	2:j:220:LEU:HD13	1.68	1.20
2:i:314:GLU:OE2	3:p:277:ALA:O	1.53	1.19
2:j:296:GLN:O	2:j:300:GLU:CG	1.89	1.19
2:F:310:LYS:HZ3	3:o:274:GLU:CG	1.37	1.19
2:F:310:LYS:HZ1	3:o:274:GLU:CG	1.45	1.18
2:j:221:GLU:OE2	2:j:233:LEU:HB3	1.43	1.18
2:O:213:ARG:HD2	2:O:236:VAL:O	1.42	1.18
2:i:149:MET:CE	2:i:196:ILE:HD13	1.62	1.18
2:O:213:ARG:HD2	2:O:236:VAL:C	1.67	1.17
2:O:213:ARG:CD	2:O:236:VAL:O	1.91	1.17
2:i:310:LYS:HZ2	3:p:274:GLU:CG	1.52	1.17
3:G:326:MET:HE1	3:o:303:TYR:CD2	1.80	1.16
3:p:272:ARG:HG2	2:r:293:TYR:CE1	1.81	1.16
2:i:328:ILE:HG21	3:p:298:ARG:HG3	1.21	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:138:GLU:OE2	3:o:114:GLN:HG2	1.46	1.15
2:i:220:LEU:HD23	2:i:233:LEU:HD21	1.29	1.15
2:j:138:GLU:OE2	3:R:114:GLN:CG	1.95	1.15
2:i:216:THR:HG21	2:i:236:VAL:CG1	1.77	1.14
2:i:138:GLU:OE1	3:p:108:GLY:CA	1.94	1.14
3:o:271:MET:SD	2:q:291:ARG:CA	2.34	1.14
3:I:296:PHE:CA	3:P:325:TYR:CE1	2.30	1.14
3:I:321:ASP:OD2	3:P:328:THR:HG22	1.48	1.14
2:i:208:GLY:O	2:i:212:ILE:HG22	1.48	1.14
2:F:138:GLU:OE2	3:o:114:GLN:CG	1.95	1.13
3:I:34:PHE:HB3	2:O:122:LEU:H	1.11	1.13
3:p:72:MET:HG3	3:p:120:LYS:HE2	1.29	1.13
2:i:191:ALA:HB1	2:i:219:GLU:HG3	1.20	1.12
3:p:119:LEU:CD1	3:p:198:MET:HE1	1.77	1.12
2:i:220:LEU:HD23	2:i:233:LEU:CD2	1.79	1.11
3:p:272:ARG:CD	2:r:293:TYR:CD1	2.33	1.11
2:O:207:GLU:HG3	2:O:211:VAL:HG21	1.19	1.11
2:j:187:ALA:O	2:j:220:LEU:HD11	1.51	1.11
2:O:188:THR:OG1	2:O:220:LEU:HD21	1.49	1.11
2:j:138:GLU:OE2	3:R:114:GLN:HG2	1.46	1.10
2:O:213:ARG:NE	2:O:236:VAL:O	1.82	1.10
2:j:213:ARG:HD3	2:j:236:VAL:O	1.50	1.10
2:j:295:ALA:O	2:j:299:LEU:HG	1.52	1.09
3:I:298:ARG:HG3	2:O:328:ILE:HG21	1.14	1.09
2:O:217:GLN:OE1	2:O:236:VAL:HG12	0.93	1.09
2:i:138:GLU:OE2	3:p:114:GLN:CG	2.01	1.09
2:j:307:ARG:HD2	3:R:269:ARG:HG2	1.27	1.09
3:I:321:ASP:CG	3:P:328:THR:HG22	1.77	1.09
2:i:149:MET:HE2	2:i:196:ILE:HD13	1.12	1.09
3:o:271:MET:HE1	2:q:291:ARG:HB2	1.22	1.08
2:i:295:ALA:HA	2:i:298:ILE:HD12	1.36	1.08
2:O:213:ARG:HD2	2:O:237:ASN:CA	1.84	1.08
2:F:234:LEU:CD2	3:o:121:ARG:NH1	2.11	1.08
2:j:234:LEU:CD2	3:R:121:ARG:NH1	2.11	1.08
3:k:324:ARG:NH2	3:m:328:THR:OG1	1.87	1.07
3:o:271:MET:SD	2:q:291:ARG:HA	1.92	1.07
2:O:213:ARG:CD	2:O:237:ASN:HA	1.84	1.07
3:k:326:MET:O	2:r:327:TYR:CE1	2.06	1.07
3:k:328:THR:HB	2:r:327:TYR:CE2	1.90	1.07
2:F:321:ILE:HD11	3:o:291:PRO:HB3	1.36	1.07
2:j:321:ILE:HD11	3:R:291:PRO:HB3	1.36	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:191:ALA:HB1	2:i:219:GLU:HG2	1.37	1.07
3:I:38:LEU:HD22	2:O:119:GLU:OE1	1.55	1.06
2:U:327:TYR:CE1	3:P:326:MET:O	2.08	1.06
3:I:121:ARG:HH11	2:O:234:LEU:HB3	1.18	1.06
3:p:79:PHE:CE2	3:p:128:ARG:HB3	1.90	1.06
3:k:324:ARG:NH2	3:m:328:THR:CG2	2.01	1.06
3:o:271:MET:CE	2:q:291:ARG:CB	2.32	1.06
3:p:72:MET:HE2	3:p:120:LYS:CG	1.83	1.06
3:I:38:LEU:CD2	2:O:119:GLU:OE1	2.04	1.05
2:i:161:MET:HE3	2:i:212:ILE:HD11	1.10	1.05
2:j:191:ALA:HB3	2:j:220:LEU:HD13	1.09	1.04
3:k:323:PHE:HA	3:p:303:TYR:OH	1.58	1.04
2:F:310:LYS:NZ	3:o:274:GLU:HG2	1.65	1.03
2:F:310:LYS:HZ1	3:o:274:GLU:CD	1.65	1.03
2:j:209:ARG:HB2	2:j:238:PHE:CD2	1.91	1.03
2:j:221:GLU:OE2	2:j:233:LEU:CB	2.05	1.03
2:F:138:GLU:OE2	3:o:114:GLN:CD	2.02	1.03
3:o:271:MET:CE	2:q:291:ARG:CA	2.36	1.03
2:O:207:GLU:O	2:O:211:VAL:HG22	1.51	1.02
2:F:138:GLU:OE1	3:o:108:GLY:CA	2.08	1.02
2:j:138:GLU:OE2	3:R:114:GLN:CD	2.02	1.02
3:p:79:PHE:HE2	3:p:128:ARG:HB3	1.18	1.02
2:i:331:MET:CB	3:k:322:PHE:HE1	1.73	1.01
3:G:326:MET:HE1	3:o:303:TYR:CE2	1.94	1.01
3:I:114:GLN:CD	2:O:138:GLU:OE2	2.04	1.01
2:i:331:MET:HB2	3:k:322:PHE:HE1	1.20	1.01
2:i:216:THR:CG2	2:i:236:VAL:CG1	2.34	1.00
2:j:223:THR:CG2	3:l:209:ARG:HE	1.72	1.00
2:j:138:GLU:OE1	3:R:108:GLY:CA	2.08	1.00
2:i:138:GLU:OE2	3:p:114:GLN:HG2	1.61	1.00
3:I:303:TYR:OH	3:P:323:PHE:HA	1.62	1.00
3:p:264:ALA:C	3:p:267:GLN:OE1	2.03	1.00
2:F:328:ILE:HG21	3:o:298:ARG:HG3	1.44	0.99
2:i:216:THR:HG21	2:i:236:VAL:HG11	1.02	0.99
3:G:326:MET:O	2:q:327:TYR:CE1	2.14	0.99
2:O:195:VAL:HG11	2:O:216:THR:OG1	1.59	0.99
2:F:308:PHE:HE1	3:G:286:ALA:O	1.44	0.99
3:k:328:THR:HG22	3:p:321:ASP:CG	1.88	0.99
2:j:328:ILE:HG21	3:R:298:ARG:HG3	1.44	0.99
2:i:294:LYS:HG2	2:i:298:ILE:HD11	1.43	0.98
3:k:328:THR:HG22	3:p:321:ASP:OD2	1.64	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:204:ILE:O	2:j:208:GLY:HA3	1.62	0.98
2:F:209:ARG:HD3	3:o:80:VAL:HG23	1.45	0.98
3:I:121:ARG:NH1	2:O:234:LEU:CD2	1.99	0.98
2:j:188:THR:HA	2:j:220:LEU:HD21	1.45	0.98
2:i:314:GLU:OE1	3:p:277:ALA:C	2.05	0.98
3:p:72:MET:HE2	3:p:120:LYS:HG3	1.46	0.97
2:i:191:ALA:CB	2:i:219:GLU:CG	2.40	0.97
2:F:119:GLU:OE1	3:o:38:LEU:HD22	1.65	0.97
3:H:321:ASP:CG	3:I:328:THR:HG22	1.90	0.97
2:j:119:GLU:OE1	3:R:38:LEU:HD22	1.65	0.97
2:i:149:MET:HB3	2:i:196:ILE:CD1	1.94	0.97
2:i:161:MET:HE1	2:i:216:THR:OG1	1.64	0.97
2:j:161:MET:CE	2:j:212:ILE:CG2	2.18	0.97
2:O:217:GLN:OE1	2:O:236:VAL:N	1.98	0.96
2:F:138:GLU:CD	3:o:108:GLY:HA3	1.91	0.96
3:o:271:MET:HE1	2:q:291:ARG:CB	1.91	0.96
3:I:303:TYR:OH	3:P:322:PHE:O	1.85	0.95
3:p:272:ARG:HG3	2:r:293:TYR:CE1	1.90	0.95
2:j:191:ALA:CB	2:j:220:LEU:CD1	2.45	0.95
2:F:304:GLU:OE2	3:G:283:PHE:CE1	2.20	0.94
3:G:326:MET:O	2:q:327:TYR:HE1	1.48	0.94
2:i:294:LYS:O	2:i:298:ILE:CG1	2.14	0.94
2:i:285:ARG:HD2	3:p:247:GLU:OE2	1.65	0.94
2:i:149:MET:CB	2:i:196:ILE:HD12	1.98	0.94
3:G:328:THR:HG22	2:q:327:TYR:CD2	2.03	0.94
3:k:324:ARG:HH12	3:m:328:THR:CG2	1.78	0.94
2:O:213:ARG:HD2	2:O:237:ASN:N	1.82	0.94
2:i:161:MET:CE	2:i:216:THR:OG1	2.16	0.94
3:k:324:ARG:HH12	3:m:328:THR:HG21	1.16	0.94
2:j:138:GLU:CD	3:R:108:GLY:HA3	1.91	0.94
3:I:263:GLU:HA	2:O:299:LEU:HD13	1.49	0.93
2:j:161:MET:HE3	2:j:212:ILE:HG22	1.47	0.93
2:i:161:MET:HE3	2:i:212:ILE:CD1	1.97	0.93
3:G:326:MET:CE	3:o:303:TYR:CE2	2.52	0.93
3:I:121:ARG:NH1	2:O:234:LEU:HB3	1.83	0.93
2:O:213:ARG:HD2	2:O:237:ASN:HA	1.44	0.92
2:i:310:LYS:HZ3	3:p:274:GLU:CG	1.69	0.92
3:k:322:PHE:O	3:p:303:TYR:OH	1.85	0.92
2:i:191:ALA:CB	2:i:219:GLU:HG3	1.99	0.92
3:p:119:LEU:HD13	3:p:198:MET:HE1	0.94	0.92
3:I:296:PHE:CA	3:P:325:TYR:HE1	1.81	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:227:TYR:OH	3:P:207:ASP:CG	2.13	0.92
2:F:199:TYR:HD2	2:F:212:ILE:HD11	1.32	0.92
3:I:34:PHE:O	2:O:121:GLY:HA3	1.69	0.92
3:k:322:PHE:CD2	3:p:303:TYR:HE1	1.88	0.92
2:i:209:ARG:HH22	3:p:78:ARG:CG	1.83	0.91
3:p:95:TRP:HZ2	3:p:116:GLU:OE2	1.52	0.91
3:I:121:ARG:CZ	2:O:234:LEU:HD22	1.99	0.91
2:O:188:THR:HA	2:O:220:LEU:CD1	2.01	0.91
2:i:209:ARG:HH22	3:p:78:ARG:CB	1.82	0.91
2:j:188:THR:HA	2:j:220:LEU:CD2	2.01	0.91
2:j:196:ILE:HD13	2:j:212:ILE:HD11	1.52	0.91
2:i:314:GLU:OE1	3:p:277:ALA:O	1.89	0.91
2:F:119:GLU:OE1	3:o:38:LEU:CD2	2.19	0.91
3:o:271:MET:HE2	2:q:291:ARG:HB2	1.51	0.91
2:j:119:GLU:OE1	3:R:38:LEU:CD2	2.19	0.91
2:j:187:ALA:C	2:j:220:LEU:HD11	1.94	0.91
2:i:216:THR:CB	2:i:236:VAL:HG11	2.00	0.90
2:O:213:ARG:HD3	2:O:237:ASN:HA	1.53	0.90
2:i:331:MET:CB	3:k:322:PHE:CE1	2.54	0.89
3:I:296:PHE:CB	3:P:325:TYR:HE1	1.86	0.89
2:i:216:THR:HG22	2:i:236:VAL:HG11	1.52	0.89
2:i:161:MET:HE2	2:i:236:VAL:HG21	1.53	0.89
3:I:121:ARG:NH1	2:O:234:LEU:CG	2.35	0.89
2:O:207:GLU:O	2:O:211:VAL:HG23	1.70	0.89
2:i:193:ARG:NH2	3:k:210:ILE:HB	1.88	0.89
2:O:227:TYR:OH	3:P:207:ASP:OD2	1.90	0.89
3:o:271:MET:HE2	2:q:291:ARG:CB	2.04	0.88
3:I:296:PHE:HB2	3:P:325:TYR:HE1	1.36	0.88
3:p:264:ALA:CA	3:p:267:GLN:CD	2.44	0.88
2:O:207:GLU:HG3	2:O:211:VAL:CG2	2.04	0.88
2:j:296:GLN:HG2	2:j:300:GLU:OE2	1.74	0.88
3:o:123:PHE:CZ	3:o:127:LEU:HD22	2.09	0.88
3:I:287:PHE:HB2	2:O:321:ILE:HG21	1.53	0.88
3:p:119:LEU:CD1	3:p:198:MET:CE	2.44	0.88
3:I:298:ARG:HG3	2:O:328:ILE:CG2	2.04	0.87
3:k:322:PHE:CE2	3:p:303:TYR:CE1	2.62	0.87
3:k:322:PHE:CE2	3:p:303:TYR:HE1	1.91	0.87
2:i:209:ARG:HH22	3:p:78:ARG:HB3	1.38	0.87
2:O:217:GLN:HB2	2:O:236:VAL:CG1	2.05	0.87
2:F:310:LYS:HZ3	3:o:274:GLU:HG3	0.70	0.87
2:F:321:ILE:CD1	3:o:291:PRO:HB3	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:161:MET:CE	2:i:212:ILE:HD11	2.01	0.86
3:k:328:THR:CB	2:r:327:TYR:CE2	2.58	0.86
3:I:247:GLU:OE2	2:O:285:ARG:HD2	1.75	0.86
2:j:321:ILE:CD1	3:R:291:PRO:HB3	2.05	0.86
2:O:213:ARG:CD	2:O:237:ASN:CA	2.50	0.85
2:i:138:GLU:CD	3:p:108:GLY:CA	2.43	0.85
2:F:314:GLU:CD	3:o:277:ALA:O	2.19	0.85
3:o:127:LEU:HD12	3:o:127:LEU:O	1.77	0.85
2:j:312:LEU:O	2:j:312:LEU:HD12	1.77	0.85
2:i:314:GLU:CD	3:p:277:ALA:C	2.43	0.85
2:j:188:THR:CA	2:j:220:LEU:HD21	2.07	0.85
3:p:95:TRP:CZ2	3:p:116:GLU:OE2	2.30	0.85
2:O:227:TYR:HH	3:P:207:ASP:CG	1.84	0.85
2:j:191:ALA:HB2	2:j:220:LEU:CD1	2.06	0.84
2:j:314:GLU:CD	3:R:277:ALA:O	2.19	0.84
3:p:130:GLU:OE1	3:p:133:ARG:NH1	2.10	0.84
2:O:217:GLN:CG	2:O:236:VAL:HG12	2.06	0.84
3:o:123:PHE:O	3:o:127:LEU:HB3	1.77	0.84
3:o:271:MET:CE	2:q:291:ARG:N	2.41	0.84
2:j:213:ARG:HD3	2:j:236:VAL:HG13	1.60	0.83
2:j:296:GLN:CG	2:j:300:GLU:OE2	2.26	0.83
2:O:188:THR:HA	2:O:220:LEU:HD13	1.58	0.83
3:o:271:MET:SD	2:q:290:ALA:O	2.36	0.83
2:i:122:LEU:H	3:p:34:PHE:HB3	1.44	0.83
2:j:122:LEU:H	3:R:34:PHE:HB3	1.42	0.83
3:I:312:ASP:OD2	2:O:340:LYS:HE2	1.78	0.83
2:F:122:LEU:H	3:o:34:PHE:HB3	1.42	0.83
2:j:187:ALA:O	2:j:220:LEU:CD1	2.25	0.83
3:p:267:GLN:OE1	3:p:267:GLN:N	2.11	0.83
2:j:294:LYS:O	2:j:298:ILE:HG13	1.79	0.83
2:j:184:LEU:HD12	2:j:229:MET:HE1	1.59	0.82
2:j:213:ARG:HH21	2:j:213:ARG:HG3	1.41	0.82
3:I:291:PRO:HB3	2:O:321:ILE:HD11	1.59	0.82
2:i:310:LYS:HZ2	3:p:274:GLU:CD	1.86	0.82
3:p:264:ALA:HA	3:p:267:GLN:CD	1.99	0.82
2:i:314:GLU:OE2	3:p:277:ALA:C	2.23	0.82
2:i:149:MET:CB	2:i:196:ILE:CD1	2.56	0.82
2:i:285:ARG:NH1	3:p:247:GLU:OE2	2.12	0.82
3:I:272:ARG:HG2	2:U:293:TYR:CD1	2.15	0.82
2:j:213:ARG:O	2:j:213:ARG:HD2	1.79	0.82
2:F:213:ARG:NH2	2:F:235:ASP:OD1	2.12	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:310:LYS:NZ	3:o:274:GLU:CD	2.31	0.81
3:I:121:ARG:NH1	2:O:234:LEU:CB	2.42	0.81
3:I:296:PHE:CB	3:P:325:TYR:CE1	2.63	0.81
3:k:326:MET:HB2	3:p:303:TYR:CE2	2.13	0.81
2:j:314:GLU:OE1	3:R:277:ALA:O	1.98	0.81
3:p:72:MET:HG3	3:p:120:LYS:CE	2.08	0.81
3:I:121:ARG:HH12	2:O:234:LEU:CG	1.92	0.81
2:O:172:LYS:HD3	2:O:228:ASP:OD2	1.80	0.81
2:F:314:GLU:OE1	3:o:277:ALA:O	1.98	0.81
2:i:149:MET:HB3	2:i:196:ILE:HD12	1.57	0.81
3:p:127:LEU:HD13	3:p:151:VAL:HG21	1.63	0.81
3:I:277:ALA:C	2:O:314:GLU:OE1	2.02	0.81
3:G:327:LYS:HB2	3:o:321:ASP:OD2	1.81	0.81
3:I:108:GLY:CA	2:O:138:GLU:CD	2.40	0.81
2:j:213:ARG:CD	2:j:236:VAL:O	2.29	0.81
2:i:213:ARG:HD3	2:i:236:VAL:O	1.79	0.81
3:I:240:SER:OG	2:O:277:PRO:HG2	1.81	0.80
3:k:324:ARG:NH2	3:m:328:THR:HB	1.95	0.80
3:k:328:THR:HB	2:r:327:TYR:CZ	2.16	0.80
2:O:217:GLN:HE22	2:O:235:ASP:HA	1.47	0.80
2:i:340:LYS:HE2	3:p:312:ASP:OD2	1.82	0.80
3:I:296:PHE:HB2	3:P:325:TYR:CE1	2.17	0.80
3:p:72:MET:CE	3:p:120:LYS:CG	2.60	0.80
2:F:209:ARG:HD3	3:o:80:VAL:CG2	2.12	0.80
3:I:121:ARG:HH11	2:O:234:LEU:CB	1.94	0.80
2:i:331:MET:HB3	3:k:322:PHE:CE1	2.14	0.79
2:F:199:TYR:CD2	2:F:212:ILE:HD11	2.15	0.79
3:I:108:GLY:N	2:O:138:GLU:OE1	2.14	0.79
3:I:305:ASN:ND2	2:O:332:GLU:OE2	2.13	0.79
3:p:265:GLU:O	3:p:269:ARG:CG	2.26	0.79
3:k:324:ARG:NH1	3:m:328:THR:CG2	2.37	0.79
2:i:192:LEU:O	2:i:192:LEU:HD23	1.83	0.79
2:i:220:LEU:HD23	2:i:233:LEU:HD22	1.65	0.79
3:p:72:MET:CG	3:p:120:LYS:HE2	2.10	0.79
2:U:331:MET:SD	3:P:326:MET:HG3	2.22	0.79
2:i:213:ARG:CD	2:i:236:VAL:O	2.31	0.79
2:i:331:MET:HB2	3:k:322:PHE:CE1	2.12	0.79
3:p:272:ARG:HD2	2:r:293:TYR:CD1	2.16	0.78
2:j:295:ALA:O	2:j:299:LEU:CG	2.31	0.78
3:H:321:ASP:OD2	3:I:328:THR:HG22	1.81	0.78
2:i:149:MET:HB3	2:i:196:ILE:HD11	1.60	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:162:ASN:CB	2:i:237:ASN:OD1	2.32	0.78
2:i:149:MET:HE1	2:i:193:ARG:HA	1.63	0.78
3:p:272:ARG:HG3	2:r:293:TYR:HD1	0.96	0.78
3:o:143:SER:HG	2:q:193:ARG:HH22	1.32	0.78
2:i:191:ALA:CB	2:i:219:GLU:OE2	2.32	0.78
2:i:209:ARG:NH2	3:p:78:ARG:HB3	1.99	0.78
3:p:143:SER:HG	2:r:193:ARG:HH22	1.32	0.78
2:i:218:ARG:HD3	2:i:218:ARG:C	2.07	0.78
3:p:72:MET:CE	3:p:120:LYS:HG2	2.14	0.78
3:p:72:MET:HE2	3:p:120:LYS:HG2	1.67	0.77
2:O:207:GLU:CG	2:O:211:VAL:HG21	2.08	0.77
2:j:213:ARG:CD	2:j:236:VAL:HG13	2.15	0.77
2:F:310:LYS:HZ1	3:o:274:GLU:HG2	1.32	0.77
3:I:312:ASP:CG	2:O:340:LYS:HE2	2.10	0.77
3:k:316:MET:HE2	3:k:323:PHE:CE2	2.20	0.76
2:j:221:GLU:HG3	2:j:233:LEU:HD22	1.67	0.76
3:p:107:THR:HG21	3:p:115:ALA:HB2	1.66	0.76
3:p:272:ARG:HG2	2:r:293:TYR:HE1	1.45	0.76
2:j:314:GLU:OE2	3:R:280:ALA:HB3	1.85	0.76
3:I:296:PHE:CA	3:P:325:TYR:CD1	2.57	0.76
2:i:209:ARG:NH2	3:p:78:ARG:CG	2.47	0.76
3:p:267:GLN:CD	3:p:267:GLN:H	1.93	0.76
2:i:277:PRO:HG2	3:p:240:SER:OG	1.86	0.76
3:k:322:PHE:HE2	3:p:303:TYR:CE1	2.01	0.76
2:O:188:THR:N	2:O:220:LEU:HD11	2.01	0.76
2:j:311:LEU:HD21	3:l:293:PHE:CZ	2.21	0.76
2:i:321:ILE:HG21	3:p:287:PHE:HB2	1.69	0.75
2:O:227:TYR:OH	3:P:207:ASP:CB	2.34	0.75
3:I:263:GLU:CA	2:O:299:LEU:HD13	2.15	0.75
2:j:311:LEU:HD21	3:l:293:PHE:CE1	2.22	0.75
2:i:119:GLU:OE1	3:p:38:LEU:CD2	2.35	0.74
3:k:328:THR:CA	2:r:327:TYR:CZ	2.70	0.74
2:j:311:LEU:CD2	3:l:293:PHE:CE1	2.69	0.74
2:i:191:ALA:HB2	2:i:219:GLU:OE2	1.86	0.74
3:k:316:MET:HE2	3:k:323:PHE:HE2	1.51	0.74
2:F:314:GLU:OE2	3:o:280:ALA:HB3	1.86	0.74
3:H:23:VAL:HG23	3:H:50:PRO:HA	1.69	0.74
3:p:119:LEU:HD13	3:p:198:MET:HE3	1.63	0.74
1:c:54:ARG:HH12	1:c:70:ILE:HB	1.53	0.74
1:d:54:ARG:HH12	1:d:70:ILE:HB	1.53	0.74
2:F:304:GLU:OE2	3:G:283:PHE:CZ	2.41	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:54:ARG:HH12	1:M:70:ILE:HB	1.53	0.74
2:j:285:ARG:NH1	3:R:247:GLU:OE2	2.21	0.74
3:k:323:PHE:HA	3:p:303:TYR:CZ	2.23	0.73
1:D:54:ARG:HH12	1:D:70:ILE:HB	1.53	0.73
3:I:321:ASP:HB2	3:P:328:THR:CG2	2.18	0.73
3:p:79:PHE:CE2	3:p:128:ARG:CB	2.70	0.73
2:F:314:GLU:OE2	3:o:277:ALA:O	2.06	0.73
3:I:281:LYS:HB2	2:O:314:GLU:HG2	1.71	0.73
2:i:162:ASN:HB3	2:i:237:ASN:OD1	1.87	0.73
2:j:205:LEU:N	2:j:205:LEU:HD23	2.01	0.73
3:n:23:VAL:HG23	3:n:50:PRO:HA	1.69	0.73
3:Q:23:VAL:HG23	3:Q:50:PRO:HA	1.69	0.73
3:R:143:SER:OG	2:S:193:ARG:NH2	2.21	0.73
3:I:108:GLY:HA3	2:O:138:GLU:CG	2.19	0.73
2:h:164:GLN:OE1	3:l:122:LYS:NZ	2.22	0.73
3:I:121:ARG:HH12	2:O:234:LEU:HD22	0.57	0.73
2:F:285:ARG:NH1	3:o:247:GLU:OE2	2.21	0.72
3:m:23:VAL:HG23	3:m:50:PRO:HA	1.69	0.72
3:p:143:SER:OG	2:r:193:ARG:NH2	2.21	0.72
3:I:143:SER:OG	2:U:193:ARG:NH2	2.21	0.72
2:i:340:LYS:HE2	3:p:312:ASP:CG	2.14	0.72
2:O:212:ILE:HD13	2:O:212:ILE:N	2.04	0.72
3:o:123:PHE:CZ	3:o:127:LEU:CD2	2.73	0.72
3:I:321:ASP:HB2	3:P:328:THR:HG21	1.71	0.72
2:g:164:GLN:OE1	3:k:122:LYS:NZ	2.22	0.72
2:j:314:GLU:OE2	3:R:277:ALA:O	2.06	0.72
2:O:217:GLN:NE2	2:O:235:ASP:HA	2.04	0.72
3:I:269:ARG:NH1	2:O:300:GLU:OE2	2.23	0.71
2:O:187:ALA:C	2:O:220:LEU:HD11	2.15	0.71
2:N:164:GLN:OE1	3:P:122:LYS:NZ	2.22	0.71
3:p:79:PHE:HE2	3:p:128:ARG:CB	1.99	0.71
2:i:119:GLU:OE1	3:p:38:LEU:HD22	1.90	0.71
1:Z:50:ARG:HB2	1:Z:57:ASN:HB2	1.73	0.71
2:j:311:LEU:HD23	2:j:311:LEU:C	2.15	0.71
2:j:234:LEU:HB3	3:R:121:ARG:HH11	1.55	0.71
2:E:164:GLN:OE1	3:G:122:LYS:NZ	2.22	0.71
2:i:138:GLU:CG	3:p:108:GLY:HA3	2.21	0.71
3:o:143:SER:OG	2:q:193:ARG:NH2	2.21	0.71
3:I:114:GLN:HG2	2:O:138:GLU:CD	2.13	0.71
2:i:216:THR:HG21	2:i:236:VAL:CB	2.20	0.71
2:j:204:ILE:O	2:j:208:GLY:CA	2.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:314:MET:HG3	2:O:342:LEU:HB2	1.73	0.70
1:K:50:ARG:HB2	1:K:57:ASN:HB2	1.73	0.70
3:l:285:ASP:OD1	3:l:286:ALA:N	2.25	0.70
2:F:234:LEU:HB3	3:o:121:ARG:HH11	1.55	0.70
1:B:50:ARG:HB2	1:B:57:ASN:HB2	1.73	0.70
3:I:280:ALA:HB3	2:O:314:GLU:OE2	1.92	0.70
2:F:308:PHE:CE1	3:G:286:ALA:O	2.36	0.70
2:i:207:GLU:O	2:i:210:THR:HG23	1.91	0.70
2:j:191:ALA:HB2	2:j:220:LEU:HD12	1.73	0.70
1:Y:50:ARG:HB2	1:Y:57:ASN:HB2	1.73	0.70
2:i:310:LYS:NZ	3:p:274:GLU:CD	2.47	0.70
2:i:314:GLU:OE1	3:p:277:ALA:HB1	1.92	0.70
2:F:298:ILE:O	2:F:302:GLN:HG2	1.90	0.70
3:P:285:ASP:OD1	3:P:286:ALA:N	2.25	0.70
2:j:223:THR:CG2	3:l:209:ARG:NE	2.52	0.69
3:k:285:ASP:OD1	3:k:286:ALA:N	2.25	0.69
3:I:287:PHE:HB2	2:O:321:ILE:CG2	2.23	0.69
3:p:116:GLU:O	3:p:120:LYS:HD2	1.91	0.69
2:E:331:MET:HE1	3:I:326:MET:HE2	1.74	0.69
2:i:216:THR:HG21	2:i:236:VAL:HG21	1.74	0.69
2:j:223:THR:HG23	3:l:209:ARG:HE	1.56	0.69
3:G:285:ASP:OD1	3:G:286:ALA:N	2.25	0.69
2:O:209:ARG:CZ	2:O:238:PHE:CD2	2.75	0.69
3:I:229:ALA:CB	2:O:266:ARG:HD2	2.22	0.69
2:j:311:LEU:CD2	3:l:293:PHE:HE1	2.05	0.69
1:e:47:ARG:O	1:e:87:LYS:HB3	1.93	0.69
1:T:47:ARG:O	1:T:87:LYS:HB3	1.93	0.69
3:I:315:VAL:CG2	2:O:343:VAL:HG12	2.24	0.69
2:i:321:ILE:HD11	3:p:291:PRO:HB3	1.75	0.68
3:k:326:MET:HB2	3:p:303:TYR:CD2	2.27	0.68
1:s:47:ARG:O	1:s:87:LYS:HB3	1.93	0.68
2:O:208:GLY:O	2:O:212:ILE:HB	1.93	0.68
2:F:109:THR:HA	2:F:114:PHE:HA	1.76	0.68
2:F:213:ARG:C	2:F:213:ARG:HD3	2.18	0.68
3:G:325:TYR:HD2	3:o:299:SER:HB3	1.59	0.68
3:o:127:LEU:HD12	3:o:127:LEU:C	2.18	0.68
2:q:135:VAL:HG11	2:q:170:PRO:HB3	1.75	0.68
3:p:121:ARG:HD2	3:p:121:ARG:O	1.94	0.68
1:t:47:ARG:O	1:t:87:LYS:HB3	1.93	0.68
2:j:223:THR:HG23	3:l:209:ARG:HH21	1.59	0.68
3:H:72:MET:HE1	3:H:120:LYS:HB2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:149:MET:HE2	2:i:192:LEU:HD22	1.75	0.68
2:j:221:GLU:OE2	2:j:233:LEU:HB2	1.93	0.68
2:F:135:VAL:HG21	2:F:170:PRO:HB3	1.76	0.68
2:r:135:VAL:HG11	2:r:170:PRO:HB3	1.75	0.68
1:f:50:ARG:NH1	1:f:91:GLU:OE2	2.27	0.68
2:i:135:VAL:HG21	2:i:170:PRO:HB3	1.76	0.68
2:j:204:ILE:HG22	2:j:205:LEU:HD23	1.75	0.68
3:I:315:VAL:HB	2:O:343:VAL:HG12	1.75	0.68
2:i:109:THR:HA	2:i:114:PHE:HA	1.76	0.68
2:j:149:MET:HE1	2:j:193:ARG:HA	1.76	0.68
2:F:310:LYS:NZ	3:o:274:GLU:OE2	2.24	0.68
2:O:217:GLN:HB2	2:O:236:VAL:HG11	1.76	0.68
3:p:156:ASN:OD1	3:p:205:VAL:HB	1.94	0.67
1:v:50:ARG:NH1	1:v:91:GLU:OE2	2.27	0.67
2:F:302:GLN:OE1	3:G:282:LEU:HD13	1.93	0.67
2:O:149:MET:HE1	2:O:193:ARG:HA	1.76	0.67
1:L:54:ARG:HH12	1:L:69:TYR:HB3	1.60	0.67
2:i:162:ASN:HB2	2:i:237:ASN:OD1	1.95	0.67
1:b:54:ARG:HH12	1:b:69:TYR:HB3	1.60	0.67
2:O:217:GLN:OE1	2:O:236:VAL:CB	2.41	0.67
3:Q:72:MET:HE1	3:Q:120:LYS:HB2	1.75	0.67
1:V:50:ARG:NH1	1:V:91:GLU:OE2	2.27	0.67
3:H:321:ASP:HB2	3:I:328:THR:CG2	2.24	0.67
2:j:135:VAL:HG21	2:j:170:PRO:HB3	1.75	0.67
3:o:271:MET:HE1	2:q:291:ARG:N	2.08	0.67
2:U:135:VAL:HG11	2:U:170:PRO:HB3	1.75	0.67
2:j:221:GLU:HG3	2:j:233:LEU:CD2	2.25	0.67
2:O:195:VAL:HG11	2:O:216:THR:HG1	1.60	0.67
2:i:300:GLU:OE2	3:p:265:GLU:HG2	1.94	0.67
1:u:50:ARG:NH1	1:u:91:GLU:OE2	2.27	0.67
2:j:209:ARG:HB2	2:j:238:PHE:CE2	2.29	0.67
1:J:46:VAL:HA	1:J:60:LYS:HA	1.77	0.67
2:S:135:VAL:HG11	2:S:170:PRO:HB3	1.75	0.67
1:A:46:VAL:HA	1:A:60:LYS:HA	1.77	0.66
2:F:277:PRO:HG2	3:o:240:SER:OG	1.95	0.66
3:G:326:MET:SD	2:q:331:MET:SD	2.93	0.66
3:I:34:PHE:HB3	2:O:122:LEU:N	1.97	0.66
3:m:72:MET:HE1	3:m:120:LYS:HB2	1.75	0.66
2:i:149:MET:CE	2:i:193:ARG:HA	2.24	0.66
2:j:109:THR:HA	2:j:114:PHE:HA	1.76	0.66
2:O:135:VAL:HG21	2:O:170:PRO:HB3	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:324:ARG:HG3	3:P:325:TYR:HD2	1.60	0.66
3:k:328:THR:HB	2:r:327:TYR:HE2	1.56	0.66
2:O:109:THR:HA	2:O:114:PHE:HA	1.76	0.66
2:F:242:ARG:HD2	2:F:248:LYS:HD2	1.78	0.66
3:k:323:PHE:CA	3:p:303:TYR:OH	2.40	0.66
3:n:72:MET:HE1	3:n:120:LYS:HB2	1.75	0.66
1:W:46:VAL:HA	1:W:60:LYS:HA	1.77	0.66
2:F:149:MET:HE1	2:F:193:ARG:HA	1.76	0.66
2:i:242:ARG:HD2	2:i:248:LYS:HD2	1.78	0.66
2:j:196:ILE:HD13	2:j:212:ILE:CD1	2.26	0.66
3:p:264:ALA:O	3:p:267:GLN:OE1	2.12	0.66
1:X:46:VAL:HA	1:X:60:LYS:HA	1.77	0.66
2:j:213:ARG:HD2	2:j:213:ARG:C	2.20	0.66
2:i:295:ALA:HA	2:i:298:ILE:CD1	2.22	0.66
2:j:296:GLN:C	2:j:300:GLU:HG2	2.13	0.66
2:j:311:LEU:HD22	3:l:293:PHE:HE1	1.59	0.66
1:L:78:LEU:HD23	1:L:82:LEU:HD23	1.78	0.66
3:R:73:ASP:OD2	2:S:186:GLN:NE2	2.29	0.66
3:o:73:ASP:OD2	2:q:186:GLN:NE2	2.29	0.66
1:b:78:LEU:HD23	1:b:82:LEU:HD23	1.78	0.66
3:p:73:ASP:OD2	2:r:186:GLN:NE2	2.29	0.66
3:I:108:GLY:N	2:O:138:GLU:CD	2.53	0.65
3:I:229:ALA:HB1	2:O:266:ARG:HD2	1.77	0.65
3:I:312:ASP:OD2	2:O:340:LYS:CE	2.44	0.65
1:a:78:LEU:HD23	1:a:82:LEU:HD23	1.78	0.65
2:i:186:GLN:OE1	3:k:92:TYR:CG	2.49	0.65
2:O:219:GLU:OE1	2:O:219:GLU:HA	1.97	0.65
3:G:328:THR:HG23	2:q:327:TYR:CE2	2.23	0.65
2:i:209:ARG:HH22	3:p:78:ARG:HG3	1.60	0.65
1:C:54:ARG:HH12	1:C:69:TYR:HB3	1.60	0.65
1:C:90:GLY:O	1:D:31:LYS:NZ	2.28	0.65
1:b:90:GLY:O	1:d:31:LYS:NZ	2.28	0.65
2:O:172:LYS:NZ	2:O:228:ASP:OD2	2.28	0.65
2:O:213:ARG:NH1	2:O:213:ARG:HB3	2.11	0.65
3:l:8:ILE:HD12	3:l:11:ILE:HD11	1.79	0.65
3:I:312:ASP:OD1	2:O:340:LYS:N	2.30	0.65
2:g:328:ILE:HG21	3:k:298:ARG:HG3	1.79	0.65
1:d:54:ARG:NH2	1:d:70:ILE:O	2.29	0.65
3:I:298:ARG:CG	2:O:328:ILE:HG21	2.09	0.65
1:c:54:ARG:NH2	1:c:70:ILE:O	2.30	0.65
2:i:204:ILE:O	2:i:208:GLY:HA3	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:328:ILE:CG2	3:p:298:ARG:HG3	2.14	0.65
3:m:102:ARG:HH12	3:m:193:ILE:HD13	1.62	0.65
2:j:161:MET:HE3	2:j:212:ILE:HG21	0.66	0.65
1:M:54:ARG:NH2	1:M:70:ILE:O	2.29	0.65
3:G:326:MET:O	2:q:327:TYR:CZ	2.50	0.65
3:H:102:ARG:HH12	3:H:193:ILE:HD13	1.62	0.65
1:a:90:GLY:O	1:c:31:LYS:NZ	2.28	0.65
2:j:277:PRO:HG2	3:R:240:SER:OG	1.95	0.65
2:F:314:GLU:OE1	3:o:277:ALA:C	2.40	0.65
2:i:191:ALA:HB1	2:i:219:GLU:CD	2.19	0.65
2:j:242:ARG:HD2	2:j:248:LYS:HD2	1.78	0.65
2:i:216:THR:HG21	2:i:236:VAL:CG2	2.27	0.65
2:i:314:GLU:OE2	3:p:277:ALA:HA	1.96	0.65
2:j:213:ARG:HH21	2:j:213:ARG:CG	2.10	0.65
1:C:78:LEU:HD23	1:C:82:LEU:HD23	1.78	0.65
1:D:54:ARG:NH2	1:D:70:ILE:O	2.29	0.65
3:I:108:GLY:H	2:O:138:GLU:CD	2.04	0.65
2:h:328:ILE:HG21	3:l:298:ARG:HG3	1.79	0.65
3:p:121:ARG:HH21	3:p:121:ARG:CG	2.10	0.65
1:L:90:GLY:O	1:M:31:LYS:NZ	2.28	0.65
1:C:45:GLN:HE22	1:C:60:LYS:HB3	1.62	0.64
1:a:54:ARG:HH12	1:a:69:TYR:HB3	1.60	0.64
2:E:328:ILE:HG21	3:G:298:ARG:HG3	1.79	0.64
3:I:73:ASP:OD2	2:U:186:GLN:NE2	2.29	0.64
3:I:114:GLN:NE2	2:O:138:GLU:OE2	2.29	0.64
3:k:8:ILE:HD12	3:k:11:ILE:HD11	1.78	0.64
3:m:152:ARG:HD3	3:m:207:ASP:HA	1.80	0.64
2:O:225:ARG:O	2:O:225:ARG:HD3	1.97	0.64
3:G:8:ILE:HD12	3:G:11:ILE:HD11	1.79	0.64
2:i:193:ARG:HD2	2:i:193:ARG:C	2.23	0.64
2:i:209:ARG:HH12	3:p:78:ARG:C	2.05	0.64
1:b:45:GLN:HE22	1:b:60:LYS:HB3	1.62	0.64
2:j:307:ARG:HD2	3:R:269:ARG:CG	2.17	0.64
3:Q:102:ARG:HH12	3:Q:193:ILE:HD13	1.62	0.64
3:I:247:GLU:OE2	2:O:285:ARG:NH1	2.28	0.64
2:i:343:VAL:HG12	3:p:315:VAL:CG2	2.27	0.64
2:j:343:VAL:HG12	3:R:315:VAL:HB	1.80	0.64
3:n:102:ARG:HH12	3:n:193:ILE:HD13	1.62	0.64
2:O:242:ARG:HD2	2:O:248:LYS:HD2	1.78	0.64
3:P:8:ILE:HD12	3:P:11:ILE:HD11	1.78	0.64
3:G:78:ARG:NH1	3:G:86:ASP:OD2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:314:GLU:OE2	3:p:277:ALA:CA	2.46	0.64
3:n:152:ARG:HD3	3:n:207:ASP:HA	1.80	0.64
3:k:328:THR:N	2:r:327:TYR:CZ	2.66	0.64
2:j:314:GLU:OE1	3:R:277:ALA:C	2.40	0.64
2:S:109:THR:HA	2:S:115:SER:H	1.63	0.64
3:I:38:LEU:HD21	2:O:119:GLU:OE1	1.93	0.64
3:k:78:ARG:NH1	3:k:86:ASP:OD2	2.31	0.64
2:j:227:TYR:OH	3:l:94:LYS:HG3	1.95	0.64
2:r:109:THR:HA	2:r:115:SER:H	1.63	0.64
1:L:45:GLN:HE22	1:L:60:LYS:HB3	1.62	0.64
3:H:152:ARG:HD3	3:H:207:ASP:HA	1.80	0.64
3:k:322:PHE:HE2	3:p:303:TYR:CD1	2.15	0.64
2:i:138:GLU:CD	3:p:114:GLN:HG2	2.23	0.63
2:i:212:ILE:C	2:i:212:ILE:HD13	2.23	0.63
1:a:45:GLN:HE22	1:a:60:LYS:HB3	1.62	0.63
2:i:209:ARG:NH1	3:p:78:ARG:O	2.31	0.63
2:O:175:TYR:HA	3:P:68:ARG:HD3	1.81	0.63
2:F:175:TYR:HA	3:G:68:ARG:HD3	1.81	0.63
2:U:143:LEU:HD11	2:U:185:ARG:HB2	1.81	0.63
2:q:109:THR:HG22	2:q:114:PHE:HA	1.81	0.63
2:F:199:TYR:CD2	2:F:212:ILE:CD1	2.81	0.63
3:I:122:LYS:NZ	3:I:196:ASN:O	2.29	0.63
2:U:109:THR:HG22	2:U:114:PHE:HA	1.81	0.63
2:j:229:MET:HE3	2:j:231:ILE:HB	1.79	0.63
3:l:78:ARG:NH1	3:l:86:ASP:OD2	2.31	0.63
3:p:121:ARG:HH21	3:p:121:ARG:HG3	1.63	0.63
2:N:328:ILE:HG21	3:P:298:ARG:HG3	1.79	0.63
3:P:78:ARG:NH1	3:P:86:ASP:OD2	2.31	0.63
2:S:143:LEU:HD11	2:S:185:ARG:HB2	1.81	0.63
3:G:322:PHE:O	3:o:303:TYR:OH	2.17	0.63
2:q:143:LEU:HD11	2:q:185:ARG:HB2	1.81	0.63
2:r:109:THR:HG22	2:r:114:PHE:HA	1.81	0.63
2:S:109:THR:HG22	2:S:114:PHE:HA	1.80	0.63
2:O:217:GLN:CD	2:O:236:VAL:H	2.04	0.63
2:j:227:TYR:HH	3:l:92:TYR:HE2	1.47	0.63
2:O:217:GLN:CB	2:O:236:VAL:CG1	2.76	0.63
3:Q:152:ARG:HD3	3:Q:207:ASP:HA	1.80	0.63
3:R:122:LYS:NZ	3:R:196:ASN:O	2.29	0.63
2:F:343:VAL:HG12	3:o:315:VAL:HB	1.80	0.62
2:U:109:THR:HA	2:U:115:SER:H	1.63	0.62
2:i:175:TYR:HA	3:k:68:ARG:HD3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:223:THR:HG21	3:l:209:ARG:HE	1.63	0.62
2:j:253:ASP:OD1	3:l:239:ARG:NH2	2.33	0.62
3:o:33:ARG:HB3	3:o:37:VAL:HG13	1.82	0.62
2:F:253:ASP:OD1	3:G:239:ARG:NH2	2.33	0.62
2:j:175:TYR:HA	3:l:68:ARG:HD3	1.81	0.62
2:O:172:LYS:CD	2:O:228:ASP:OD2	2.48	0.62
3:I:296:PHE:N	3:P:325:TYR:CE1	2.68	0.62
2:g:102:GLU:HB2	3:k:36:LYS:HA	1.82	0.62
2:i:342:LEU:HB2	3:p:314:MET:HG3	1.81	0.62
2:j:188:THR:OG1	2:j:220:LEU:HD21	1.99	0.62
1:K:74:ASP:HB3	1:K:77:LEU:HD22	1.82	0.62
2:N:102:GLU:HB2	3:P:36:LYS:HA	1.82	0.62
2:q:109:THR:HA	2:q:115:SER:H	1.63	0.62
2:r:143:LEU:HD11	2:r:185:ARG:HB2	1.81	0.62
3:I:33:ARG:HB3	3:I:37:VAL:HG13	1.82	0.62
3:l:322:PHE:O	3:R:303:TYR:OH	2.17	0.62
2:h:102:GLU:HB2	3:l:36:LYS:HA	1.82	0.62
2:j:222:GLU:OE1	2:j:222:GLU:HA	2.00	0.62
2:E:102:GLU:HB2	3:G:36:LYS:HA	1.82	0.62
2:E:331:MET:HE2	3:I:326:MET:O	1.98	0.61
2:i:253:ASP:OD1	3:k:239:ARG:NH2	2.33	0.61
2:i:343:VAL:HG12	3:p:315:VAL:HB	1.81	0.61
2:O:188:THR:CA	2:O:220:LEU:HD11	2.29	0.61
2:O:267:GLU:OE1	3:P:250:ARG:NH2	2.33	0.61
2:F:267:GLU:OE1	3:G:250:ARG:NH2	2.33	0.61
2:j:267:GLU:OE1	3:l:250:ARG:NH2	2.33	0.61
3:H:314:MET:HE2	2:U:342:LEU:HD22	1.83	0.61
3:I:315:VAL:CB	2:O:343:VAL:HG12	2.30	0.61
1:Z:74:ASP:HB3	1:Z:77:LEU:HD22	1.82	0.61
2:j:119:GLU:OE1	3:R:38:LEU:HD21	2.00	0.61
2:i:149:MET:CG	2:i:196:ILE:CD1	2.79	0.61
2:O:253:ASP:OD1	3:P:239:ARG:NH2	2.32	0.61
3:I:321:ASP:CB	3:P:328:THR:HG22	2.31	0.61
2:i:121:GLY:HA3	3:p:34:PHE:O	2.00	0.61
2:i:267:GLU:OE1	3:k:250:ARG:NH2	2.33	0.61
2:i:285:ARG:CD	3:p:247:GLU:OE2	2.45	0.61
3:o:79:PHE:CE2	3:o:128:ARG:HG3	2.36	0.61
2:j:188:THR:CB	2:j:220:LEU:HD21	2.31	0.61
3:l:325:TYR:C	3:l:327:LYS:H	2.09	0.61
3:I:121:ARG:NH1	2:O:234:LEU:HD13	2.16	0.61
1:Y:74:ASP:HB3	1:Y:77:LEU:HD22	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:k:328:THR:CG2	3:p:321:ASP:OD2	2.45	0.61
2:j:138:GLU:OE2	3:R:114:GLN:NE2	2.34	0.61
2:j:219:GLU:OE1	2:j:219:GLU:HA	2.00	0.61
1:B:74:ASP:HB3	1:B:77:LEU:HD22	1.82	0.61
2:O:188:THR:HA	2:O:220:LEU:HD11	1.83	0.61
2:i:160:GLU:CD	2:i:240:ALA:HB3	2.25	0.61
1:a:54:ARG:NH1	1:a:70:ILE:O	2.34	0.60
2:i:300:GLU:HA	2:i:300:GLU:OE1	1.99	0.60
3:k:78:ARG:O	3:k:128:ARG:NH1	2.34	0.60
3:m:314:MET:HE2	2:q:342:LEU:HD22	1.83	0.60
3:R:33:ARG:HB3	3:R:37:VAL:HG13	1.82	0.60
1:C:42:ASN:HA	1:C:84:LYS:HE2	1.83	0.60
3:I:265:GLU:OE1	3:I:265:GLU:HA	1.99	0.60
2:j:223:THR:HG23	3:l:209:ARG:NH2	2.16	0.60
3:n:314:MET:HE2	2:r:342:LEU:HD22	1.83	0.60
2:O:217:GLN:OE1	2:O:236:VAL:CA	2.49	0.60
3:I:263:GLU:N	2:O:299:LEU:CD1	2.64	0.60
3:k:328:THR:CG2	3:p:321:ASP:CG	2.69	0.60
2:j:225:ARG:HB3	2:j:226:PRO:HD3	1.83	0.60
2:i:191:ALA:CB	2:i:219:GLU:CD	2.74	0.60
3:k:328:THR:HA	2:r:327:TYR:CZ	2.36	0.60
3:o:228:ARG:O	3:o:232:GLU:HG2	2.02	0.60
2:j:340:LYS:HE2	3:R:312:ASP:CG	2.27	0.60
1:L:42:ASN:HA	1:L:84:LYS:HE2	1.83	0.60
2:O:188:THR:CA	2:O:220:LEU:CD1	2.77	0.60
2:F:340:LYS:HE2	3:o:312:ASP:CG	2.27	0.60
3:I:228:ARG:O	3:I:232:GLU:HG2	2.02	0.60
1:b:42:ASN:HA	1:b:84:LYS:HE2	1.83	0.60
1:b:56:ILE:HD13	1:b:68:THR:HG23	1.84	0.60
3:p:228:ARG:O	3:p:232:GLU:HG2	2.02	0.60
1:L:56:ILE:HD13	1:L:68:THR:HG23	1.84	0.60
1:A:42:ASN:HA	1:A:84:LYS:HE2	1.84	0.60
2:i:314:GLU:OE2	3:p:280:ALA:HB3	2.01	0.60
3:k:326:MET:HG3	2:r:331:MET:SD	2.40	0.60
3:o:271:MET:CE	2:q:291:ARG:HA	2.17	0.60
1:b:54:ARG:NH1	1:b:70:ILE:O	2.34	0.60
3:p:117:VAL:HA	3:p:120:LYS:HD2	1.84	0.60
3:Q:298:ARG:HG3	2:S:328:ILE:HG21	1.84	0.60
3:I:321:ASP:OD2	3:P:328:THR:CG2	2.39	0.60
1:W:42:ASN:HA	1:W:84:LYS:HE2	1.84	0.60
3:H:298:ARG:HG3	2:U:328:ILE:HG21	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:294:LYS:O	2:i:298:ILE:CD1	2.49	0.60
3:l:78:ARG:O	3:l:128:ARG:NH1	2.34	0.60
2:O:188:THR:OG1	2:O:220:LEU:CD2	2.39	0.60
2:S:315:TYR:OH	2:S:323:ARG:NH1	2.35	0.60
1:B:46:VAL:HG13	1:B:86:VAL:HG11	1.84	0.60
2:F:119:GLU:OE1	3:o:38:LEU:HD21	2.00	0.60
1:a:42:ASN:HA	1:a:84:LYS:HE2	1.83	0.60
1:T:40:GLU:OE1	1:T:66:TYR:OH	2.16	0.60
2:U:327:TYR:CZ	3:P:328:THR:HA	2.37	0.60
1:Y:46:VAL:HG13	1:Y:86:VAL:HG11	1.84	0.60
2:i:340:LYS:CE	3:p:312:ASP:OD2	2.50	0.60
3:p:33:ARG:HB3	3:p:37:VAL:HG13	1.82	0.60
2:r:315:TYR:OH	2:r:323:ARG:NH1	2.35	0.60
1:J:42:ASN:HA	1:J:84:LYS:HE2	1.84	0.60
3:R:228:ARG:O	3:R:232:GLU:HG2	2.02	0.60
3:P:78:ARG:O	3:P:128:ARG:NH1	2.34	0.59
1:C:54:ARG:NH1	1:C:70:ILE:O	2.34	0.59
1:C:56:ILE:HD13	1:C:68:THR:HG23	1.84	0.59
3:I:303:TYR:CZ	3:P:323:PHE:HA	2.36	0.59
2:q:315:TYR:OH	2:q:323:ARG:NH1	2.35	0.59
1:b:50:ARG:HG2	1:b:89:VAL:HB	1.84	0.59
3:p:152:ARG:NH1	3:p:206:VAL:O	2.35	0.59
1:L:54:ARG:NH1	1:L:70:ILE:O	2.34	0.59
3:R:152:ARG:NH1	3:R:206:VAL:O	2.35	0.59
1:a:50:ARG:HG2	1:a:89:VAL:HB	1.84	0.59
3:k:328:THR:CB	2:r:327:TYR:CZ	2.82	0.59
3:Q:314:MET:HE2	2:S:342:LEU:HD22	1.83	0.59
2:F:138:GLU:OE2	3:o:114:GLN:NE2	2.34	0.59
3:H:79:PHE:HB3	3:H:131:ILE:HG21	1.85	0.59
3:G:78:ARG:O	3:G:128:ARG:NH1	2.34	0.59
2:U:315:TYR:OH	2:U:323:ARG:NH1	2.35	0.59
2:i:192:LEU:HD23	2:i:192:LEU:C	2.26	0.59
1:L:50:ARG:HG2	1:L:89:VAL:HB	1.84	0.59
2:F:304:GLU:OE2	3:G:283:PHE:HE1	1.80	0.59
1:a:56:ILE:HD13	1:a:68:THR:HG23	1.84	0.59
3:o:79:PHE:HE2	3:o:128:ARG:CB	2.16	0.59
3:p:264:ALA:C	3:p:267:GLN:CD	2.70	0.59
2:O:172:LYS:CE	2:O:228:ASP:OD2	2.50	0.59
1:X:42:ASN:HA	1:X:84:LYS:HE2	1.84	0.59
3:p:130:GLU:OE1	3:p:130:GLU:HA	2.01	0.59
3:I:152:ARG:NH1	3:I:206:VAL:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:m:79:PHE:HB3	3:m:131:ILE:HG21	1.85	0.59
3:o:152:ARG:NH1	3:o:206:VAL:O	2.35	0.59
3:p:119:LEU:HD12	3:p:119:LEU:O	2.02	0.59
2:U:238:PHE:HZ	2:U:241:ALA:HB2	1.68	0.59
1:a:60:LYS:HD2	1:a:64:ASN:HB2	1.85	0.59
1:b:60:LYS:HD2	1:b:64:ASN:HB2	1.85	0.59
2:j:223:THR:HG23	3:l:209:ARG:NE	2.16	0.58
2:j:227:TYR:OH	3:l:94:LYS:CG	2.39	0.58
1:K:46:VAL:HG13	1:K:86:VAL:HG11	1.84	0.58
2:F:328:ILE:CG2	3:o:298:ARG:HG3	2.27	0.58
3:n:298:ARG:HG3	2:r:328:ILE:HG21	1.84	0.58
2:O:217:GLN:CB	2:O:236:VAL:HG12	2.33	0.58
3:I:34:PHE:O	2:O:121:GLY:CA	2.49	0.58
3:k:317:SER:O	3:k:320:SER:OG	2.15	0.58
2:O:208:GLY:C	2:O:212:ILE:HG12	2.25	0.58
3:G:326:MET:O	2:q:327:TYR:OH	2.22	0.58
3:I:121:ARG:NH1	2:O:234:LEU:CD1	2.66	0.58
1:C:50:ARG:HG2	1:C:89:VAL:HB	1.84	0.58
3:m:298:ARG:HG3	2:q:328:ILE:HG21	1.84	0.58
1:Z:46:VAL:HG13	1:Z:86:VAL:HG11	1.84	0.58
2:j:221:GLU:CG	2:j:233:LEU:HD22	2.33	0.58
3:p:72:MET:HE2	3:p:120:LYS:CE	2.33	0.58
3:G:223:ILE:O	3:G:227:MET:HG3	2.04	0.57
2:O:172:LYS:O	2:O:176:SER:OG	2.18	0.57
3:P:223:ILE:O	3:P:227:MET:HG3	2.04	0.57
2:q:238:PHE:HZ	2:q:241:ALA:HB2	1.68	0.57
2:j:311:LEU:HD23	2:j:311:LEU:O	2.03	0.57
1:L:60:LYS:HD2	1:L:64:ASN:HB2	1.85	0.57
2:S:238:PHE:HZ	2:S:241:ALA:HB2	1.68	0.57
3:o:130:GLU:OE1	3:o:133:ARG:NH1	2.37	0.57
2:F:183:SER:HB2	3:G:94:LYS:HZ1	1.69	0.57
3:H:321:ASP:CB	3:I:328:THR:HG22	2.34	0.57
3:I:321:ASP:CB	3:P:328:THR:CG2	2.82	0.57
2:i:294:LYS:CG	2:i:298:ILE:HD11	2.27	0.57
2:j:109:THR:HG22	2:j:114:PHE:HB3	1.87	0.57
3:n:79:PHE:HB3	3:n:131:ILE:HG21	1.85	0.57
1:C:60:LYS:HD2	1:C:64:ASN:HB2	1.85	0.57
2:U:327:TYR:CE2	3:P:328:THR:HA	2.39	0.57
2:i:149:MET:HB2	2:i:196:ILE:HD12	1.86	0.57
3:o:122:LYS:NZ	3:o:196:ASN:O	2.29	0.57
2:r:238:PHE:HZ	2:r:241:ALA:HB2	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:l:323:PHE:HA	3:r:303:TYR:OH	2.04	0.57
3:G:90:ASP:OD2	3:G:212:GLN:NE2	2.37	0.57
3:l:90:ASP:OD2	3:l:212:GLN:NE2	2.37	0.57
3:Q:79:PHE:HB3	3:Q:131:ILE:HG21	1.85	0.57
3:k:223:ILE:O	3:k:227:MET:HG3	2.04	0.57
3:P:316:MET:HE2	3:P:323:PHE:CE2	2.39	0.57
2:i:183:SER:HB2	3:k:94:LYS:HZ1	1.70	0.56
2:i:199:TYR:CE2	2:i:211:VAL:HG11	2.40	0.56
2:i:109:THR:HG22	2:i:114:PHE:HB3	1.87	0.56
3:o:79:PHE:CD2	3:o:128:ARG:HG3	2.40	0.56
1:T:87:LYS:NZ	1:V:33:ASP:OD2	2.31	0.56
2:F:285:ARG:HD2	3:o:247:GLU:OE2	2.05	0.56
3:G:323:PHE:HA	3:o:303:TYR:OH	2.05	0.56
3:I:262:ALA:CB	2:O:299:LEU:HD12	2.35	0.56
3:I:315:VAL:HG21	2:O:343:VAL:HG12	1.85	0.56
3:o:226:ARG:HH22	2:q:154:GLU:HG3	1.70	0.56
2:j:183:SER:HB2	3:l:94:LYS:HZ1	1.70	0.56
3:l:158:GLY:H	3:l:197:SER:HB3	1.71	0.56
1:t:87:LYS:NZ	1:v:33:ASP:OD2	2.31	0.56
3:R:139:ILE:HD12	3:R:147:LEU:HD21	1.88	0.56
3:G:327:LYS:CB	3:o:321:ASP:OD2	2.52	0.56
2:O:183:SER:HB2	3:P:94:LYS:HZ1	1.69	0.56
2:F:109:THR:HG22	2:F:114:PHE:HB3	1.87	0.56
2:j:196:ILE:CD1	2:j:212:ILE:CD1	2.83	0.56
2:i:161:MET:HE2	2:i:236:VAL:CG2	2.31	0.56
2:i:314:GLU:OE1	3:p:277:ALA:CB	2.54	0.56
3:l:223:ILE:O	3:l:227:MET:HG3	2.04	0.56
2:O:209:ARG:HG2	2:O:238:PHE:CE2	2.40	0.56
2:j:188:THR:HA	2:j:220:LEU:CD1	2.36	0.56
3:p:139:ILE:HD12	3:p:147:LEU:HD21	1.88	0.56
2:j:312:LEU:HD12	2:j:312:LEU:C	2.28	0.56
3:P:316:MET:HE2	3:P:323:PHE:HE2	1.69	0.56
2:i:216:THR:HB	2:i:236:VAL:HG11	1.86	0.56
2:j:178:THR:HG22	3:l:68:ARG:NH1	2.21	0.56
3:p:226:ARG:HH22	2:r:154:GLU:HG3	1.70	0.56
1:W:30:ARG:NH1	1:W:31:LYS:O	2.39	0.56
3:p:199:ALA:O	3:p:201:LEU:O	2.24	0.56
2:O:109:THR:HG22	2:O:114:PHE:HB3	1.87	0.56
3:G:325:TYR:HD2	3:o:299:SER:CB	2.18	0.55
3:I:226:ARG:HH22	2:U:154:GLU:HG3	1.70	0.55
2:i:178:THR:HG22	3:k:68:ARG:NH1	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:209:ARG:NH2	3:p:78:ARG:HG3	2.18	0.55
3:k:326:MET:CB	3:p:303:TYR:CE2	2.86	0.55
2:F:178:THR:HG22	3:G:68:ARG:NH1	2.21	0.55
3:I:144:ARG:NH1	2:U:219:GLU:OE1	2.39	0.55
3:I:296:PHE:HA	3:P:325:TYR:HD1	1.56	0.55
3:I:321:ASP:CG	3:P:328:THR:CG2	2.66	0.55
3:k:158:GLY:H	3:k:197:SER:HB3	1.71	0.55
3:o:144:ARG:NH1	2:q:219:GLU:OE1	2.39	0.55
2:j:296:GLN:O	2:j:300:GLU:N	2.34	0.55
3:p:272:ARG:CD	2:r:293:TYR:CG	2.88	0.55
3:I:139:ILE:HD12	3:I:147:LEU:HD21	1.88	0.55
2:j:285:ARG:HD2	3:R:247:GLU:OE2	2.05	0.55
3:p:144:ARG:NH1	2:r:219:GLU:OE1	2.39	0.55
3:P:158:GLY:H	3:P:197:SER:HB3	1.71	0.55
3:I:263:GLU:N	2:O:299:LEU:HD13	2.21	0.55
1:a:45:GLN:NE2	1:a:60:LYS:HB3	2.22	0.55
3:m:248:LYS:HG2	2:q:284:GLN:HG2	1.89	0.55
3:I:291:PRO:HB3	2:O:321:ILE:CD1	2.32	0.55
2:j:234:LEU:CG	3:R:121:ARG:NH1	2.70	0.55
3:R:226:ARG:HH22	2:S:154:GLU:HG3	1.70	0.55
1:A:30:ARG:NH1	1:A:31:LYS:O	2.39	0.55
2:i:331:MET:HA	2:i:334:VAL:HG12	1.88	0.55
2:i:343:VAL:HG12	3:p:315:VAL:CB	2.36	0.55
3:o:45:PRO:HD2	3:o:101:SER:HB2	1.89	0.55
3:p:272:ARG:HD2	2:r:293:TYR:CG	2.42	0.55
1:C:45:GLN:NE2	1:C:60:LYS:HB3	2.22	0.55
3:n:83:GLU:HB2	3:n:85:LYS:HE2	1.89	0.55
3:n:248:LYS:HG2	2:r:284:GLN:HG2	1.89	0.55
3:p:45:PRO:HD2	3:p:101:SER:HB2	1.89	0.55
3:p:155:LEU:HD23	3:p:205:VAL:HG21	1.89	0.55
2:O:331:MET:HA	2:O:334:VAL:HG12	1.88	0.55
3:R:144:ARG:NH1	2:S:219:GLU:OE1	2.39	0.55
3:I:240:SER:OG	2:O:277:PRO:CG	2.55	0.55
3:m:83:GLU:HB2	3:m:85:LYS:HE2	1.89	0.55
2:O:208:GLY:HA2	2:O:212:ILE:HG12	0.67	0.55
3:H:83:GLU:HB2	3:H:85:LYS:HE2	1.89	0.55
3:o:131:ILE:CG2	3:o:132:GLY:N	2.70	0.55
2:j:234:LEU:HD22	3:R:121:ARG:CZ	2.22	0.55
3:p:272:ARG:CG	2:r:293:TYR:HD1	1.77	0.55
3:R:155:LEU:HD23	3:R:205:VAL:HG21	1.89	0.55
2:j:331:MET:HA	2:j:334:VAL:HG12	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:30:ARG:NH1	1:J:31:LYS:O	2.39	0.54
2:F:331:MET:HA	2:F:334:VAL:HG12	1.88	0.54
3:G:158:GLY:H	3:G:197:SER:HB3	1.71	0.54
3:I:324:ARG:O	3:I:327:LYS:HD3	2.07	0.54
1:e:40:GLU:OE1	1:e:66:TYR:OH	2.16	0.54
1:e:51:ILE:HG12	1:e:56:ILE:HG12	1.89	0.54
3:o:139:ILE:HD12	3:o:147:LEU:HD21	1.88	0.54
1:X:30:ARG:NH1	1:X:31:LYS:O	2.39	0.54
2:j:308:PHE:CD1	2:j:308:PHE:C	2.85	0.54
2:O:178:THR:HG22	3:P:68:ARG:NH1	2.21	0.54
2:O:222:GLU:OE1	2:O:222:GLU:HA	2.08	0.54
3:k:322:PHE:CD2	3:k:322:PHE:C	2.86	0.54
1:s:51:ILE:HG12	1:s:56:ILE:HG12	1.89	0.54
1:L:45:GLN:NE2	1:L:60:LYS:HB3	2.22	0.54
3:Q:83:GLU:HB2	3:Q:85:LYS:HE2	1.89	0.54
2:i:340:LYS:N	3:p:312:ASP:OD1	2.35	0.54
2:F:310:LYS:CE	3:o:274:GLU:HG2	2.37	0.54
2:g:110:ARG:H	2:g:115:SER:HB3	1.73	0.54
2:i:314:GLU:HG2	3:p:281:LYS:HB2	1.89	0.54
1:b:45:GLN:NE2	1:b:60:LYS:HB3	2.22	0.54
2:j:343:VAL:HG12	3:R:315:VAL:CB	2.38	0.54
3:p:121:ARG:HD2	3:p:121:ARG:C	2.32	0.54
3:R:45:PRO:HD2	3:R:101:SER:HB2	1.89	0.54
1:T:51:ILE:HG12	1:T:56:ILE:HG12	1.89	0.54
2:E:110:ARG:H	2:E:115:SER:HB3	1.73	0.54
3:o:155:LEU:HD23	3:o:205:VAL:HG21	1.89	0.54
2:h:143:LEU:HD11	2:h:185:ARG:HB2	1.90	0.54
3:P:90:ASP:OD2	3:P:212:GLN:NE2	2.37	0.54
3:Q:93:ILE:HD11	3:Q:123:PHE:CG	2.43	0.54
3:I:38:LEU:CD1	2:O:119:GLU:OE1	2.56	0.54
3:o:130:GLU:OE1	3:o:130:GLU:HA	2.07	0.54
2:j:188:THR:HA	2:j:220:LEU:HD11	1.90	0.54
2:F:295:ALA:O	2:F:299:LEU:HG	2.07	0.54
3:I:45:PRO:HD2	3:I:101:SER:HB2	1.89	0.54
2:i:216:THR:CB	2:i:236:VAL:CG1	2.82	0.54
3:m:93:ILE:HD11	3:m:123:PHE:CG	2.43	0.54
3:o:271:MET:SD	2:q:290:ALA:CB	2.96	0.54
2:E:143:LEU:HD11	2:E:185:ARG:HB2	1.90	0.53
2:U:331:MET:HA	2:U:334:VAL:HG12	1.90	0.53
3:p:72:MET:CE	3:p:120:LYS:HG3	2.27	0.53
2:r:163:VAL:HG22	2:r:236:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:23:VAL:HA	3:G:64:MET:HE1	1.91	0.53
2:i:266:ARG:HD2	3:p:229:ALA:CB	2.38	0.53
3:k:323:PHE:CD2	3:k:323:PHE:N	2.75	0.53
2:j:121:GLY:HA3	3:R:34:PHE:O	2.09	0.53
2:S:163:VAL:HG22	2:S:236:VAL:HG22	1.91	0.53
3:I:258:THR:HG21	2:O:292:ALA:HB1	1.89	0.53
2:j:328:ILE:CG2	3:R:298:ARG:HG3	2.27	0.53
3:H:93:ILE:HD11	3:H:123:PHE:CG	2.43	0.53
2:g:143:LEU:HD11	2:g:185:ARG:HB2	1.90	0.53
3:o:21:PHE:HD2	3:o:53:HIS:HB2	1.73	0.53
2:N:110:ARG:H	2:N:115:SER:HB3	1.73	0.53
3:I:155:LEU:HD23	3:I:205:VAL:HG21	1.89	0.53
2:i:343:VAL:HG12	3:p:315:VAL:HG21	1.89	0.53
3:k:322:PHE:CD2	3:p:303:TYR:CE1	2.81	0.53
3:k:328:THR:N	2:r:327:TYR:OH	2.41	0.53
2:j:308:PHE:HE2	3:l:294:TYR:HB2	1.73	0.53
3:n:93:ILE:HD11	3:n:123:PHE:CG	2.43	0.53
1:W:48:GLU:HG3	1:W:59:THR:HB	1.91	0.53
3:P:23:VAL:HA	3:P:64:MET:HE1	1.91	0.53
3:Q:248:LYS:HG2	2:S:284:GLN:HG2	1.89	0.53
3:G:325:TYR:CD2	3:o:299:SER:HB3	2.42	0.53
2:i:310:LYS:HZ3	3:p:274:GLU:HG2	0.73	0.53
2:j:229:MET:HE3	2:j:231:ILE:HD12	1.90	0.53
3:o:79:PHE:CE2	3:o:128:ARG:CG	2.91	0.53
3:o:79:PHE:CD2	3:o:128:ARG:CG	2.91	0.53
1:t:51:ILE:HG12	1:t:56:ILE:HG12	1.89	0.53
2:S:331:MET:HA	2:S:334:VAL:HG12	1.91	0.53
1:T:47:ARG:HB2	1:T:61:LYS:HD2	1.91	0.53
3:I:21:PHE:HD2	3:I:53:HIS:HB2	1.73	0.53
3:I:143:SER:HG	2:U:193:ARG:HH22	1.53	0.53
2:i:223:THR:O	2:i:226:PRO:HD2	2.09	0.53
2:h:110:ARG:H	2:h:115:SER:HB3	1.73	0.53
2:N:143:LEU:HD11	2:N:185:ARG:HB2	1.90	0.53
2:O:217:GLN:CG	2:O:236:VAL:CG1	2.85	0.53
3:H:248:LYS:HG2	2:U:284:GLN:HG2	1.89	0.53
1:X:48:GLU:HG3	1:X:59:THR:HB	1.91	0.53
1:A:50:ARG:HB3	1:A:57:ASN:HB2	1.91	0.52
2:i:321:ILE:CG2	3:p:287:PHE:HB2	2.37	0.52
1:B:40:GLU:OE2	1:B:60:LYS:NZ	2.42	0.52
2:E:163:VAL:HG22	2:E:236:VAL:HG22	1.91	0.52
2:F:343:VAL:HG12	3:o:315:VAL:CB	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:296:PHE:CD2	3:P:325:TYR:CD1	2.97	0.52
1:Y:40:GLU:OE2	1:Y:60:LYS:NZ	2.42	0.52
2:i:193:ARG:HH22	3:k:210:ILE:HB	1.71	0.52
3:H:223:ILE:HG22	3:H:227:MET:HE2	1.92	0.52
2:q:163:VAL:HG22	2:q:236:VAL:HG22	1.91	0.52
3:p:21:PHE:HD2	3:p:53:HIS:HB2	1.74	0.52
2:F:234:LEU:CG	3:o:121:ARG:NH1	2.70	0.52
2:U:163:VAL:HG22	2:U:236:VAL:HG22	1.91	0.52
1:e:47:ARG:HB2	1:e:61:LYS:HD2	1.91	0.52
2:g:163:VAL:HG22	2:g:236:VAL:HG22	1.91	0.52
3:k:23:VAL:HA	3:k:64:MET:HE1	1.91	0.52
3:l:23:VAL:HA	3:l:64:MET:HE1	1.91	0.52
3:n:223:ILE:HG22	3:n:227:MET:HE2	1.92	0.52
2:N:163:VAL:HG22	2:N:236:VAL:HG22	1.92	0.52
3:G:328:THR:CG2	2:q:327:TYR:CZ	2.83	0.52
3:k:90:ASP:OD2	3:k:212:GLN:NE2	2.37	0.52
2:r:331:MET:HA	2:r:334:VAL:HG12	1.90	0.52
2:S:108:VAL:HG13	2:S:115:SER:HB2	1.92	0.52
1:C:52:ASN:HB3	1:C:55:GLU:HB3	1.91	0.52
3:m:223:ILE:HG22	3:m:227:MET:HE2	1.92	0.52
3:n:21:PHE:HB3	3:n:53:HIS:HB2	1.91	0.52
3:Q:78:ARG:HD2	3:Q:88:ILE:HG12	1.92	0.52
3:R:21:PHE:HD2	3:R:53:HIS:HB2	1.73	0.52
2:i:149:MET:HE3	2:i:196:ILE:HD11	0.54	0.52
1:t:47:ARG:HB2	1:t:61:LYS:HD2	1.91	0.52
1:L:88:VAL:HG23	1:M:34:TYR:HB3	1.92	0.52
3:Q:223:ILE:HG22	3:Q:227:MET:HE2	1.92	0.52
2:F:121:GLY:HA3	3:o:34:PHE:O	2.09	0.52
2:F:234:LEU:HB3	3:o:121:ARG:NH1	2.24	0.52
2:i:218:ARG:HD3	2:i:218:ARG:O	2.09	0.52
3:o:267:GLN:O	3:o:270:ILE:HB	2.10	0.52
2:h:142:GLU:OE2	2:h:162:ASN:ND2	2.40	0.52
1:J:50:ARG:HB3	1:J:57:ASN:HB2	1.91	0.52
1:L:52:ASN:HB3	1:L:55:GLU:HB3	1.92	0.52
1:A:48:GLU:HG3	1:A:59:THR:HB	1.91	0.52
1:s:47:ARG:HB2	1:s:61:LYS:HD2	1.91	0.52
2:N:330:THR:HG23	3:Q:304:GLU:HG3	1.92	0.52
3:Q:115:ALA:HB1	3:Q:203:ILE:HD11	1.92	0.52
2:E:251:PHE:HE2	3:G:84:LYS:HD3	1.75	0.52
3:H:21:PHE:HB3	3:H:53:HIS:HB2	1.91	0.52
3:I:321:ASP:OD1	3:I:322:PHE:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:108:VAL:HG13	2:U:115:SER:HB2	1.92	0.52
2:g:251:PHE:HE2	3:k:84:LYS:HD3	1.75	0.52
2:i:209:ARG:HA	2:i:212:ILE:CG2	2.40	0.52
3:o:271:MET:HE2	2:q:291:ARG:CA	2.30	0.52
2:h:330:THR:HG23	3:n:304:GLU:HG3	1.92	0.52
2:r:108:VAL:HG13	2:r:115:SER:HB2	1.92	0.52
2:N:251:PHE:HE2	3:P:84:LYS:HD3	1.75	0.52
2:O:187:ALA:C	2:O:220:LEU:CD1	2.82	0.52
3:I:66:ASP:OD1	3:I:67:ALA:N	2.43	0.51
2:i:149:MET:HE3	2:i:196:ILE:CG1	2.25	0.51
2:i:207:GLU:O	2:i:210:THR:CG2	2.57	0.51
3:m:21:PHE:HB3	3:m:53:HIS:HB2	1.91	0.51
1:X:50:ARG:HB3	1:X:57:ASN:HB2	1.91	0.51
1:b:88:VAL:HG23	1:d:34:TYR:HB3	1.92	0.51
2:h:163:VAL:HG22	2:h:236:VAL:HG22	1.91	0.51
1:J:48:GLU:HG3	1:J:59:THR:HB	1.91	0.51
3:H:78:ARG:HD2	3:H:88:ILE:HG12	1.92	0.51
3:I:262:ALA:C	2:O:299:LEU:CD1	2.83	0.51
2:i:277:PRO:CG	3:p:240:SER:OG	2.57	0.51
2:q:108:VAL:HG13	2:q:115:SER:HB2	1.92	0.51
3:R:321:ASP:OD1	3:R:322:PHE:N	2.43	0.51
3:I:303:TYR:OH	3:P:323:PHE:CA	2.49	0.51
3:o:66:ASP:OD1	3:o:67:ALA:N	2.43	0.51
3:l:71:THR:HG1	3:l:94:LYS:HZ2	1.55	0.51
3:Q:21:PHE:HB3	3:Q:53:HIS:HB2	1.91	0.51
1:A:34:TYR:HE2	1:A:70:ILE:HG22	1.76	0.51
3:m:78:ARG:HD2	3:m:88:ILE:HG12	1.92	0.51
1:b:52:ASN:HB3	1:b:55:GLU:HB3	1.91	0.51
1:a:52:ASN:HB3	1:a:55:GLU:HB3	1.91	0.51
2:i:332:GLU:OE2	3:p:305:ASN:ND2	2.27	0.51
2:j:209:ARG:HB2	2:j:238:PHE:HD2	1.66	0.51
3:n:115:ALA:HB1	3:n:203:ILE:HD11	1.92	0.51
3:p:66:ASP:OD1	3:p:67:ALA:N	2.43	0.51
3:p:321:ASP:OD1	3:p:322:PHE:N	2.43	0.51
2:O:188:THR:HG23	2:O:220:LEU:HD22	1.93	0.51
3:o:321:ASP:OD1	3:o:322:PHE:N	2.43	0.51
2:N:275:VAL:HG12	3:Q:257:VAL:HG21	1.93	0.51
3:m:303:TYR:OH	3:o:322:PHE:O	2.26	0.51
2:q:331:MET:HA	2:q:334:VAL:HG12	1.91	0.51
2:j:225:ARG:N	2:j:226:PRO:CD	2.74	0.51
2:j:296:GLN:C	2:j:300:GLU:CG	2.77	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:314:GLU:OE1	3:R:277:ALA:HB1	2.11	0.51
3:n:78:ARG:HD2	3:n:88:ILE:HG12	1.92	0.51
1:J:34:TYR:HE2	1:J:70:ILE:HG22	1.76	0.51
3:R:66:ASP:OD1	3:R:67:ALA:N	2.43	0.51
3:R:81:THR:OG1	3:R:134:LEU:O	2.29	0.51
1:W:50:ARG:HB3	1:W:57:ASN:HB2	1.91	0.51
3:o:271:MET:HE1	2:q:291:ARG:CA	2.23	0.51
2:j:182:ASP:O	2:j:186:GLN:HG3	2.11	0.51
1:K:40:GLU:OE2	1:K:60:LYS:NZ	2.42	0.51
2:N:331:MET:HA	2:N:334:VAL:HG12	1.93	0.51
1:C:88:VAL:HG23	1:D:34:TYR:HB3	1.92	0.51
3:G:327:LYS:CA	3:o:321:ASP:OD2	2.59	0.51
2:i:119:GLU:OE1	3:p:38:LEU:HD21	2.11	0.51
3:I:33:ARG:H	3:I:37:VAL:HG11	1.76	0.51
2:g:330:THR:HG23	3:m:304:GLU:HG3	1.93	0.51
2:i:314:GLU:CD	3:p:277:ALA:CA	2.84	0.51
1:X:34:TYR:HE2	1:X:70:ILE:HG22	1.76	0.51
2:h:126:PRO:HB2	2:h:129:ILE:HB	1.93	0.51
2:E:330:THR:HG23	3:H:304:GLU:HG3	1.92	0.50
2:F:209:ARG:CD	3:o:80:VAL:CG2	2.87	0.50
3:I:56:ILE:HB	3:I:59:ILE:HG22	1.93	0.50
3:I:81:THR:OG1	3:I:134:LEU:O	2.29	0.50
3:I:303:TYR:CE1	3:P:323:PHE:CD1	2.99	0.50
3:o:33:ARG:H	3:o:37:VAL:HG11	1.76	0.50
1:J:81:LEU:HD21	1:J:88:VAL:HB	1.94	0.50
2:O:208:GLY:CA	2:O:212:ILE:CG1	2.42	0.50
3:H:115:ALA:HB1	3:H:203:ILE:HD11	1.92	0.50
2:i:149:MET:HE2	2:i:192:LEU:CD2	2.39	0.50
3:m:115:ALA:HB1	3:m:203:ILE:HD11	1.92	0.50
2:j:196:ILE:CD1	2:j:212:ILE:HD11	2.31	0.50
2:E:331:MET:HA	2:E:334:VAL:HG12	1.93	0.50
1:a:88:VAL:HG23	1:c:34:TYR:HB3	1.92	0.50
2:g:331:MET:HA	2:g:334:VAL:HG12	1.93	0.50
3:k:324:ARG:CZ	3:m:328:THR:CG2	2.53	0.50
2:j:311:LEU:HD22	3:l:293:PHE:CE1	2.43	0.50
3:p:95:TRP:CZ2	3:p:116:GLU:CG	2.95	0.50
2:O:182:ASP:O	2:O:186:GLN:HG3	2.11	0.50
3:P:321:ASP:O	3:P:324:ARG:HG2	2.12	0.50
1:A:81:LEU:HD21	1:A:88:VAL:HB	1.94	0.50
3:k:326:MET:N	3:p:303:TYR:HE2	2.10	0.50
3:o:56:ILE:HB	3:o:59:ILE:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:h:251:PHE:HE2	3:l:84:LYS:HD3	1.75	0.50
3:p:78:ARG:HE	3:p:86:ASP:HB3	1.77	0.50
3:p:116:GLU:C	3:p:120:LYS:HD2	2.35	0.50
2:F:182:ASP:O	2:F:186:GLN:HG3	2.11	0.50
3:k:90:ASP:HB2	3:k:212:GLN:HG2	1.93	0.50
3:R:143:SER:HG	2:S:193:ARG:HH22	1.54	0.50
3:G:90:ASP:HB2	3:G:212:GLN:HG2	1.93	0.50
3:H:39:ARG:HA	3:H:45:PRO:HA	1.94	0.50
3:I:78:ARG:HE	3:I:86:ASP:HB3	1.77	0.50
2:g:126:PRO:HB2	2:g:129:ILE:HB	1.93	0.50
2:i:162:ASN:O	2:i:236:VAL:HG23	2.12	0.50
2:i:284:GLN:HG2	3:p:248:LYS:HG2	1.92	0.50
3:o:71:THR:HG22	3:o:94:LYS:HG2	1.93	0.50
3:l:328:THR:HA	2:S:327:TYR:CE2	2.47	0.50
2:N:161:MET:HE3	2:N:238:PHE:HD1	1.77	0.50
1:D:92:PRO:HA	1:e:54:ARG:HH22	1.77	0.50
2:E:161:MET:HE3	2:E:238:PHE:HD1	1.77	0.50
2:E:279:ALA:HB2	3:H:257:VAL:HG13	1.94	0.50
3:I:273:GLY:HA3	2:O:307:ARG:HG2	1.92	0.50
1:W:34:TYR:HE2	1:W:70:ILE:HG22	1.76	0.50
2:g:161:MET:HE3	2:g:238:PHE:HD1	1.77	0.50
2:i:183:SER:OG	2:i:229:MET:SD	2.70	0.50
2:h:275:VAL:HG12	3:n:257:VAL:HG21	1.93	0.50
2:N:109:THR:HG22	2:N:114:PHE:HA	1.94	0.50
2:N:126:PRO:HB2	2:N:129:ILE:HB	1.93	0.50
3:I:92:TYR:HB3	3:I:211:LYS:HE2	1.94	0.50
2:g:275:VAL:HG12	3:m:257:VAL:HG21	1.93	0.50
2:i:216:THR:HB	2:i:236:VAL:CG1	2.41	0.50
2:h:161:MET:HE3	2:h:238:PHE:HD1	1.77	0.50
3:p:33:ARG:H	3:p:37:VAL:HG11	1.76	0.50
3:p:92:TYR:HB3	3:p:211:LYS:HE2	1.94	0.50
3:p:156:ASN:ND2	3:p:205:VAL:O	2.41	0.50
1:t:40:GLU:OE1	1:t:66:TYR:OH	2.16	0.50
1:M:92:PRO:HA	1:T:54:ARG:HH22	1.77	0.50
2:O:209:ARG:CZ	2:O:238:PHE:HD2	2.23	0.50
3:R:71:THR:HG22	3:R:94:LYS:HG2	1.93	0.50
2:i:149:MET:CE	2:i:192:LEU:HD22	2.42	0.49
3:k:103:TYR:HB2	3:k:202:GLY:HA3	1.94	0.49
3:m:39:ARG:HA	3:m:45:PRO:HA	1.94	0.49
2:j:342:LEU:HB2	3:R:314:MET:HG3	1.94	0.49
3:p:71:THR:HG22	3:p:94:LYS:HG2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:39:ARG:HA	3:Q:45:PRO:HA	1.94	0.49
2:E:242:ARG:HH22	2:E:248:LYS:HD2	1.77	0.49
2:F:314:GLU:OE1	3:o:277:ALA:HB1	2.11	0.49
3:I:272:ARG:HG2	2:U:293:TYR:HD1	1.75	0.49
2:g:109:THR:HG22	2:g:114:PHE:HA	1.94	0.49
2:i:192:LEU:C	2:i:192:LEU:CD2	2.85	0.49
3:o:92:TYR:HB3	3:o:211:LYS:HE2	1.94	0.49
3:o:271:MET:HE1	2:q:291:ARG:H	1.76	0.49
2:h:109:THR:HG22	2:h:114:PHE:HA	1.94	0.49
2:j:234:LEU:HB3	3:R:121:ARG:NH1	2.24	0.49
3:n:39:ARG:HA	3:n:45:PRO:HA	1.94	0.49
3:R:78:ARG:HE	3:R:86:ASP:HB3	1.77	0.49
2:F:183:SER:OG	2:F:229:MET:SD	2.70	0.49
2:i:254:ALA:HA	3:k:235:ALA:HB2	1.95	0.49
3:k:322:PHE:HD2	3:p:303:TYR:HE1	1.50	0.49
3:o:81:THR:OG1	3:o:134:LEU:O	2.29	0.49
1:s:36:THR:HA	1:s:39:GLN:CD	2.37	0.49
3:n:64:MET:HA	3:n:64:MET:HE2	1.95	0.49
3:p:81:THR:OG1	3:p:134:LEU:O	2.29	0.49
3:p:95:TRP:CE3	3:p:203:ILE:HD12	2.48	0.49
3:p:119:LEU:HD11	3:p:155:LEU:HD21	1.95	0.49
1:t:36:THR:HA	1:t:39:GLN:CD	2.37	0.49
3:G:103:TYR:HB2	3:G:202:GLY:HA3	1.94	0.49
3:H:303:TYR:OH	3:I:322:PHE:O	2.26	0.49
1:W:81:LEU:HD21	1:W:88:VAL:HB	1.94	0.49
2:g:142:GLU:OE2	2:g:162:ASN:ND2	2.40	0.49
2:i:328:ILE:HG21	3:p:298:ARG:CG	2.15	0.49
2:h:331:MET:HA	2:h:334:VAL:HG12	1.93	0.49
1:v:38:LEU:HA	1:v:41:VAL:HG12	1.94	0.49
3:Q:64:MET:HE2	3:Q:64:MET:HA	1.95	0.49
2:E:275:VAL:HG12	3:H:257:VAL:HG21	1.93	0.49
3:I:263:GLU:CA	2:O:299:LEU:CD1	2.88	0.49
2:i:138:GLU:CD	3:p:108:GLY:N	2.69	0.49
3:l:90:ASP:HB2	3:l:212:GLN:HG2	1.93	0.49
3:l:103:TYR:HB2	3:l:202:GLY:HA3	1.94	0.49
3:l:314:MET:HE2	3:l:316:MET:SD	2.53	0.49
1:T:36:THR:HA	1:T:39:GLN:CD	2.37	0.49
3:I:95:TRP:CE3	3:I:203:ILE:HD12	2.48	0.49
1:X:81:LEU:HD21	1:X:88:VAL:HB	1.94	0.49
2:j:149:MET:HE2	2:j:192:LEU:HD23	1.95	0.49
2:j:312:LEU:HB3	2:j:313:PRO:HD3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:90:ASP:HB2	3:P:212:GLN:HG2	1.93	0.49
2:E:109:THR:HG22	2:E:114:PHE:HA	1.94	0.49
2:g:242:ARG:HH22	2:g:248:LYS:HD2	1.77	0.49
3:l:77:ASP:OD2	3:l:77:ASP:N	2.46	0.49
3:P:314:MET:HE2	3:P:316:MET:SD	2.53	0.49
3:R:95:TRP:CE3	3:R:203:ILE:HD12	2.48	0.49
3:H:227:MET:O	3:H:230:GLU:HG3	2.13	0.49
3:o:124:SER:O	3:o:128:ARG:HB2	2.13	0.49
1:u:38:LEU:HA	1:u:41:VAL:HG12	1.94	0.49
2:O:254:ALA:HA	3:P:235:ALA:HB2	1.94	0.49
3:H:64:MET:HA	3:H:64:MET:HE2	1.95	0.49
3:I:71:THR:HG22	3:I:94:LYS:HG2	1.93	0.49
2:g:159:VAL:HG11	2:g:196:ILE:HD11	1.95	0.49
2:g:279:ALA:HB2	3:m:257:VAL:HG13	1.94	0.49
3:p:56:ILE:HB	3:p:59:ILE:HG22	1.93	0.49
2:O:183:SER:OG	2:O:229:MET:SD	2.70	0.49
3:P:324:ARG:HG3	3:P:325:TYR:CD2	2.44	0.49
3:R:33:ARG:H	3:R:37:VAL:CG1	2.26	0.49
2:E:126:PRO:HB2	2:E:129:ILE:HB	1.93	0.49
2:E:142:GLU:OE2	2:E:162:ASN:ND2	2.40	0.49
2:F:234:LEU:HD22	3:o:121:ARG:CZ	2.22	0.49
1:e:36:THR:HA	1:e:39:GLN:CD	2.37	0.49
2:i:213:ARG:NE	2:i:237:ASN:HA	2.27	0.49
3:m:64:MET:HE2	3:m:64:MET:HA	1.95	0.49
3:o:33:ARG:H	3:o:37:VAL:CG1	2.26	0.49
1:s:87:LYS:NZ	1:u:33:ASP:OD2	2.31	0.49
2:h:279:ALA:HB2	3:n:257:VAL:HG13	1.94	0.49
2:N:279:ALA:HB2	3:Q:257:VAL:HG13	1.94	0.49
3:P:103:TYR:HB2	3:P:202:GLY:HA3	1.94	0.49
3:R:33:ARG:H	3:R:37:VAL:HG11	1.76	0.49
3:R:56:ILE:HB	3:R:59:ILE:HG22	1.93	0.49
2:F:342:LEU:HB2	3:o:314:MET:HG3	1.95	0.48
3:G:77:ASP:OD2	3:G:77:ASP:N	2.46	0.48
3:H:19:SER:HB3	3:H:57:PRO:HG3	1.95	0.48
3:p:264:ALA:CA	3:p:267:GLN:OE1	2.50	0.48
3:R:92:TYR:HB3	3:R:211:LYS:HE2	1.94	0.48
2:S:268:ALA:O	2:S:272:THR:HG23	2.13	0.48
3:p:121:ARG:CG	3:p:121:ARG:NH2	2.72	0.48
2:N:238:PHE:CZ	2:N:241:ALA:HB2	2.48	0.48
2:E:159:VAL:HG11	2:E:196:ILE:HD11	1.95	0.48
2:F:149:MET:HE2	2:F:192:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:92:PRO:HA	1:s:54:ARG:HH22	1.77	0.48
3:k:314:MET:HE2	3:k:316:MET:SD	2.53	0.48
3:o:78:ARG:HE	3:o:86:ASP:HB3	1.77	0.48
3:o:95:TRP:CE3	3:o:203:ILE:HD12	2.48	0.48
1:Z:40:GLU:OE2	1:Z:60:LYS:NZ	2.42	0.48
2:h:159:VAL:HG11	2:h:196:ILE:HD11	1.95	0.48
2:j:254:ALA:HA	3:l:235:ALA:HB2	1.95	0.48
3:n:227:MET:O	3:n:230:GLU:HG3	2.13	0.48
3:I:33:ARG:H	3:I:37:VAL:CG1	2.26	0.48
2:g:330:THR:HG21	3:m:300:LEU:HD22	1.96	0.48
3:m:19:SER:HB3	3:m:57:PRO:HG3	1.95	0.48
3:n:21:PHE:HD1	3:n:53:HIS:HB2	1.79	0.48
2:r:215:ASP:OD1	2:r:218:ARG:NH2	2.47	0.48
2:O:217:GLN:CB	2:O:236:VAL:HG11	2.41	0.48
3:Q:19:SER:HB3	3:Q:57:PRO:HG3	1.95	0.48
2:E:238:PHE:CZ	2:E:241:ALA:HB2	2.48	0.48
3:G:314:MET:HE2	3:G:316:MET:SD	2.53	0.48
3:H:93:ILE:HD11	3:H:123:PHE:CD2	2.48	0.48
2:U:215:ASP:OD1	2:U:218:ARG:NH2	2.47	0.48
2:U:268:ALA:O	2:U:272:THR:HG23	2.13	0.48
2:q:215:ASP:OD1	2:q:218:ARG:NH2	2.47	0.48
2:j:272:THR:HA	2:j:275:VAL:HG12	1.96	0.48
3:p:33:ARG:H	3:p:37:VAL:CG1	2.26	0.48
3:p:256:GLU:O	3:p:260:THR:HG23	2.13	0.48
1:v:48:GLU:HG3	1:v:59:THR:HB	1.96	0.48
2:O:272:THR:HA	2:O:275:VAL:HG12	1.96	0.48
1:f:48:GLU:HG3	1:f:59:THR:HB	1.96	0.48
2:i:172:LYS:O	2:i:176:SER:OG	2.18	0.48
3:o:256:GLU:O	3:o:260:THR:HG23	2.13	0.48
3:n:93:ILE:HD11	3:n:123:PHE:CD2	2.48	0.48
3:n:303:TYR:OH	3:p:322:PHE:O	2.26	0.48
2:N:242:ARG:HH22	2:N:248:LYS:HD2	1.77	0.48
2:O:225:ARG:N	2:O:226:PRO:CD	2.76	0.48
3:Q:93:ILE:HD11	3:Q:123:PHE:CD2	2.48	0.48
3:R:135:ASP:O	3:R:139:ILE:HG12	2.14	0.48
2:F:254:ALA:HA	3:G:235:ALA:HB2	1.95	0.48
3:G:327:LYS:HA	3:o:321:ASP:OD2	2.14	0.48
3:o:1:MET:HG2	3:o:3:LYS:H	1.79	0.48
1:d:92:PRO:HA	1:t:54:ARG:HH22	1.77	0.48
2:h:238:PHE:CZ	2:h:241:ALA:HB2	2.48	0.48
2:r:268:ALA:O	2:r:272:THR:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:54:ARG:HH22	1:M:70:ILE:N	2.12	0.48
1:V:48:GLU:HG3	1:V:59:THR:HB	1.96	0.48
1:D:54:ARG:HH22	1:D:70:ILE:N	2.12	0.48
2:F:340:LYS:HE2	3:o:312:ASP:OD2	2.14	0.48
1:f:38:LEU:HA	1:f:41:VAL:HG12	1.94	0.48
2:g:238:PHE:CZ	2:g:241:ALA:HB2	2.48	0.48
1:t:42:ASN:HA	1:t:84:LYS:HE2	1.96	0.48
3:Q:21:PHE:HD1	3:Q:53:HIS:HB2	1.79	0.48
3:I:135:ASP:O	3:I:139:ILE:HG12	2.14	0.48
2:i:110:ARG:N	2:i:113:LYS:O	2.47	0.48
2:i:327:TYR:O	2:i:331:MET:HG2	2.14	0.48
3:k:328:THR:CA	2:r:327:TYR:CE2	2.95	0.48
1:u:48:GLU:HG3	1:u:59:THR:HB	1.96	0.48
3:n:19:SER:HB3	3:n:57:PRO:HG3	1.95	0.48
2:r:148:VAL:HG22	2:r:158:ARG:HG2	1.96	0.48
3:R:231:ARG:HB2	2:S:250:ALA:HB1	1.96	0.48
3:R:256:GLU:O	3:R:260:THR:HG23	2.13	0.48
2:F:250:ALA:HB1	3:G:231:ARG:HB2	1.96	0.48
2:g:102:GLU:HA	2:g:120:PRO:HB2	1.96	0.48
3:m:21:PHE:HD1	3:m:53:HIS:HB2	1.79	0.48
3:m:93:ILE:HD11	3:m:123:PHE:CD2	2.48	0.48
3:m:227:MET:O	3:m:230:GLU:HG3	2.13	0.48
3:p:1:MET:HG2	3:p:3:LYS:H	1.79	0.48
3:Q:227:MET:O	3:Q:230:GLU:HG3	2.13	0.48
1:C:34:TYR:CD2	1:C:71:PRO:HD3	2.49	0.47
3:H:21:PHE:HD1	3:H:53:HIS:HB2	1.79	0.47
3:I:256:GLU:O	3:I:260:THR:HG23	2.13	0.47
3:m:201:LEU:HD12	3:m:202:GLY:H	1.79	0.47
3:p:231:ARG:HB2	2:r:250:ALA:HB1	1.96	0.47
3:P:77:ASP:OD2	3:P:77:ASP:N	2.46	0.47
3:Q:201:LEU:HD12	3:Q:202:GLY:H	1.79	0.47
2:F:110:ARG:N	2:F:113:LYS:O	2.47	0.47
3:m:126:ARG:HH22	3:m:160:ALA:HA	1.80	0.47
2:j:110:ARG:N	2:j:113:LYS:O	2.47	0.47
3:p:119:LEU:CD1	3:p:198:MET:HE3	2.34	0.47
2:O:149:MET:HE2	2:O:192:LEU:HD23	1.95	0.47
2:E:102:GLU:HA	2:E:120:PRO:HB2	1.96	0.47
2:F:302:GLN:OE1	3:G:282:LEU:CD1	2.60	0.47
3:I:231:ARG:HB2	2:U:250:ALA:HB1	1.96	0.47
3:I:247:GLU:OE2	2:O:285:ARG:CD	2.56	0.47
3:I:296:PHE:CD2	3:P:325:TYR:HD1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:199:TYR:CE2	2:i:211:VAL:CG1	2.97	0.47
2:h:102:GLU:HA	2:h:120:PRO:HB2	1.96	0.47
2:h:242:ARG:HH22	2:h:248:LYS:HD2	1.77	0.47
2:j:327:TYR:O	2:j:331:MET:HG2	2.14	0.47
3:p:33:ARG:HA	3:p:60:GLU:HA	1.96	0.47
3:p:121:ARG:C	3:p:121:ARG:CD	2.86	0.47
2:S:215:ASP:OD1	2:S:218:ARG:NH2	2.47	0.47
3:G:93:ILE:HG23	3:G:208:VAL:HG22	1.97	0.47
3:I:312:ASP:OD2	2:O:340:LYS:NZ	2.47	0.47
1:a:34:TYR:CD2	1:a:71:PRO:HD3	2.49	0.47
1:b:56:ILE:HD11	1:b:70:ILE:CD1	2.45	0.47
1:d:54:ARG:HH22	1:d:70:ILE:N	2.12	0.47
2:j:213:ARG:NH1	2:j:235:ASP:OD1	2.46	0.47
2:j:250:ALA:HB1	3:l:231:ARG:HB2	1.96	0.47
2:N:135:VAL:HG21	2:N:170:PRO:HB3	1.97	0.47
2:N:159:VAL:HG11	2:N:196:ILE:HD11	1.95	0.47
2:N:330:THR:HG21	3:Q:300:LEU:HD22	1.96	0.47
3:Q:126:ARG:HH22	3:Q:160:ALA:HA	1.80	0.47
1:V:38:LEU:HA	1:V:41:VAL:HG12	1.94	0.47
2:E:135:VAL:HG21	2:E:170:PRO:HB3	1.97	0.47
3:G:316:MET:HE3	3:G:316:MET:HB3	1.76	0.47
2:i:250:ALA:HB1	3:k:231:ARG:HB2	1.96	0.47
3:k:77:ASP:OD2	3:k:77:ASP:N	2.46	0.47
2:q:268:ALA:O	2:q:272:THR:HG23	2.13	0.47
1:L:56:ILE:HD11	1:L:70:ILE:CD1	2.45	0.47
3:P:93:ILE:HG23	3:P:208:VAL:HG22	1.97	0.47
2:F:327:TYR:O	2:F:331:MET:HG2	2.14	0.47
1:e:42:ASN:HA	1:e:84:LYS:HE2	1.96	0.47
1:c:54:ARG:HH22	1:c:70:ILE:N	2.12	0.47
2:j:340:LYS:HE2	3:R:312:ASP:OD2	2.14	0.47
3:n:201:LEU:HD12	3:n:202:GLY:H	1.80	0.47
3:H:126:ARG:HH22	3:H:160:ALA:HA	1.80	0.47
3:H:201:LEU:HD12	3:H:202:GLY:H	1.79	0.47
3:I:1:MET:HG2	3:I:3:LYS:H	1.79	0.47
3:I:121:ARG:NH2	2:O:234:LEU:HD22	2.29	0.47
1:e:89:VAL:HG22	1:f:33:ASP:CG	2.40	0.47
2:g:135:VAL:HG21	2:g:170:PRO:HB3	1.97	0.47
3:o:8:ILE:O	3:o:11:ILE:HG22	2.15	0.47
3:o:43:ASN:OD1	3:o:44:LYS:N	2.47	0.47
3:o:123:PHE:O	3:o:127:LEU:CB	2.58	0.47
2:q:148:VAL:HG22	2:q:158:ARG:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:s:40:GLU:OE1	1:s:66:TYR:OH	2.16	0.47
2:h:330:THR:HG21	3:n:300:LEU:HD22	1.96	0.47
3:l:327:LYS:HB3	3:R:321:ASP:OD2	2.14	0.47
1:t:89:VAL:HG22	1:v:33:ASP:CG	2.40	0.47
1:L:34:TYR:CD2	1:L:71:PRO:HD3	2.49	0.47
1:L:51:ILE:HD12	1:M:71:PRO:HB3	1.97	0.47
2:N:142:GLU:OE2	2:N:162:ASN:ND2	2.40	0.47
3:Q:71:THR:HB	3:Q:94:LYS:HZ3	1.80	0.47
3:R:1:MET:HG2	3:R:3:LYS:H	1.79	0.47
3:R:43:ASN:OD1	3:R:44:LYS:N	2.47	0.47
2:F:209:ARG:CZ	3:o:78:ARG:HG2	2.44	0.47
3:I:108:GLY:H	3:I:114:GLN:HG2	1.80	0.47
2:i:272:THR:HA	2:i:275:VAL:HG12	1.96	0.47
3:m:321:ASP:OD1	3:m:322:PHE:N	2.48	0.47
3:o:33:ARG:HA	3:o:60:GLU:HA	1.96	0.47
3:o:231:ARG:HB2	2:q:250:ALA:HB1	1.96	0.47
1:s:89:VAL:HG22	1:u:33:ASP:CG	2.40	0.47
2:j:213:ARG:HD2	2:j:236:VAL:HG13	1.95	0.47
3:R:8:ILE:O	3:R:11:ILE:HG22	2.15	0.47
2:F:272:THR:HA	2:F:275:VAL:HG12	1.96	0.47
1:W:45:GLN:HE22	1:W:60:LYS:HD3	1.80	0.47
2:j:188:THR:CA	2:j:220:LEU:HD11	2.45	0.47
3:n:321:ASP:OD1	3:n:322:PHE:N	2.48	0.47
3:p:43:ASN:OD1	3:p:44:LYS:N	2.48	0.47
2:O:110:ARG:N	2:O:113:LYS:O	2.47	0.47
2:O:250:ALA:HB1	3:P:231:ARG:HB2	1.96	0.47
3:Q:321:ASP:OD1	3:Q:322:PHE:N	2.48	0.47
1:B:48:GLU:HG3	1:B:59:THR:OG1	2.15	0.47
2:E:330:THR:HG21	3:H:300:LEU:HD22	1.96	0.47
2:F:274:GLU:OE2	2:F:278:ARG:NH2	2.48	0.47
3:I:277:ALA:HB1	2:O:314:GLU:OE1	2.15	0.47
3:o:257:VAL:HG21	2:q:275:VAL:HG12	1.97	0.47
3:o:292:ASP:OD1	3:o:293:PHE:N	2.48	0.47
2:h:135:VAL:HG21	2:h:170:PRO:HB3	1.97	0.47
2:j:138:GLU:CD	3:R:108:GLY:CA	2.74	0.47
2:j:227:TYR:OH	3:l:92:TYR:HE2	1.97	0.47
2:j:229:MET:CE	2:j:231:ILE:HD12	2.45	0.47
3:l:11:ILE:HA	3:l:14:VAL:HG12	1.97	0.47
3:p:8:ILE:O	3:p:11:ILE:HG22	2.15	0.47
3:Q:87:LEU:HD13	3:Q:213:ILE:HG23	1.97	0.47
3:R:108:GLY:H	3:R:114:GLN:HG2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:138:GLU:CD	3:o:108:GLY:CA	2.74	0.46
3:H:87:LEU:HD13	3:H:213:ILE:HG23	1.97	0.46
3:H:225:ASN:ND2	2:U:259:GLU:OE2	2.48	0.46
3:I:292:ASP:OD1	3:I:293:PHE:N	2.48	0.46
3:m:225:ASN:ND2	2:q:259:GLU:OE2	2.48	0.46
2:j:340:LYS:NZ	3:R:312:ASP:OD2	2.45	0.46
3:p:131:ILE:O	3:p:133:ARG:N	2.48	0.46
2:O:209:ARG:HG2	2:O:238:PHE:CD2	2.50	0.46
3:I:43:ASN:OD1	3:I:44:LYS:N	2.47	0.46
3:I:262:ALA:C	2:O:299:LEU:HD13	2.40	0.46
1:a:56:ILE:HD11	1:a:70:ILE:CD1	2.44	0.46
2:i:149:MET:HE1	2:i:193:ARG:CA	2.40	0.46
2:i:299:LEU:HD13	3:p:263:GLU:HA	1.96	0.46
1:s:42:ASN:HA	1:s:84:LYS:HE2	1.96	0.46
1:X:45:GLN:HE22	1:X:60:LYS:HD3	1.80	0.46
1:b:34:TYR:CD2	1:b:71:PRO:HD3	2.49	0.46
1:K:48:GLU:HG3	1:K:59:THR:OG1	2.15	0.46
2:N:239:GLN:OE1	3:P:124:SER:OG	2.33	0.46
2:S:148:VAL:HG22	2:S:158:ARG:HG2	1.96	0.46
2:E:251:PHE:CE2	3:G:84:LYS:HD3	2.50	0.46
2:F:340:LYS:NZ	3:o:312:ASP:OD2	2.45	0.46
3:I:33:ARG:HA	3:I:60:GLU:HA	1.96	0.46
2:i:274:GLU:OE2	2:i:278:ARG:NH2	2.48	0.46
2:i:314:GLU:OE1	3:p:277:ALA:CA	2.63	0.46
3:k:93:ILE:HG23	3:k:208:VAL:HG22	1.97	0.46
3:o:135:ASP:O	3:o:139:ILE:HG12	2.14	0.46
1:b:51:ILE:HD12	1:d:71:PRO:HB3	1.97	0.46
2:j:213:ARG:CG	2:j:213:ARG:NH2	2.72	0.46
3:p:135:ASP:O	3:p:139:ILE:HG12	2.14	0.46
1:C:56:ILE:HD11	1:C:70:ILE:CD1	2.45	0.46
3:I:257:VAL:HG21	2:U:275:VAL:HG12	1.97	0.46
2:U:148:VAL:HG22	2:U:158:ARG:HG2	1.96	0.46
3:k:11:ILE:HA	3:k:14:VAL:HG12	1.97	0.46
3:m:87:LEU:HD13	3:m:213:ILE:HG23	1.97	0.46
3:n:87:LEU:HD13	3:n:213:ILE:HG23	1.97	0.46
3:n:225:ASN:ND2	2:r:259:GLU:OE2	2.48	0.46
3:p:292:ASP:OD1	3:p:293:PHE:N	2.48	0.46
2:N:102:GLU:HA	2:N:120:PRO:HB2	1.96	0.46
3:P:11:ILE:HA	3:P:14:VAL:HG12	1.97	0.46
1:C:51:ILE:HD12	1:D:71:PRO:HB3	1.97	0.46
2:U:327:TYR:CZ	3:P:328:THR:CA	2.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:81:LEU:HD22	1:Y:86:VAL:HG21	1.98	0.46
1:a:51:ILE:HD12	1:c:71:PRO:HB3	1.97	0.46
1:Z:48:GLU:HG3	1:Z:59:THR:OG1	2.16	0.46
1:Z:81:LEU:HD22	1:Z:86:VAL:HG21	1.98	0.46
1:K:56:ILE:HD11	1:K:70:ILE:HD11	1.97	0.46
2:O:327:TYR:O	2:O:331:MET:HG2	2.14	0.46
1:T:89:VAL:HG22	1:V:33:ASP:CG	2.40	0.46
2:E:239:GLN:OE1	3:G:124:SER:OG	2.33	0.46
3:I:8:ILE:O	3:I:11:ILE:HG22	2.15	0.46
1:Z:54:ARG:NH2	1:v:91:GLU:O	2.49	0.46
2:j:299:LEU:HD13	3:R:262:ALA:HB3	1.98	0.46
3:l:93:ILE:HG23	3:l:208:VAL:HG22	1.97	0.46
3:H:95:TRP:HA	3:H:205:VAL:HA	1.98	0.46
3:H:321:ASP:OD1	3:H:322:PHE:N	2.48	0.46
3:I:298:ARG:CZ	3:I:301:ARG:HH21	2.28	0.46
3:n:126:ARG:HH22	3:n:160:ALA:HA	1.79	0.46
1:J:45:GLN:HE22	1:J:60:LYS:HD3	1.80	0.46
3:P:321:ASP:O	3:P:324:ARG:NH1	2.36	0.46
3:Q:225:ASN:ND2	2:S:259:GLU:OE2	2.48	0.46
1:A:91:GLU:HG2	1:A:92:PRO:HD2	1.98	0.46
3:I:284:ALA:HB1	2:O:318:ALA:HB3	1.97	0.46
2:g:251:PHE:CE2	3:k:84:LYS:HD3	2.50	0.46
1:Z:56:ILE:HD11	1:Z:70:ILE:HD11	1.97	0.46
2:j:172:LYS:O	2:j:176:SER:OG	2.18	0.46
3:Q:95:TRP:HA	3:Q:205:VAL:HA	1.98	0.46
3:G:11:ILE:HA	3:G:14:VAL:HG12	1.97	0.46
1:a:34:TYR:OH	1:a:77:LEU:HD12	2.16	0.46
3:o:108:GLY:H	3:o:114:GLN:HG2	1.80	0.46
3:p:257:VAL:HG21	2:r:275:VAL:HG12	1.97	0.46
3:p:298:ARG:CZ	3:p:301:ARG:HH21	2.28	0.46
3:R:33:ARG:HA	3:R:60:GLU:HA	1.97	0.46
1:T:42:ASN:HA	1:T:84:LYS:HE2	1.96	0.46
1:B:56:ILE:HD11	1:B:70:ILE:HD11	1.97	0.46
1:B:81:LEU:HD22	1:B:86:VAL:HG21	1.98	0.46
3:o:123:PHE:O	3:o:127:LEU:N	2.38	0.46
2:h:251:PHE:CE2	3:l:84:LYS:HD3	2.50	0.46
2:j:195:VAL:HG21	2:j:215:ASP:HB3	1.78	0.46
2:j:274:GLU:OE2	2:j:278:ARG:NH2	2.48	0.46
3:p:272:ARG:HD3	2:r:293:TYR:CD1	2.41	0.46
3:R:257:VAL:HG21	2:S:275:VAL:HG12	1.97	0.46
3:R:298:ARG:CZ	3:R:301:ARG:HH21	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:161:MET:CE	2:j:212:ILE:HG22	2.20	0.45
2:j:244:PRO:HG2	2:j:247:VAL:HG22	1.98	0.45
3:p:83:GLU:HG3	3:p:85:LYS:HG3	1.98	0.45
2:r:85:ALA:HA	2:r:88:ILE:HG12	1.98	0.45
1:K:54:ARG:NH2	1:V:91:GLU:O	2.49	0.45
1:L:34:TYR:OH	1:L:77:LEU:HD12	2.17	0.45
2:O:119:GLU:HB3	2:O:120:PRO:HD2	1.99	0.45
2:O:148:VAL:HG13	2:O:156:VAL:HG13	1.99	0.45
2:O:188:THR:CB	2:O:220:LEU:HD21	2.44	0.45
2:F:299:LEU:HD12	3:o:262:ALA:HB1	1.97	0.45
3:H:321:ASP:HB2	3:I:328:THR:HG21	1.95	0.45
3:k:328:THR:HB	2:r:327:TYR:OH	2.15	0.45
2:j:119:GLU:HB3	2:j:120:PRO:HD2	1.98	0.45
2:O:244:PRO:HG2	2:O:247:VAL:HG22	1.98	0.45
3:R:292:ASP:OD1	3:R:293:PHE:N	2.48	0.45
3:I:130:GLU:OE1	3:I:130:GLU:HA	2.16	0.45
2:q:85:ALA:HA	2:q:88:ILE:HG12	1.98	0.45
2:j:172:LYS:HD3	2:j:228:ASP:OD2	2.17	0.45
1:A:45:GLN:HE22	1:A:60:LYS:HD3	1.80	0.45
2:E:238:PHE:HZ	2:E:241:ALA:HB2	1.82	0.45
2:U:85:ALA:HA	2:U:88:ILE:HG12	1.98	0.45
1:Y:48:GLU:HG3	1:Y:59:THR:OG1	2.15	0.45
2:i:138:GLU:OE1	3:p:108:GLY:N	2.44	0.45
3:p:307:PHE:HB2	2:r:334:VAL:HG23	1.99	0.45
2:N:251:PHE:CE2	3:P:84:LYS:HD3	2.50	0.45
1:A:36:THR:HA	1:A:39:GLN:CD	2.42	0.45
2:F:148:VAL:HG13	2:F:156:VAL:HG13	1.99	0.45
1:Y:54:ARG:NH2	1:u:91:GLU:O	2.49	0.45
1:Y:56:ILE:HD11	1:Y:70:ILE:HD11	1.97	0.45
2:i:119:GLU:HB3	2:i:120:PRO:HD2	1.99	0.45
2:i:344:ASN:OD1	2:i:345:ASP:N	2.50	0.45
3:o:307:PHE:HB2	2:q:334:VAL:HG23	1.99	0.45
3:p:119:LEU:CD1	3:p:155:LEU:HD21	2.46	0.45
3:m:95:TRP:HA	3:m:205:VAL:HA	1.98	0.45
3:o:267:GLN:C	3:o:267:GLN:CD	2.85	0.45
1:u:46:VAL:HA	1:u:60:LYS:HA	1.99	0.45
1:b:91:GLU:HA	1:d:31:LYS:HZ1	1.81	0.45
2:j:308:PHE:CE2	3:l:294:TYR:HB2	2.52	0.45
3:p:130:GLU:CD	3:p:133:ARG:NH1	2.73	0.45
2:r:223:THR:O	2:r:226:PRO:HD2	2.17	0.45
2:U:223:THR:O	2:U:226:PRO:HD2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:238:PHE:HZ	2:g:241:ALA:HB2	1.82	0.45
3:o:298:ARG:CZ	3:o:301:ARG:HH21	2.28	0.45
1:X:91:GLU:HG2	1:X:92:PRO:HD2	1.98	0.45
2:j:223:THR:HG23	3:l:209:ARG:CZ	2.47	0.45
1:K:81:LEU:HD22	1:K:86:VAL:HG21	1.98	0.45
1:M:36:THR:HA	1:M:39:GLN:HE21	1.82	0.45
2:O:344:ASN:OD1	2:O:345:ASP:N	2.50	0.45
3:P:30:ILE:HD11	3:P:100:PHE:HB3	1.98	0.45
3:Q:303:TYR:OH	3:R:322:PHE:O	2.26	0.45
2:F:119:GLU:HB3	2:F:120:PRO:HD2	1.99	0.45
2:F:292:ALA:HB1	3:o:258:THR:HG21	1.99	0.45
3:H:43:ASN:OD1	3:H:44:LYS:N	2.50	0.45
3:I:262:ALA:C	2:O:299:LEU:HD12	2.42	0.45
1:f:46:VAL:HA	1:f:60:LYS:HA	1.99	0.45
1:c:54:ARG:NH1	1:c:70:ILE:HB	2.28	0.45
3:o:271:MET:HE2	2:q:291:ARG:HA	1.95	0.45
3:l:30:ILE:HD11	3:l:100:PHE:HB3	1.98	0.45
3:p:263:GLU:HG2	3:p:267:GLN:NE2	2.32	0.45
1:J:36:THR:HA	1:J:39:GLN:CD	2.42	0.45
3:R:83:GLU:HG3	3:R:85:LYS:HG3	1.98	0.45
2:S:85:ALA:HA	2:S:88:ILE:HG12	1.98	0.45
1:T:38:LEU:HD23	1:T:38:LEU:HA	1.86	0.45
1:A:74:ASP:OD1	1:A:76:LYS:HG2	2.17	0.45
1:B:54:ARG:NH2	1:f:91:GLU:O	2.49	0.45
1:C:34:TYR:OH	1:C:77:LEU:HD12	2.16	0.45
2:F:217:GLN:HG2	2:F:221:GLU:OE2	2.17	0.45
2:F:244:PRO:HG2	2:F:247:VAL:HG22	1.98	0.45
3:G:326:MET:HE2	3:G:326:MET:CA	2.45	0.45
1:W:74:ASP:OD1	1:W:76:LYS:HG2	2.17	0.45
1:a:37:PHE:CE1	1:a:58:VAL:HG21	2.52	0.45
2:j:344:ASN:OD1	2:j:345:ASP:N	2.50	0.45
3:n:95:TRP:HA	3:n:205:VAL:HA	1.98	0.45
1:J:91:GLU:HG2	1:J:92:PRO:HD2	1.98	0.45
2:O:274:GLU:OE2	2:O:278:ARG:NH2	2.48	0.45
1:C:70:ILE:H	1:C:70:ILE:HD12	1.82	0.45
3:G:30:ILE:HD11	3:G:100:PHE:HB3	1.98	0.45
3:I:158:GLY:HA3	3:I:197:SER:HB2	1.99	0.45
2:i:285:ARG:HH11	3:p:247:GLU:CD	2.18	0.45
3:k:30:ILE:HD11	3:k:100:PHE:HB3	1.98	0.45
2:j:333:LYS:HE3	2:j:333:LYS:HB2	1.74	0.45
1:v:46:VAL:HA	1:v:60:LYS:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:74:ASP:OD1	1:J:76:LYS:HG2	2.17	0.45
1:L:37:PHE:CE1	1:L:58:VAL:HG21	2.52	0.45
1:V:46:VAL:HA	1:V:60:LYS:HA	1.99	0.45
3:I:83:GLU:HG3	3:I:85:LYS:HG3	1.98	0.44
3:m:43:ASN:OD1	3:m:44:LYS:N	2.50	0.44
1:b:70:ILE:H	1:b:70:ILE:HD12	1.82	0.44
1:d:40:GLU:HG3	1:d:45:GLN:NE2	2.32	0.44
2:j:283:ALA:HB1	3:l:264:ALA:HB2	1.98	0.44
3:p:37:VAL:HA	3:p:40:ASP:OD2	2.18	0.44
1:M:40:GLU:HG3	1:M:45:GLN:NE2	2.32	0.44
2:O:283:ALA:HB1	3:P:264:ALA:HB2	1.99	0.44
3:R:307:PHE:HB2	2:S:334:VAL:HG23	1.99	0.44
2:S:238:PHE:CZ	2:S:241:ALA:HB2	2.52	0.44
1:W:36:THR:HA	1:W:39:GLN:CD	2.42	0.44
1:W:91:GLU:HG2	1:W:92:PRO:HD2	1.98	0.44
1:c:36:THR:HA	1:c:39:GLN:HE21	1.82	0.44
2:g:239:GLN:OE1	3:k:124:SER:OG	2.33	0.44
3:o:79:PHE:HE2	3:o:128:ARG:HB2	1.81	0.44
1:X:87:LYS:HD2	1:X:87:LYS:C	2.42	0.44
1:b:34:TYR:OH	1:b:77:LEU:HD12	2.16	0.44
1:b:37:PHE:CE1	1:b:58:VAL:HG21	2.52	0.44
3:l:31:THR:HG21	3:l:38:LEU:HD12	2.00	0.44
1:J:34:TYR:O	1:J:38:LEU:HD23	2.17	0.44
1:L:70:ILE:H	1:L:70:ILE:HD12	1.82	0.44
1:M:45:GLN:O	1:M:60:LYS:HE2	2.17	0.44
3:R:158:GLY:HA3	3:R:197:SER:HB2	1.99	0.44
2:S:223:THR:O	2:S:226:PRO:HD2	2.17	0.44
1:V:50:ARG:HG2	1:V:89:VAL:HB	1.99	0.44
1:A:87:LYS:HD2	1:A:87:LYS:C	2.42	0.44
1:C:56:ILE:HD11	1:C:70:ILE:HD12	1.99	0.44
2:F:344:ASN:OD1	2:F:345:ASP:N	2.50	0.44
2:U:288:GLU:OE1	2:U:291:ARG:NH1	2.51	0.44
2:i:244:PRO:HG2	2:i:247:VAL:HG22	1.98	0.44
2:i:283:ALA:HB1	3:k:264:ALA:HB2	1.98	0.44
3:o:83:GLU:HG3	3:o:85:LYS:HG3	1.98	0.44
1:u:50:ARG:HG2	1:u:89:VAL:HB	1.99	0.44
3:n:158:GLY:HA3	3:n:194:ASN:ND2	2.33	0.44
1:L:79:ASP:O	1:L:82:LEU:HG	2.18	0.44
3:P:31:THR:HG21	3:P:38:LEU:HD12	1.99	0.44
3:P:117:VAL:O	3:P:121:ARG:HG2	2.17	0.44
3:Q:21:PHE:CE2	3:Q:62:VAL:HG11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:37:VAL:HA	3:R:40:ASP:OD2	2.18	0.44
1:C:37:PHE:CE1	1:C:58:VAL:HG21	2.52	0.44
1:C:79:ASP:O	1:C:82:LEU:HG	2.18	0.44
2:F:283:ALA:HB1	3:G:264:ALA:HB2	1.98	0.44
2:F:343:VAL:HG12	3:o:315:VAL:CG2	2.47	0.44
3:G:198:MET:HE3	3:G:203:ILE:HB	2.00	0.44
3:H:158:GLY:HA3	3:H:194:ASN:ND2	2.33	0.44
1:W:34:TYR:O	1:W:38:LEU:HD23	2.18	0.44
2:i:148:VAL:HG13	2:i:156:VAL:HG13	1.99	0.44
2:i:331:MET:HB3	3:k:322:PHE:CD1	2.53	0.44
1:d:45:GLN:O	1:d:60:LYS:HE2	2.17	0.44
2:j:84:ALA:O	2:j:88:ILE:HG12	2.18	0.44
2:r:238:PHE:CZ	2:r:241:ALA:HB2	2.52	0.44
2:O:213:ARG:HB3	2:O:213:ARG:CZ	2.47	0.44
3:Q:148:THR:HB	3:Q:208:VAL:O	2.18	0.44
1:D:36:THR:HA	1:D:39:GLN:HE21	1.82	0.44
1:D:40:GLU:HG3	1:D:45:GLN:NE2	2.33	0.44
1:D:45:GLN:O	1:D:60:LYS:HE2	2.17	0.44
2:F:84:ALA:O	2:F:88:ILE:HG12	2.18	0.44
3:G:326:MET:CE	3:o:303:TYR:CD2	2.72	0.44
3:I:307:PHE:HB2	2:U:334:VAL:HG23	1.99	0.44
1:W:87:LYS:HD2	1:W:87:LYS:C	2.42	0.44
2:i:84:ALA:O	2:i:88:ILE:HG12	2.18	0.44
2:i:266:ARG:HD2	3:p:229:ALA:HB1	1.99	0.44
3:o:139:ILE:O	3:o:143:SER:HB3	2.18	0.44
1:d:54:ARG:NH1	1:d:70:ILE:HB	2.28	0.44
2:h:162:ASN:HB3	2:h:237:ASN:OD1	2.18	0.44
2:h:238:PHE:HZ	2:h:241:ALA:HB2	1.82	0.44
2:j:292:ALA:HB1	3:R:258:THR:HG21	1.99	0.44
3:n:43:ASN:OD1	3:n:44:LYS:N	2.50	0.44
1:J:87:LYS:HD2	1:J:87:LYS:C	2.42	0.44
1:K:37:PHE:HB2	1:K:68:THR:HG21	2.00	0.44
3:I:37:VAL:HA	3:I:40:ASP:OD2	2.18	0.44
1:c:45:GLN:O	1:c:60:LYS:HE2	2.17	0.44
2:g:162:ASN:HB3	2:g:237:ASN:OD1	2.18	0.44
2:i:227:TYR:OH	3:k:94:LYS:HG3	2.14	0.44
2:i:305:VAL:HG13	3:k:286:ALA:CB	2.48	0.44
3:m:103:TYR:O	3:m:107:THR:OG1	2.31	0.44
1:X:36:THR:HA	1:X:39:GLN:CD	2.42	0.44
2:h:120:PRO:O	3:l:36:LYS:HB3	2.18	0.44
1:L:56:ILE:HD11	1:L:70:ILE:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:158:GLY:HA3	3:Q:194:ASN:ND2	2.33	0.44
1:A:34:TYR:O	1:A:38:LEU:HD23	2.17	0.44
2:F:199:TYR:CE2	2:F:212:ILE:CD1	3.01	0.44
3:G:31:THR:HG21	3:G:38:LEU:HD12	2.00	0.44
1:a:56:ILE:HD11	1:a:70:ILE:HD12	1.99	0.44
1:a:70:ILE:HD12	1:a:70:ILE:H	1.82	0.44
2:i:143:LEU:HD22	2:i:165:TYR:HE1	1.83	0.44
3:k:117:VAL:O	3:k:121:ARG:HG2	2.17	0.44
3:m:88:ILE:O	3:m:214:ASN:N	2.51	0.44
1:d:36:THR:HA	1:d:39:GLN:HE21	1.82	0.44
2:j:148:VAL:HG13	2:j:156:VAL:HG13	1.99	0.44
3:l:316:MET:HE3	3:l:316:MET:HB3	1.76	0.44
1:K:60:LYS:HD3	1:K:64:ASN:HB2	2.00	0.44
2:N:238:PHE:HZ	2:N:241:ALA:HB2	1.82	0.44
3:P:198:MET:HE3	3:P:203:ILE:HB	2.00	0.44
3:Q:90:ASP:N	3:Q:90:ASP:OD1	2.50	0.44
1:T:50:ARG:HG2	1:T:89:VAL:HB	2.00	0.44
3:G:78:ARG:HA	3:G:87:LEU:O	2.18	0.44
3:G:117:VAL:O	3:G:121:ARG:HG2	2.17	0.44
3:I:81:THR:HG22	3:I:85:LYS:H	1.83	0.44
1:Y:41:VAL:HG22	1:Y:46:VAL:HG11	2.00	0.44
3:k:31:THR:HG21	3:k:38:LEU:HD12	2.00	0.44
3:o:127:LEU:C	3:o:127:LEU:CD1	2.86	0.44
1:X:34:TYR:O	1:X:38:LEU:HD23	2.17	0.44
1:X:74:ASP:OD1	1:X:76:LYS:HG2	2.17	0.44
2:j:225:ARG:N	2:j:226:PRO:HD2	2.33	0.44
3:l:117:VAL:O	3:l:121:ARG:HG2	2.17	0.44
3:p:307:PHE:HD2	2:r:338:THR:HG21	1.83	0.44
3:P:78:ARG:HA	3:P:87:LEU:O	2.18	0.44
2:F:307:ARG:HH12	3:o:272:ARG:HB3	1.83	0.44
2:U:126:PRO:HB2	2:U:129:ILE:HB	2.00	0.44
2:j:343:VAL:HG12	3:R:315:VAL:CG2	2.47	0.44
2:N:137:VAL:HA	2:N:167:VAL:HG13	2.00	0.44
2:N:162:ASN:HB3	2:N:237:ASN:OD1	2.18	0.44
3:Q:43:ASN:OD1	3:Q:44:LYS:N	2.50	0.44
1:A:45:GLN:NE2	1:A:60:LYS:HB3	2.33	0.43
2:E:120:PRO:O	3:G:36:LYS:HB3	2.18	0.43
2:F:143:LEU:HD22	2:F:165:TYR:HE1	1.83	0.43
3:H:21:PHE:CE2	3:H:62:VAL:HG11	2.53	0.43
1:e:31:LYS:HB2	1:e:31:LYS:HE2	1.76	0.43
1:e:50:ARG:HG2	1:e:89:VAL:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:137:VAL:HA	2:g:167:VAL:HG13	2.00	0.43
2:i:105:ARG:HD2	2:i:120:PRO:HD3	2.00	0.43
2:i:138:GLU:OE1	3:p:108:GLY:HA2	2.06	0.43
2:i:208:GLY:O	2:i:212:ILE:CG2	2.41	0.43
3:m:158:GLY:HA3	3:m:194:ASN:ND2	2.33	0.43
3:o:69:ILE:HB	2:q:177:VAL:HG22	2.00	0.43
2:q:223:THR:O	2:q:226:PRO:HD2	2.17	0.43
1:b:79:ASP:O	1:b:82:LEU:HG	2.18	0.43
2:h:242:ARG:HH11	2:h:242:ARG:HG3	1.83	0.43
2:j:216:THR:O	2:j:220:LEU:HB2	2.17	0.43
2:j:341:VAL:HB	3:l:315:VAL:HG22	2.00	0.43
3:p:139:ILE:O	3:p:143:SER:HB3	2.18	0.43
1:v:50:ARG:HG2	1:v:89:VAL:HB	1.99	0.43
1:C:91:GLU:HA	1:D:31:LYS:NZ	2.34	0.43
3:H:148:THR:HB	3:H:208:VAL:O	2.17	0.43
1:a:79:ASP:O	1:a:82:LEU:HG	2.18	0.43
1:c:40:GLU:HG3	1:c:45:GLN:NE2	2.33	0.43
2:g:242:ARG:HH11	2:g:242:ARG:HG3	1.83	0.43
3:o:37:VAL:HA	3:o:40:ASP:OD2	2.18	0.43
2:O:84:ALA:O	2:O:88:ILE:HG12	2.18	0.43
2:O:225:ARG:HB3	2:O:226:PRO:HD3	2.00	0.43
3:R:69:ILE:HB	2:S:177:VAL:HG22	2.01	0.43
1:B:60:LYS:HD3	1:B:64:ASN:HB2	2.00	0.43
3:I:139:ILE:O	3:I:143:SER:HB3	2.18	0.43
3:I:272:ARG:HG2	2:U:293:TYR:CE1	2.52	0.43
2:i:219:GLU:CD	2:i:219:GLU:C	2.87	0.43
3:k:78:ARG:HA	3:k:87:LEU:O	2.18	0.43
3:m:148:THR:HB	3:m:208:VAL:O	2.17	0.43
2:q:288:GLU:OE1	2:q:291:ARG:NH1	2.51	0.43
1:u:40:GLU:OE1	1:u:66:TYR:OH	2.27	0.43
2:j:234:LEU:HD22	3:R:121:ARG:HH12	0.54	0.43
3:n:66:ASP:OD1	3:n:66:ASP:N	2.51	0.43
3:p:79:PHE:CD2	3:p:128:ARG:CB	3.01	0.43
2:O:225:ARG:HD3	2:O:225:ARG:C	2.43	0.43
2:O:341:VAL:HB	3:P:315:VAL:HG22	2.00	0.43
1:A:36:THR:HA	1:A:39:GLN:NE2	2.34	0.43
1:B:37:PHE:HB2	1:B:68:THR:HG21	2.00	0.43
2:E:242:ARG:HH11	2:E:242:ARG:HG3	1.83	0.43
2:F:333:LYS:HB2	2:F:333:LYS:HE3	1.74	0.43
3:I:244:GLU:OE1	2:O:277:PRO:HB3	2.18	0.43
2:g:229:MET:HE3	2:g:229:MET:HB2	1.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:k:327:LYS:HE3	3:k:327:LYS:HB2	1.62	0.43
2:q:126:PRO:HB2	2:q:129:ILE:HB	2.00	0.43
1:b:56:ILE:HD11	1:b:70:ILE:HD12	1.99	0.43
3:n:88:ILE:O	3:n:214:ASN:N	2.51	0.43
3:p:95:TRP:CZ2	3:p:116:GLU:CD	2.95	0.43
2:O:213:ARG:CD	2:O:237:ASN:C	2.92	0.43
3:R:139:ILE:O	3:R:143:SER:HB3	2.18	0.43
2:E:162:ASN:HB3	2:E:237:ASN:OD1	2.18	0.43
3:I:69:ILE:HB	2:U:177:VAL:HG22	2.01	0.43
3:I:225:ASN:ND2	2:O:259:GLU:OE2	2.35	0.43
3:o:158:GLY:HA3	3:o:197:SER:HB2	1.99	0.43
2:q:243:PRO:HB2	2:q:247:VAL:HG23	2.00	0.43
1:X:36:THR:HA	1:X:39:GLN:NE2	2.34	0.43
1:Z:41:VAL:HG22	1:Z:46:VAL:HG11	2.00	0.43
1:b:91:GLU:HA	1:d:31:LYS:NZ	2.34	0.43
2:j:105:ARG:HD2	2:j:120:PRO:HD3	2.00	0.43
2:r:288:GLU:OE1	2:r:291:ARG:NH1	2.51	0.43
1:t:50:ARG:HG2	1:t:89:VAL:HB	2.00	0.43
1:J:36:THR:HA	1:J:39:GLN:NE2	2.34	0.43
1:J:87:LYS:HD3	1:L:33:ASP:OD2	2.19	0.43
2:N:120:PRO:O	3:P:36:LYS:HB3	2.18	0.43
2:F:105:ARG:HD2	2:F:120:PRO:HD3	2.00	0.43
3:I:17:TYR:O	3:I:20:VAL:HG12	2.19	0.43
1:f:50:ARG:HG2	1:f:89:VAL:HB	1.99	0.43
1:Y:60:LYS:HD3	1:Y:64:ASN:HB2	2.00	0.43
1:Z:37:PHE:HB2	1:Z:68:THR:HG21	2.00	0.43
2:j:296:GLN:O	2:j:300:GLU:HG3	2.05	0.43
1:t:31:LYS:HB2	1:t:31:LYS:HE2	1.76	0.43
1:M:54:ARG:NH1	1:M:70:ILE:HB	2.28	0.43
2:N:242:ARG:HG3	2:N:242:ARG:HH11	1.83	0.43
2:O:187:ALA:O	2:O:220:LEU:CD1	2.67	0.43
3:P:107:THR:HG21	3:P:115:ALA:HB2	2.01	0.43
1:A:87:LYS:HD3	1:C:33:ASP:OD2	2.19	0.43
2:E:137:VAL:HA	2:E:167:VAL:HG13	2.00	0.43
2:E:182:ASP:OD1	2:E:185:ARG:NH2	2.52	0.43
2:i:138:GLU:CD	3:p:108:GLY:H	2.27	0.43
3:m:21:PHE:CE2	3:m:62:VAL:HG11	2.53	0.43
1:X:87:LYS:HD3	1:b:33:ASP:OD2	2.19	0.43
3:l:78:ARG:HA	3:l:87:LEU:O	2.18	0.43
3:n:21:PHE:CE2	3:n:62:VAL:HG11	2.53	0.43
3:n:148:THR:HB	3:n:208:VAL:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:45:GLN:NE2	1:J:60:LYS:HB3	2.33	0.43
2:S:288:GLU:OE1	2:S:291:ARG:NH1	2.51	0.43
3:I:263:GLU:HA	2:O:299:LEU:CD1	2.35	0.43
2:U:165:TYR:OH	2:U:181:ASP:OD1	2.32	0.43
1:Y:87:LYS:HB2	1:Y:87:LYS:HE2	1.82	0.43
2:g:120:PRO:O	3:k:36:LYS:HB3	2.18	0.43
3:k:198:MET:HE3	3:k:203:ILE:HB	2.00	0.43
3:k:322:PHE:O	3:k:322:PHE:CD2	2.72	0.43
1:s:50:ARG:HG2	1:s:89:VAL:HB	2.00	0.43
2:j:143:LEU:HD22	2:j:165:TYR:HE1	1.83	0.43
3:p:103:TYR:HB2	3:p:202:GLY:HA3	2.01	0.43
2:r:243:PRO:HB2	2:r:247:VAL:HG23	2.00	0.43
1:L:91:GLU:HA	1:M:31:LYS:NZ	2.34	0.43
2:N:246:GLU:H	2:N:246:GLU:CD	2.26	0.43
3:G:325:TYR:CD2	3:o:299:SER:CB	2.99	0.43
3:H:90:ASP:OD1	3:H:90:ASP:N	2.50	0.43
2:U:243:PRO:HB2	2:U:247:VAL:HG23	2.00	0.43
1:Y:59:THR:HG22	1:Y:65:ARG:HG2	2.00	0.43
3:o:17:TYR:O	3:o:20:VAL:HG12	2.19	0.43
1:Z:59:THR:HG22	1:Z:65:ARG:HG2	2.00	0.43
2:j:220:LEU:O	2:j:224:ILE:HG12	2.18	0.43
3:p:69:ILE:HB	2:r:177:VAL:HG22	2.01	0.43
2:r:298:ILE:O	2:r:302:GLN:HG3	2.19	0.43
3:R:307:PHE:HD2	2:S:338:THR:HG21	1.83	0.43
2:S:126:PRO:HB2	2:S:129:ILE:HB	2.00	0.43
1:W:36:THR:HA	1:W:39:GLN:NE2	2.34	0.43
1:W:45:GLN:NE2	1:W:60:LYS:HB3	2.33	0.43
1:a:91:GLU:HA	1:c:31:LYS:NZ	2.34	0.43
2:i:192:LEU:HD23	2:i:196:ILE:HG23	1.99	0.43
1:X:45:GLN:NE2	1:X:60:LYS:HB3	2.34	0.43
1:Z:60:LYS:HD3	1:Z:64:ASN:HB2	2.00	0.43
2:h:239:GLN:OE1	3:l:124:SER:OG	2.33	0.43
3:n:90:ASP:OD1	3:n:90:ASP:N	2.50	0.43
2:r:126:PRO:HB2	2:r:129:ILE:HB	2.00	0.43
2:O:143:LEU:HD22	2:O:165:TYR:HE1	1.83	0.43
1:T:60:LYS:HB3	1:T:60:LYS:HE2	1.79	0.43
1:V:40:GLU:OE1	1:V:66:TYR:OH	2.27	0.43
3:o:52:LEU:HG	2:q:111:PHE:CG	2.54	0.42
3:o:103:TYR:HB2	3:o:202:GLY:HA3	2.01	0.42
3:o:307:PHE:HD2	2:q:338:THR:HG21	1.83	0.42
2:h:246:GLU:H	2:h:246:GLU:CD	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:l:107:THR:HG21	3:l:115:ALA:HB2	2.01	0.42
3:l:198:MET:HE3	3:l:203:ILE:HB	2.00	0.42
1:k:41:VAL:HG22	1:k:46:VAL:HG11	2.00	0.42
2:n:179:SER:O	2:n:179:SER:OG	2.32	0.42
3:p:51:GLY:O	3:p:53:HIS:ND1	2.50	0.42
2:s:298:ILE:O	2:s:302:GLN:HG3	2.19	0.42
1:d:45:GLN:N	1:d:45:GLN:OE1	2.52	0.42
3:i:68:ARG:NE	2:u:178:THR:HG22	2.34	0.42
3:i:269:ARG:HE	3:i:269:ARG:HB2	1.72	0.42
1:c:45:GLN:OE1	1:c:45:GLN:N	2.52	0.42
2:i:333:LYS:HE3	2:i:333:LYS:HB2	1.74	0.42
3:o:68:ARG:NE	2:q:178:THR:HG22	2.34	0.42
1:z:55:GLU:HG3	1:z:69:TYR:CE2	2.54	0.42
1:b:57:ASN:HB3	1:b:65:ARG:NH2	2.34	0.42
2:h:182:ASP:OD1	2:h:185:ARG:NH2	2.52	0.42
2:j:299:LEU:HD13	3:r:262:ALA:CB	2.48	0.42
2:j:311:LEU:HD21	3:l:293:PHE:HZ	1.77	0.42
3:p:17:TYR:O	3:p:20:VAL:HG12	2.19	0.42
3:p:131:ILE:C	3:p:133:ARG:N	2.77	0.42
3:i:148:THR:HB	3:i:208:VAL:O	2.20	0.42
3:i:307:PHE:HD2	2:u:338:THR:HG21	1.83	0.42
2:i:303:GLY:O	2:i:307:ARG:HG3	2.18	0.42
1:x:44:ASP:OD1	1:x:84:LYS:HE3	2.19	0.42
2:h:137:VAL:HA	2:h:167:VAL:HG13	2.00	0.42
3:n:5:VAL:HA	3:n:8:ILE:HG12	2.01	0.42
2:o:209:ARG:NH1	2:o:238:PHE:CE2	2.87	0.42
2:o:227:TYR:N	2:o:227:TYR:CD1	2.82	0.42
3:r:81:THR:HG22	3:r:85:LYS:H	1.83	0.42
2:s:243:PRO:HB2	2:s:247:VAL:HG23	2.00	0.42
2:f:341:VAL:HB	3:g:315:VAL:HG22	2.00	0.42
3:g:107:THR:HG21	3:g:115:ALA:HB2	2.01	0.42
2:i:310:LYS:NZ	3:p:274:GLU:OE2	2.48	0.42
2:i:341:VAL:HB	3:k:315:VAL:HG22	2.01	0.42
3:k:90:ASP:O	3:k:211:LYS:N	2.43	0.42
1:x:76:LYS:HB2	1:x:76:LYS:HE3	1.92	0.42
1:m:40:GLU:HG3	1:m:45:GLN:HE21	1.84	0.42
1:a:44:ASP:OD1	1:a:84:LYS:HE3	2.19	0.42
1:b:41:VAL:HG22	1:b:46:VAL:HG11	2.00	0.42
2:e:327:TYR:OH	3:i:326:MET:O	2.36	0.42
3:g:328:THR:HG22	2:q:327:TYR:HE2	0.67	0.42
3:h:88:ILE:O	3:h:214:ASN:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:268:GLY:O	3:H:272:ARG:HG3	2.20	0.42
1:Y:37:PHE:HB2	1:Y:68:THR:HG21	2.00	0.42
2:g:85:ALA:HA	2:g:88:ILE:HG12	2.02	0.42
2:g:210:THR:HG21	3:k:133:ARG:HH21	1.85	0.42
3:o:30:ILE:HA	3:o:48:TYR:HD2	1.85	0.42
3:o:81:THR:HG22	3:o:85:LYS:H	1.83	0.42
3:o:148:THR:HB	3:o:208:VAL:O	2.20	0.42
2:h:321:ILE:HD11	3:l:291:PRO:HB3	2.02	0.42
2:j:216:THR:O	2:j:220:LEU:CB	2.68	0.42
3:l:326:MET:HG2	3:l:326:MET:O	2.20	0.42
3:n:270:ILE:O	3:n:274:GLU:HG3	2.20	0.42
1:K:59:THR:HG22	1:K:65:ARG:HG2	2.00	0.42
3:P:79:PHE:CE2	3:P:128:ARG:HG2	2.55	0.42
3:Q:93:ILE:HG21	3:Q:119:LEU:HD21	2.02	0.42
2:E:85:ALA:HA	2:E:88:ILE:HG12	2.02	0.42
3:H:71:THR:HB	3:H:94:LYS:HZ3	1.85	0.42
1:Y:55:GLU:HG3	1:Y:69:TYR:CE2	2.55	0.42
1:c:50:ARG:HD3	1:c:91:GLU:OE1	2.20	0.42
2:g:182:ASP:OD1	2:g:185:ARG:NH2	2.52	0.42
2:g:333:LYS:HE3	2:g:333:LYS:HB2	1.75	0.42
3:m:66:ASP:OD1	3:m:66:ASP:N	2.51	0.42
3:p:52:LEU:HG	2:r:111:PHE:CG	2.54	0.42
3:p:116:GLU:O	3:p:120:LYS:CD	2.62	0.42
2:N:182:ASP:OD1	2:N:185:ARG:NH2	2.52	0.42
2:O:105:ARG:HD2	2:O:120:PRO:HD3	2.00	0.42
3:R:11:ILE:HA	3:R:14:VAL:HG22	2.01	0.42
1:D:50:ARG:HD3	1:D:91:GLU:OE1	2.20	0.42
2:F:307:ARG:NH1	3:o:272:ARG:HB3	2.35	0.42
2:U:238:PHE:CZ	2:U:241:ALA:HB2	2.52	0.42
1:W:87:LYS:HD3	1:a:33:ASP:OD2	2.19	0.42
1:a:57:ASN:HB3	1:a:65:ARG:NH2	2.35	0.42
2:g:188:THR:HA	2:g:220:LEU:HD13	2.02	0.42
3:m:270:ILE:O	3:m:274:GLU:HG3	2.20	0.42
1:d:40:GLU:HG3	1:d:45:GLN:HE21	1.84	0.42
2:h:292:ALA:HB1	3:l:258:THR:HG21	2.02	0.42
2:O:209:ARG:NE	2:O:238:PHE:HD2	2.18	0.42
2:O:217:GLN:CD	2:O:236:VAL:N	2.69	0.42
3:R:17:TYR:O	3:R:20:VAL:HG12	2.19	0.42
1:C:57:ASN:HB3	1:C:65:ARG:NH2	2.34	0.42
2:E:188:THR:HA	2:E:220:LEU:HD13	2.02	0.42
2:E:229:MET:HE3	2:E:229:MET:HB2	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:282:GLN:O	2:F:286:ILE:HG23	2.20	0.42
3:G:79:PHE:CE2	3:G:128:ARG:HG2	2.55	0.42
3:I:103:TYR:HB2	3:I:202:GLY:HA3	2.01	0.42
1:W:44:ASP:OD1	1:W:84:LYS:HE3	2.19	0.42
2:i:213:ARG:HD2	2:i:236:VAL:O	2.18	0.42
3:m:90:ASP:OD1	3:m:90:ASP:N	2.50	0.42
2:q:101:LYS:HE3	2:q:101:LYS:HB3	1.78	0.42
3:p:263:GLU:HG2	3:p:267:GLN:HE21	1.85	0.42
1:K:55:GLU:HG3	1:K:69:TYR:CE2	2.55	0.42
3:P:56:ILE:HB	3:P:60:GLU:OE1	2.19	0.42
3:R:52:LEU:HG	2:S:111:PHE:CG	2.54	0.42
3:R:148:THR:HB	3:R:208:VAL:O	2.20	0.42
1:B:55:GLU:HG3	1:B:69:TYR:CE2	2.55	0.42
1:C:91:GLU:HA	1:D:31:LYS:HZ1	1.85	0.42
1:D:54:ARG:NH1	1:D:70:ILE:HB	2.28	0.42
2:E:210:THR:HG21	3:G:133:ARG:HH21	1.85	0.42
2:E:246:GLU:H	2:E:246:GLU:CD	2.26	0.42
2:F:195:VAL:HG11	2:F:216:THR:OG1	2.20	0.42
3:I:30:ILE:HA	3:I:48:TYR:HD2	1.85	0.42
2:U:298:ILE:O	2:U:302:GLN:HG3	2.19	0.42
2:i:186:GLN:HE22	3:k:73:ASP:HB3	1.84	0.42
3:k:51:GLY:O	3:k:53:HIS:ND1	2.50	0.42
2:q:298:ILE:O	2:q:302:GLN:HG3	2.19	0.42
3:n:37:VAL:HG13	3:n:104:TYR:HE2	1.85	0.42
3:p:30:ILE:HA	3:p:48:TYR:HD2	1.84	0.42
3:R:68:ARG:NE	2:S:178:THR:HG22	2.34	0.42
3:R:113:SER:O	3:R:117:VAL:HG13	2.20	0.42
1:B:43:ASN:CG	1:B:45:GLN:HE22	2.28	0.42
2:F:340:LYS:CE	3:o:312:ASP:OD2	2.68	0.42
3:G:137:LYS:HA	3:G:140:VAL:HG22	2.02	0.42
3:H:37:VAL:HG13	3:H:104:TYR:HE2	1.85	0.42
2:i:209:ARG:HD2	2:i:238:PHE:HB3	2.01	0.42
2:i:282:GLN:O	2:i:286:ILE:HG23	2.20	0.42
3:k:107:THR:HG21	3:k:115:ALA:HB2	2.01	0.42
2:q:238:PHE:CZ	2:q:241:ALA:HB2	2.52	0.42
3:p:81:THR:HG22	3:p:85:LYS:H	1.83	0.42
1:J:44:ASP:OD1	1:J:84:LYS:HE3	2.19	0.42
2:N:292:ALA:HB1	3:P:258:THR:HG21	2.02	0.42
3:R:23:VAL:HG22	3:R:64:MET:HE1	2.02	0.42
1:A:60:LYS:HB2	1:A:62:ASP:OD1	2.20	0.41
3:G:56:ILE:HB	3:G:60:GLU:OE1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:5:VAL:HA	3:H:8:ILE:HG12	2.01	0.41
3:H:93:ILE:HG21	3:H:119:LEU:HD21	2.02	0.41
1:W:60:LYS:HB2	1:W:62:ASP:OD1	2.20	0.41
3:k:79:PHE:CE2	3:k:128:ARG:HG2	2.55	0.41
2:q:90:ILE:HD13	2:q:90:ILE:HA	1.91	0.41
3:l:65:LEU:HD22	3:l:103:TYR:HE2	1.85	0.41
3:p:23:VAL:HG22	3:p:64:MET:HE1	2.02	0.41
3:p:68:ARG:NE	2:r:178:THR:HG22	2.34	0.41
3:p:148:THR:HB	3:p:208:VAL:O	2.20	0.41
1:K:87:LYS:HB2	1:K:87:LYS:HE2	1.82	0.41
3:Q:88:ILE:O	3:Q:214:ASN:N	2.51	0.41
3:R:224:TYR:HE1	2:S:156:VAL:HG21	1.85	0.41
1:B:59:THR:HG22	1:B:65:ARG:HG2	2.00	0.41
3:G:328:THR:HA	3:G:329:PRO:HD3	1.84	0.41
3:H:270:ILE:O	3:H:274:GLU:HG3	2.20	0.41
3:I:38:LEU:HD13	2:O:119:GLU:OE1	2.20	0.41
3:I:253:ALA:HB2	2:U:272:THR:HG22	2.02	0.41
3:I:262:ALA:HB3	2:O:299:LEU:HD12	2.02	0.41
3:I:296:PHE:N	3:P:325:TYR:HE1	2.12	0.41
2:U:195:VAL:HG11	2:U:216:THR:OG1	2.20	0.41
1:c:40:GLU:HG3	1:c:45:GLN:HE21	1.85	0.41
3:m:5:VAL:HA	3:m:8:ILE:HG12	2.01	0.41
3:o:113:SER:O	3:o:117:VAL:HG13	2.20	0.41
3:o:268:GLY:O	3:o:271:MET:HB3	2.20	0.41
1:s:38:LEU:HD23	1:s:38:LEU:HA	1.87	0.41
2:h:91:ILE:HD13	2:h:91:ILE:HA	1.92	0.41
2:j:311:LEU:CD2	2:j:311:LEU:C	2.86	0.41
3:l:79:PHE:CE2	3:l:128:ARG:HG2	2.55	0.41
3:n:268:GLY:O	3:n:272:ARG:HG3	2.20	0.41
1:t:38:LEU:HD23	1:t:38:LEU:HA	1.86	0.41
1:M:45:GLN:OE1	1:M:45:GLN:N	2.52	0.41
1:M:50:ARG:HD3	1:M:91:GLU:OE1	2.20	0.41
3:P:65:LEU:HD22	3:P:103:TYR:HE2	1.85	0.41
3:R:253:ALA:HB2	2:S:272:THR:HG22	2.02	0.41
1:B:36:THR:O	1:B:40:GLU:HG3	2.21	0.41
3:I:223:ILE:O	3:I:227:MET:HG3	2.21	0.41
3:k:328:THR:HA	2:r:327:TYR:CE2	2.55	0.41
3:m:37:VAL:HG13	3:m:104:TYR:HE2	1.85	0.41
3:m:268:GLY:O	3:m:272:ARG:HG3	2.20	0.41
2:q:151:THR:OG1	2:q:155:ASN:HB2	2.20	0.41
1:Z:43:ASN:CG	1:Z:45:GLN:HE22	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:n:31:THR:OG1	3:n:60:GLU:OE2	2.28	0.41
2:N:321:ILE:HD11	3:P:291:PRO:HB3	2.02	0.41
3:P:49:GLU:O	3:P:51:GLY:N	2.53	0.41
3:Q:37:VAL:HG13	3:Q:104:TYR:HE2	1.85	0.41
3:R:103:TYR:HB2	3:R:202:GLY:HA3	2.01	0.41
3:R:223:ILE:O	3:R:227:MET:HG3	2.21	0.41
2:S:195:VAL:HG11	2:S:216:THR:OG1	2.20	0.41
1:D:48:GLU:HB3	1:D:59:THR:HB	2.03	0.41
3:I:52:LEU:HG	2:U:111:PHE:CG	2.54	0.41
3:I:113:SER:O	3:I:117:VAL:HG13	2.20	0.41
2:i:149:MET:SD	2:i:196:ILE:HD11	2.49	0.41
1:s:45:GLN:C	1:s:61:LYS:HG2	2.46	0.41
1:Z:36:THR:O	1:Z:40:GLU:HG3	2.21	0.41
2:j:192:LEU:HA	2:j:195:VAL:HG12	2.02	0.41
3:l:56:ILE:HB	3:l:60:GLU:OE1	2.19	0.41
3:p:29:GLY:HA3	3:p:64:MET:SD	2.61	0.41
2:N:188:THR:HA	2:N:220:LEU:HD13	2.02	0.41
2:O:333:LYS:HB2	2:O:333:LYS:HE3	1.74	0.41
3:Q:5:VAL:HA	3:Q:8:ILE:HG12	2.01	0.41
3:R:30:ILE:HA	3:R:48:TYR:HD2	1.85	0.41
1:D:40:GLU:HG3	1:D:45:GLN:HE21	1.85	0.41
2:F:192:LEU:HA	2:F:195:VAL:HG12	2.02	0.41
3:H:31:THR:OG1	3:H:60:GLU:OE2	2.28	0.41
3:I:258:THR:CG2	2:O:292:ALA:HB1	2.50	0.41
1:e:45:GLN:C	1:e:61:LYS:HG2	2.46	0.41
1:c:34:TYR:OH	1:c:77:LEU:HD12	2.21	0.41
3:k:56:ILE:HB	3:k:60:GLU:OE1	2.19	0.41
3:k:124:SER:O	3:k:128:ARG:HG3	2.21	0.41
3:o:11:ILE:HA	3:o:14:VAL:HG22	2.01	0.41
1:X:60:LYS:HB2	1:X:62:ASP:OD1	2.20	0.41
2:h:85:ALA:HA	2:h:88:ILE:HG12	2.02	0.41
2:h:210:THR:HG21	3:l:133:ARG:HH21	1.84	0.41
3:p:223:ILE:O	3:p:227:MET:HG3	2.21	0.41
3:p:224:TYR:HE1	2:r:156:VAL:HG21	1.85	0.41
1:L:57:ASN:HB3	1:L:65:ARG:NH2	2.34	0.41
2:N:210:THR:HG21	3:P:133:ARG:HH21	1.85	0.41
2:O:213:ARG:HB3	2:O:213:ARG:HH11	1.83	0.41
2:O:242:ARG:HG2	2:O:243:PRO:O	2.21	0.41
3:P:124:SER:O	3:P:128:ARG:HG3	2.21	0.41
3:Q:270:ILE:O	3:Q:274:GLU:HG3	2.20	0.41
1:B:34:TYR:OH	1:B:74:ASP:OD1	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:211:VAL:HG23	2:F:212:ILE:N	2.36	0.41
3:G:298:ARG:HD2	3:G:298:ARG:HA	1.87	0.41
3:I:121:ARG:HH12	2:O:234:LEU:CD1	2.30	0.41
3:I:261:LEU:HD23	3:I:261:LEU:HA	1.90	0.41
2:U:229:MET:HE3	2:U:229:MET:HB2	1.86	0.41
3:m:93:ILE:HG21	3:m:119:LEU:HD21	2.02	0.41
3:o:29:GLY:HA3	3:o:64:MET:SD	2.61	0.41
3:o:223:ILE:O	3:o:227:MET:HG3	2.21	0.41
1:d:50:ARG:HD3	1:d:91:GLU:OE1	2.20	0.41
2:j:282:GLN:O	2:j:286:ILE:HG23	2.20	0.41
3:p:264:ALA:HB2	2:r:283:ALA:HB1	2.03	0.41
1:J:60:LYS:HB2	1:J:62:ASP:OD1	2.20	0.41
1:K:36:THR:O	1:K:40:GLU:HG3	2.21	0.41
3:Q:268:GLY:O	3:Q:272:ARG:HG3	2.20	0.41
3:R:40:ASP:HB3	3:R:46:LEU:HD23	2.03	0.41
1:B:84:LYS:HA	1:B:84:LYS:HD3	1.86	0.41
1:D:34:TYR:OH	1:D:77:LEU:HD12	2.21	0.41
2:F:340:LYS:HE2	2:F:340:LYS:HB2	1.90	0.41
3:I:29:GLY:HA3	3:I:64:MET:SD	2.61	0.41
3:I:224:TYR:HE1	2:U:156:VAL:HG21	1.85	0.41
1:Y:43:ASN:CG	1:Y:45:GLN:HE22	2.28	0.41
1:Y:74:ASP:HA	1:Y:75:PRO:HD3	1.91	0.41
1:c:48:GLU:HB3	1:c:59:THR:HB	2.03	0.41
2:i:191:ALA:CB	2:i:219:GLU:HG2	2.28	0.41
2:i:242:ARG:HG2	2:i:243:PRO:O	2.20	0.41
3:k:137:LYS:HA	3:k:140:VAL:HG22	2.02	0.41
3:o:40:ASP:HB3	3:o:46:LEU:HD23	2.03	0.41
1:Z:87:LYS:HB2	1:Z:87:LYS:HE2	1.82	0.41
1:d:34:TYR:OH	1:d:77:LEU:HD12	2.21	0.41
1:d:45:GLN:N	1:d:45:GLN:OE1	2.52	0.41
2:h:188:THR:HA	2:h:220:LEU:HD13	2.02	0.41
2:j:242:ARG:HG2	2:j:243:PRO:O	2.20	0.41
2:r:151:THR:OG1	2:r:155:ASN:HB2	2.20	0.41
2:O:246:GLU:OE1	2:O:246:GLU:N	2.53	0.41
2:O:282:GLN:O	2:O:286:ILE:HG23	2.20	0.41
3:R:29:GLY:HA3	3:R:64:MET:SD	2.61	0.41
2:F:195:VAL:HG21	2:F:215:ASP:HB3	2.02	0.41
3:I:296:PHE:HD2	3:P:325:TYR:CD1	2.38	0.41
2:i:307:ARG:HG2	3:p:273:GLY:HA3	2.03	0.41
3:p:40:ASP:HB3	3:p:46:LEU:HD23	2.03	0.41
3:p:253:ALA:HB2	2:r:272:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:r:195:VAL:HG11	2:r:216:THR:OG1	2.20	0.41
2:S:151:THR:OG1	2:S:155:ASN:HB2	2.20	0.41
1:T:31:LYS:HE2	1:T:31:LYS:HB2	1.76	0.41
2:E:292:ALA:HB1	3:G:258:THR:HG21	2.02	0.41
2:E:321:ILE:HD11	3:G:291:PRO:HB3	2.02	0.41
2:F:246:GLU:OE1	2:F:246:GLU:N	2.53	0.41
3:G:65:LEU:HD22	3:G:103:TYR:HE2	1.85	0.41
3:G:134:LEU:HD11	3:G:146:ARG:HH22	1.86	0.41
3:I:11:ILE:HA	3:I:14:VAL:HG22	2.01	0.41
3:I:18:MET:HE2	3:I:58:PHE:HE1	1.86	0.41
3:I:23:VAL:HG22	3:I:64:MET:HE1	2.02	0.41
2:U:151:THR:OG1	2:U:155:ASN:HB2	2.20	0.41
1:e:87:LYS:NZ	1:f:33:ASP:OD2	2.31	0.41
1:Y:36:THR:O	1:Y:40:GLU:HG3	2.21	0.41
3:m:121:ARG:HD2	2:q:213:ARG:CZ	2.51	0.41
3:o:84:LYS:HE3	3:o:84:LYS:HB2	1.87	0.41
1:b:31:LYS:HE3	1:b:31:LYS:HB2	1.82	0.41
2:j:340:LYS:CE	3:R:312:ASP:OD2	2.68	0.41
3:l:137:LYS:HA	3:l:140:VAL:HG22	2.02	0.41
3:p:18:MET:HE2	3:p:58:PHE:HE1	1.86	0.41
2:r:208:GLY:O	2:r:209:ARG:C	2.64	0.41
1:t:45:GLN:C	1:t:61:LYS:HG2	2.46	0.41
1:v:38:LEU:HA	1:v:38:LEU:HD23	1.84	0.41
1:K:43:ASN:CG	1:K:45:GLN:HE22	2.28	0.41
2:N:85:ALA:HA	2:N:88:ILE:HG12	2.02	0.41
2:F:142:GLU:HG3	2:F:164:GLN:HG2	2.03	0.41
3:G:124:SER:O	3:G:128:ARG:HG3	2.21	0.41
1:a:91:GLU:HA	1:c:31:LYS:HZ1	1.85	0.41
2:i:298:ILE:HG13	2:i:298:ILE:H	1.46	0.41
3:o:18:MET:HE2	3:o:58:PHE:HE1	1.86	0.41
2:j:138:GLU:OE1	3:R:108:GLY:N	2.54	0.41
2:j:234:LEU:CB	3:R:121:ARG:NH1	2.84	0.41
3:l:134:LEU:HD11	3:l:146:ARG:HH22	1.86	0.41
3:p:261:LEU:HD23	3:p:261:LEU:HA	1.90	0.41
1:M:34:TYR:OH	1:M:77:LEU:HD12	2.21	0.41
2:N:160:GLU:OE2	2:N:240:ALA:HB3	2.21	0.41
2:E:160:GLU:OE2	2:E:240:ALA:HB3	2.21	0.40
2:F:242:ARG:HG2	2:F:243:PRO:O	2.20	0.40
3:H:121:ARG:HD2	2:U:213:ARG:CZ	2.51	0.40
2:U:90:ILE:HD13	2:U:90:ILE:HA	1.90	0.40
1:Y:34:TYR:OH	1:Y:74:ASP:OD1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:160:GLU:OE2	2:g:240:ALA:HB3	2.21	0.40
2:g:321:ILE:HD11	3:k:291:PRO:HB3	2.02	0.40
2:i:91:ILE:HD13	2:i:91:ILE:HA	1.93	0.40
2:i:149:MET:SD	2:i:196:ILE:CD1	3.02	0.40
3:o:23:VAL:HG22	3:o:64:MET:HE1	2.02	0.40
1:X:57:ASN:OD1	1:X:67:THR:HG22	2.22	0.40
2:j:296:GLN:HA	2:j:299:LEU:HD12	2.03	0.40
2:j:343:VAL:HG12	3:R:315:VAL:HG21	2.03	0.40
3:p:102:ARG:HH22	3:p:193:ILE:HD12	1.86	0.40
1:t:33:ASP:OD1	1:t:36:THR:HG22	2.21	0.40
2:S:333:LYS:HE3	2:S:333:LYS:HB2	1.80	0.40
3:I:40:ASP:HB3	3:I:46:LEU:HD23	2.03	0.40
3:I:296:PHE:CB	3:P:325:TYR:CD1	3.02	0.40
1:e:33:ASP:OD1	1:e:36:THR:HG22	2.21	0.40
2:g:292:ALA:HB1	3:k:258:THR:HG21	2.02	0.40
2:g:344:ASN:OD1	2:g:345:ASP:N	2.55	0.40
3:o:253:ALA:HB2	2:q:272:THR:HG22	2.02	0.40
3:l:120:LYS:HB3	3:l:120:LYS:HE2	1.96	0.40
2:r:229:MET:HE3	2:r:229:MET:HB2	1.86	0.40
3:P:66:ASP:OD1	3:P:66:ASP:N	2.54	0.40
3:Q:47:VAL:HG11	3:Q:100:PHE:HB2	2.03	0.40
3:Q:66:ASP:N	3:Q:66:ASP:OD1	2.51	0.40
2:E:91:ILE:HD13	2:E:91:ILE:HA	1.92	0.40
2:E:344:ASN:OD1	2:E:345:ASP:N	2.55	0.40
2:F:223:THR:O	2:F:226:PRO:HD2	2.21	0.40
2:i:195:VAL:CG1	2:i:196:ILE:N	2.84	0.40
2:i:246:GLU:OE1	2:i:246:GLU:N	2.53	0.40
3:k:65:LEU:HD22	3:k:103:TYR:HE2	1.85	0.40
3:o:224:TYR:HE1	2:q:156:VAL:HG21	1.85	0.40
3:P:92:TYR:CE1	3:P:209:ARG:HB2	2.57	0.40
2:S:229:MET:HE3	2:S:229:MET:HB2	1.86	0.40
1:T:33:ASP:OD1	1:T:36:THR:HG22	2.21	0.40
1:T:45:GLN:C	1:T:61:LYS:HG2	2.46	0.40
2:F:234:LEU:CB	3:o:121:ARG:NH1	2.84	0.40
2:F:302:GLN:OE1	2:F:302:GLN:HA	2.21	0.40
3:G:261:LEU:HD23	3:G:261:LEU:HA	1.91	0.40
3:H:47:VAL:HG11	3:H:100:PHE:HB2	2.03	0.40
3:I:11:ILE:HA	3:I:11:ILE:HD12	1.93	0.40
2:i:193:ARG:C	2:i:193:ARG:CD	2.92	0.40
3:o:79:PHE:CE2	3:o:128:ARG:CB	3.00	0.40
2:q:188:THR:HA	2:q:220:LEU:HD13	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:h:90:ILE:HD13	2:h:90:ILE:HA	1.98	0.40
3:p:11:ILE:HA	3:p:14:VAL:HG22	2.01	0.40
3:p:272:ARG:HD2	2:r:293:TYR:CE1	2.54	0.40
1:t:52:ASN:HA	1:t:91:GLU:HB2	2.04	0.40
1:J:35:SER:O	1:J:39:GLN:OE1	2.40	0.40
1:L:45:GLN:HE22	1:L:60:LYS:HD3	1.86	0.40
1:M:48:GLU:HB3	1:M:59:THR:HB	2.03	0.40
2:O:91:ILE:HD13	2:O:91:ILE:HA	1.93	0.40
2:O:142:GLU:HG3	2:O:164:GLN:HG2	2.03	0.40
2:O:192:LEU:HA	2:O:195:VAL:HG12	2.02	0.40
3:P:137:LYS:HA	3:P:140:VAL:HG22	2.02	0.40
3:Q:9:ILE:O	3:Q:13:LEU:HD23	2.21	0.40
3:Q:102:ARG:HE	3:Q:102:ARG:HB3	1.72	0.40
3:Q:121:ARG:HD2	2:S:213:ARG:CZ	2.51	0.40
3:R:18:MET:HE2	3:R:58:PHE:HE1	1.86	0.40
3:R:264:ALA:HB2	2:S:283:ALA:HB1	2.03	0.40
1:A:35:SER:O	1:A:39:GLN:OE1	2.40	0.40
3:G:87:LEU:HD23	3:G:87:LEU:HA	1.95	0.40
2:U:188:THR:HA	2:U:220:LEU:HD13	2.04	0.40
3:o:79:PHE:CE2	3:o:128:ARG:HA	2.56	0.40
2:q:208:GLY:O	2:q:209:ARG:C	2.64	0.40
3:n:9:ILE:O	3:n:13:LEU:HD23	2.21	0.40
3:p:272:ARG:CG	2:r:293:TYR:HE1	2.01	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	B	61/644 (10%)	58 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	D	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	J	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	K	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	L	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	M	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	T	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	V	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
1	W	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	X	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	Y	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	Z	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	a	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	b	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	c	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	d	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	e	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	f	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
1	s	61/644 (10%)	58 (95%)	3 (5%)	0	100	100
1	t	61/644 (10%)	59 (97%)	2 (3%)	0	100	100
1	u	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
1	v	61/644 (10%)	60 (98%)	1 (2%)	0	100	100
2	E	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	F	265/419 (63%)	257 (97%)	8 (3%)	0	100	100
2	N	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	O	265/419 (63%)	256 (97%)	8 (3%)	1 (0%)	30	60
2	S	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
2	U	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
2	g	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	h	265/419 (63%)	256 (97%)	9 (3%)	0	100	100
2	i	265/419 (63%)	256 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	j	265/419 (63%)	257 (97%)	8 (3%)	0	100	100
2	q	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
2	r	265/419 (63%)	254 (96%)	11 (4%)	0	100	100
3	G	295/334 (88%)	287 (97%)	8 (3%)	0	100	100
3	H	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	I	295/334 (88%)	290 (98%)	5 (2%)	0	100	100
3	P	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	Q	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	R	295/334 (88%)	290 (98%)	5 (2%)	0	100	100
3	k	295/334 (88%)	287 (97%)	8 (3%)	0	100	100
3	l	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	m	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	n	295/334 (88%)	286 (97%)	9 (3%)	0	100	100
3	o	295/334 (88%)	289 (98%)	5 (2%)	1 (0%)	36	66
3	p	295/334 (88%)	289 (98%)	5 (2%)	1 (0%)	36	66
All	All	8184/24492 (33%)	7925 (97%)	256 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	o	264	ALA
2	O	229	MET
3	p	132	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	60/527 (11%)	60 (100%)	0	100	100
1	B	60/527 (11%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	60/527 (11%)	60 (100%)	0	100	100
1	D	60/527 (11%)	60 (100%)	0	100	100
1	J	60/527 (11%)	60 (100%)	0	100	100
1	K	60/527 (11%)	60 (100%)	0	100	100
1	L	60/527 (11%)	60 (100%)	0	100	100
1	M	60/527 (11%)	60 (100%)	0	100	100
1	T	60/527 (11%)	60 (100%)	0	100	100
1	V	60/527 (11%)	60 (100%)	0	100	100
1	W	60/527 (11%)	60 (100%)	0	100	100
1	X	60/527 (11%)	60 (100%)	0	100	100
1	Y	60/527 (11%)	60 (100%)	0	100	100
1	Z	60/527 (11%)	60 (100%)	0	100	100
1	a	60/527 (11%)	60 (100%)	0	100	100
1	b	60/527 (11%)	60 (100%)	0	100	100
1	c	60/527 (11%)	60 (100%)	0	100	100
1	d	60/527 (11%)	60 (100%)	0	100	100
1	e	60/527 (11%)	60 (100%)	0	100	100
1	f	60/527 (11%)	60 (100%)	0	100	100
1	s	60/527 (11%)	60 (100%)	0	100	100
1	t	60/527 (11%)	60 (100%)	0	100	100
1	u	60/527 (11%)	60 (100%)	0	100	100
1	v	60/527 (11%)	60 (100%)	0	100	100
2	E	224/336 (67%)	224 (100%)	0	100	100
2	F	224/336 (67%)	223 (100%)	1 (0%)	84	85
2	N	224/336 (67%)	224 (100%)	0	100	100
2	O	224/336 (67%)	218 (97%)	6 (3%)	39	63
2	S	224/336 (67%)	224 (100%)	0	100	100
2	U	224/336 (67%)	224 (100%)	0	100	100
2	g	224/336 (67%)	224 (100%)	0	100	100
2	h	224/336 (67%)	224 (100%)	0	100	100
2	i	224/336 (67%)	220 (98%)	4 (2%)	51	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	j	224/336 (67%)	221 (99%)	3 (1%)	61	75
2	q	224/336 (67%)	224 (100%)	0	100	100
2	r	224/336 (67%)	224 (100%)	0	100	100
3	G	258/283 (91%)	258 (100%)	0	100	100
3	H	258/283 (91%)	258 (100%)	0	100	100
3	I	258/283 (91%)	255 (99%)	3 (1%)	63	75
3	P	258/283 (91%)	258 (100%)	0	100	100
3	Q	258/283 (91%)	258 (100%)	0	100	100
3	R	258/283 (91%)	258 (100%)	0	100	100
3	k	258/283 (91%)	258 (100%)	0	100	100
3	l	258/283 (91%)	258 (100%)	0	100	100
3	m	258/283 (91%)	258 (100%)	0	100	100
3	n	258/283 (91%)	258 (100%)	0	100	100
3	o	258/283 (91%)	256 (99%)	2 (1%)	73	79
3	p	258/283 (91%)	255 (99%)	3 (1%)	63	75
All	All	7224/20076 (36%)	7202 (100%)	22 (0%)	84	86

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	212	ILE
3	I	131	ILE
3	I	270	ILE
3	I	328	THR
2	i	195	VAL
2	i	210	THR
2	i	212	ILE
2	i	298	ILE
3	o	127	LEU
3	o	128	ARG
2	j	205	LEU
2	j	210	THR
2	j	213	ARG
3	p	121	ARG
3	p	131	ILE
3	p	267	GLN
2	O	210	THR

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Mol	Chain	Res	Type
2	O	211	VAL
2	O	212	ILE
2	O	221	GLU
2	O	223	THR
2	O	225	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	85	ASN
2	F	162	ASN
3	H	196	ASN
3	H	243	GLN
3	I	310	ASN
2	U	186	GLN
1	Y	85	ASN
3	m	196	ASN
3	m	243	GLN
2	q	186	GLN
1	Z	85	ASN
2	j	162	ASN
3	n	196	ASN
3	n	243	GLN
2	r	186	GLN
1	K	85	ASN
1	L	42	ASN
1	M	39	GLN
2	N	262	GLN
2	O	162	ASN
3	Q	196	ASN
3	Q	243	GLN
3	R	70	GLN
2	S	186	GLN

5.3.3 RNA ⓘ

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.

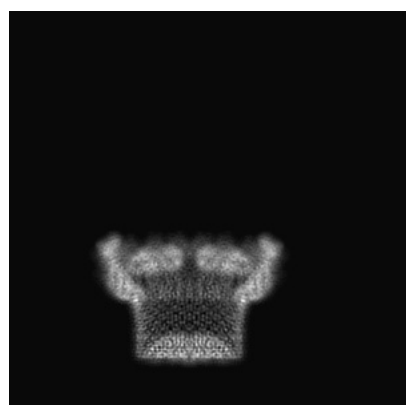
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32002. These allow visual inspection of the internal detail of the map and identification of artifacts.

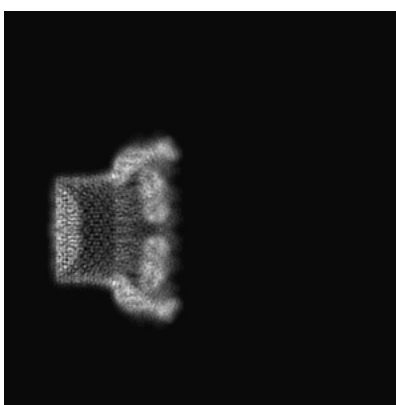
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

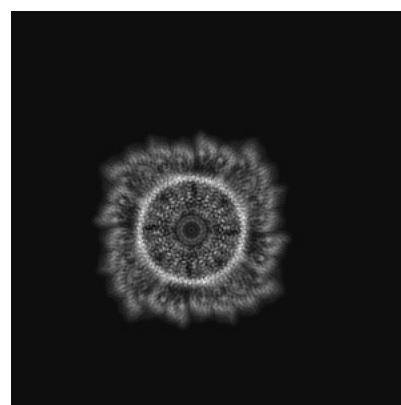
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

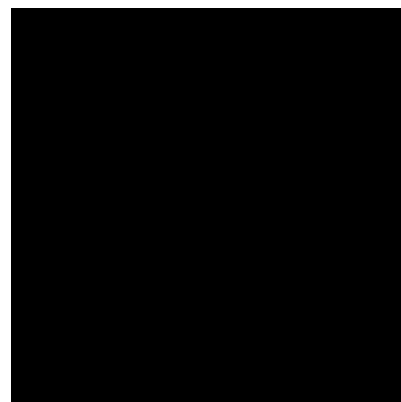
6.2.1 Primary map



X Index: 200



Y Index: 200

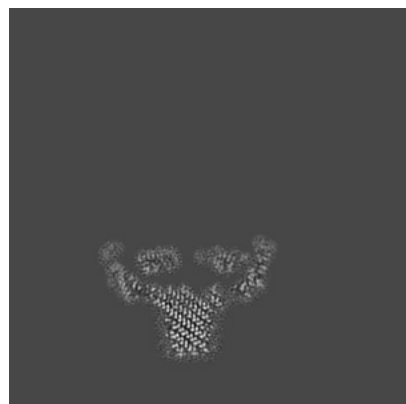


Z Index: 200

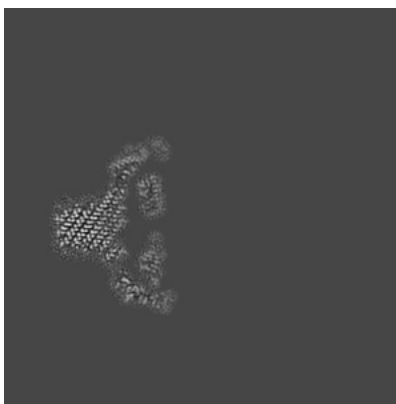
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

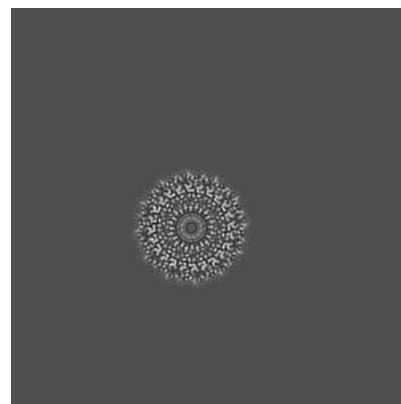
6.3.1 Primary map



X Index: 129



Y Index: 129

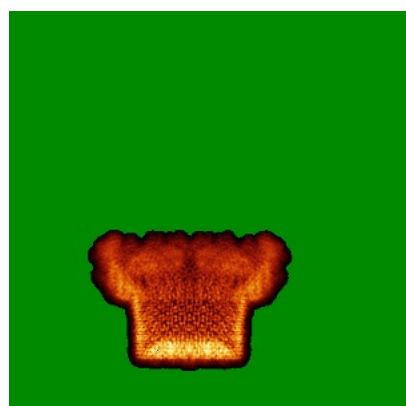


Z Index: 60

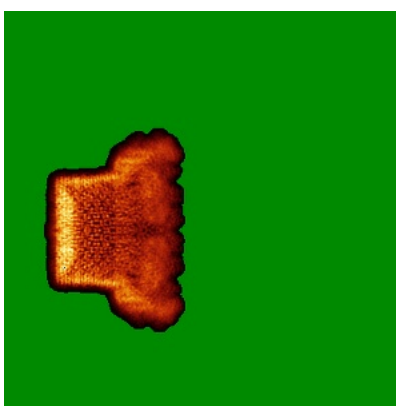
The images above show the largest variance slices of the map in three orthogonal directions.

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

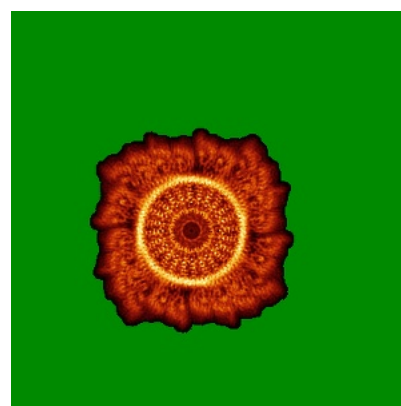
6.4.1 Primary map



X



Y

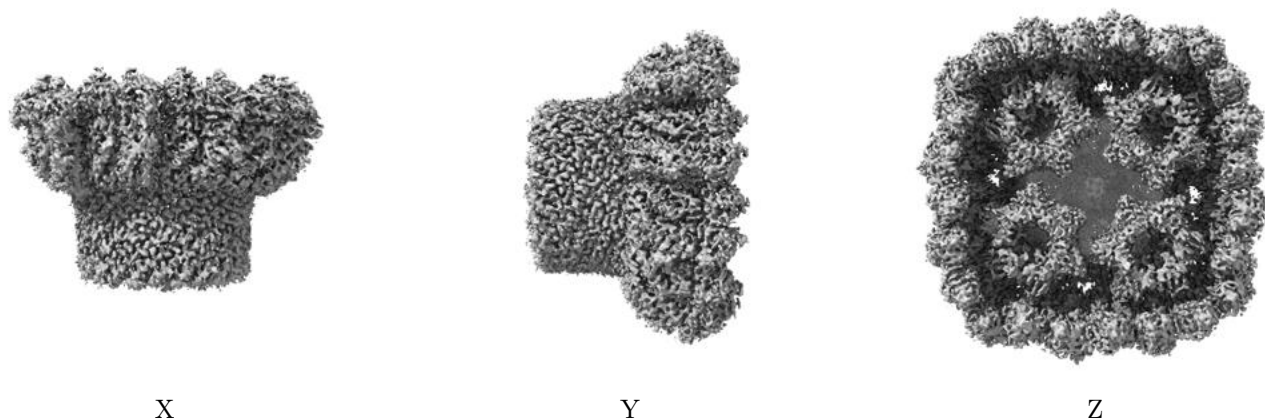


Z

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 0.0146. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

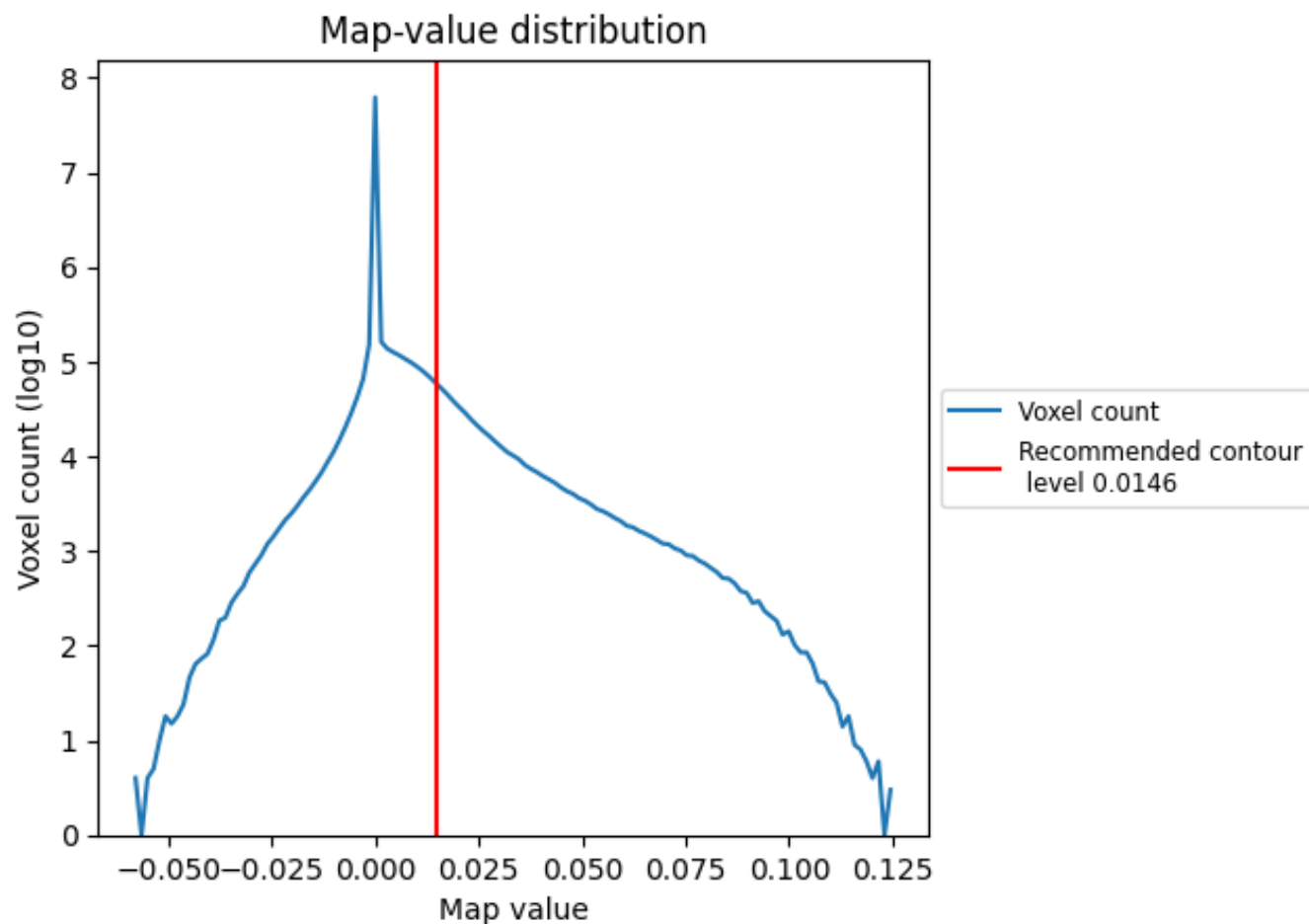
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

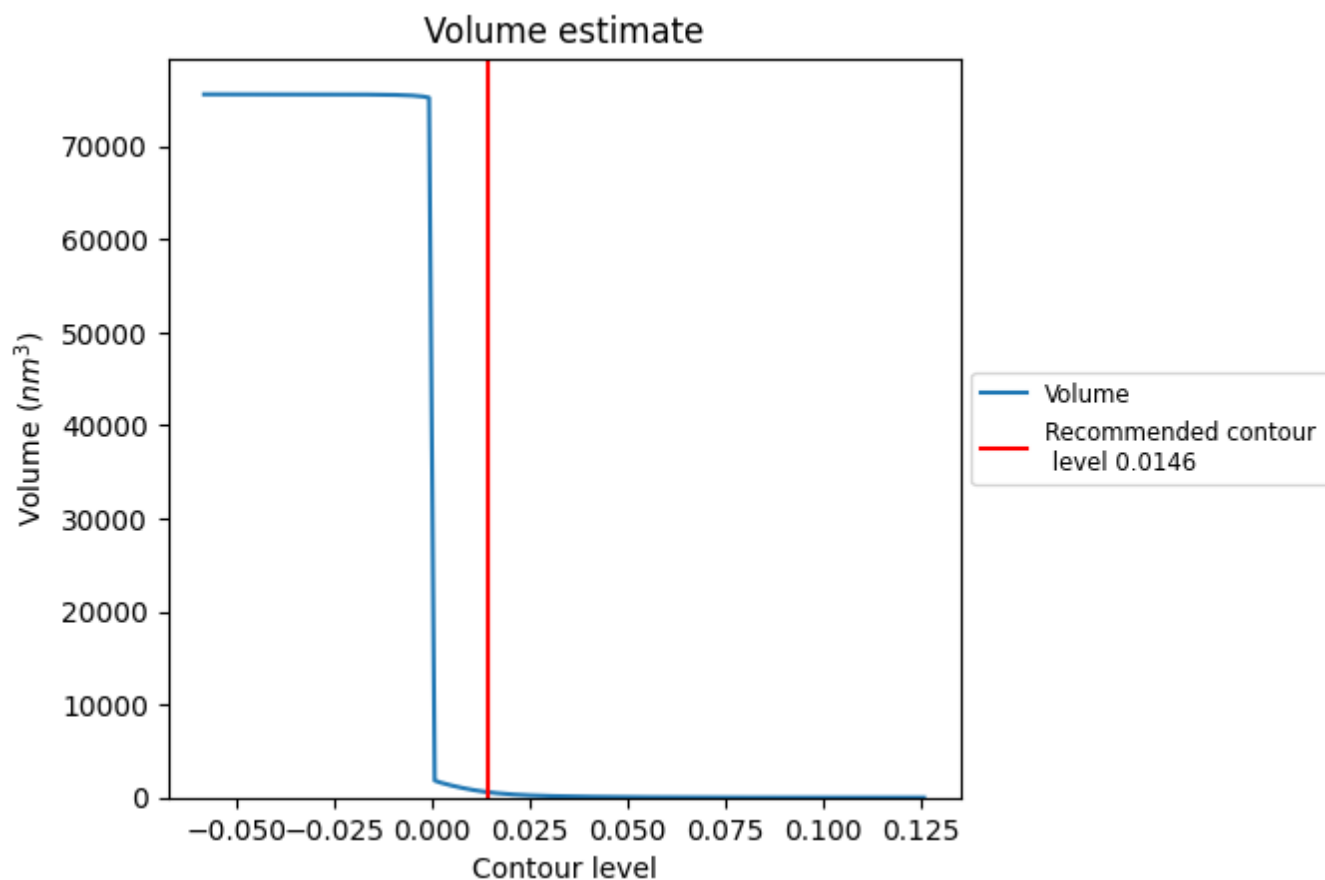
This section contains the results of statistical analysis of the map.

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.

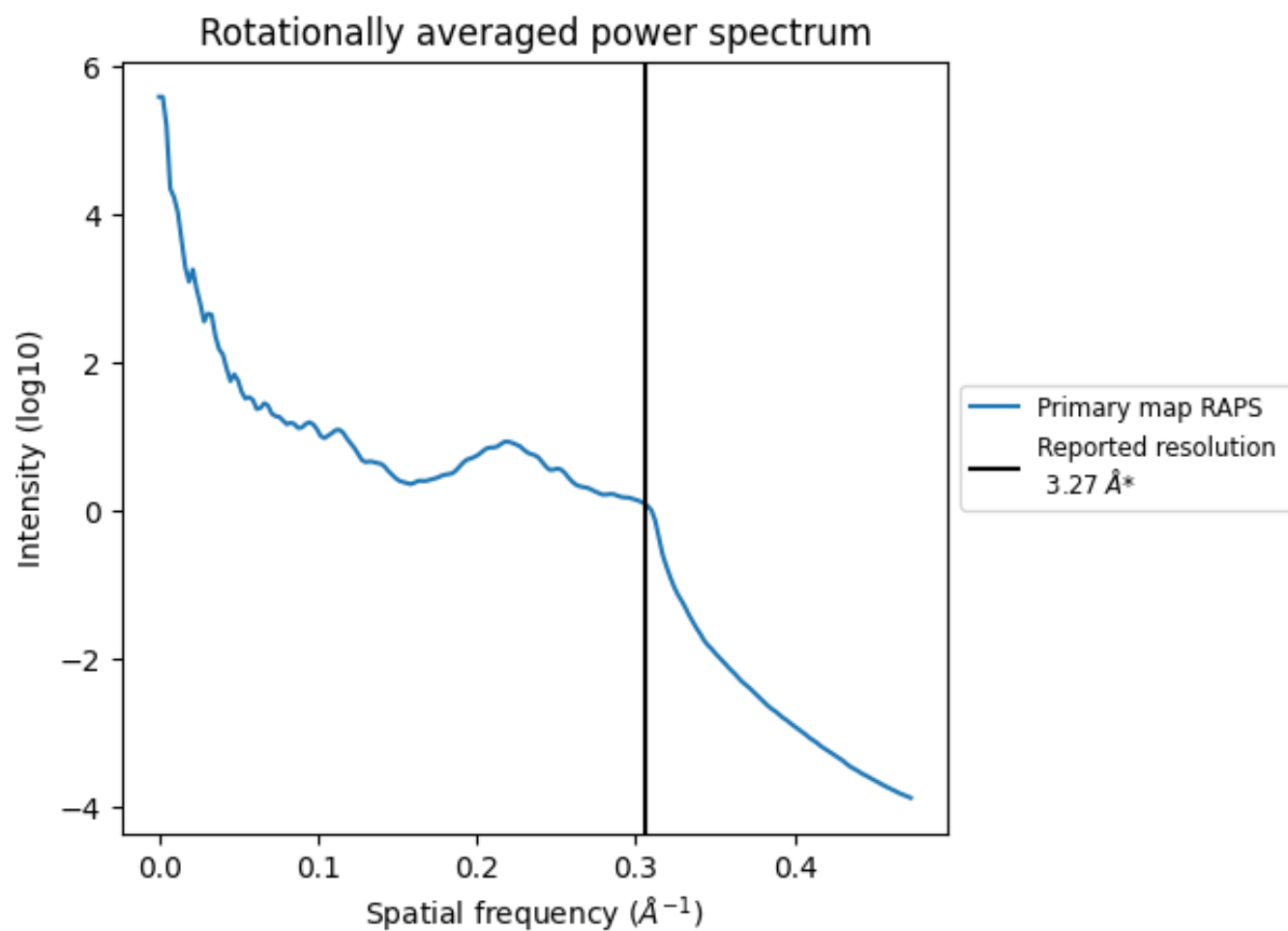
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 576 nm^3 ; this corresponds to an approximate mass of 520 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 0.306 Å⁻¹

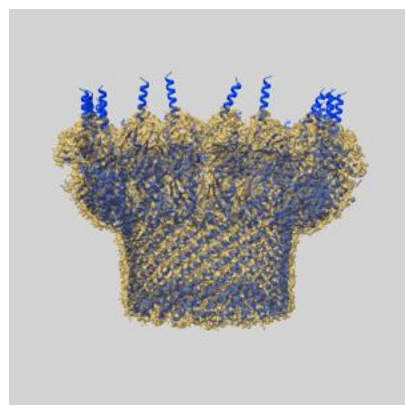
8 Fourier-Shell correlation

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

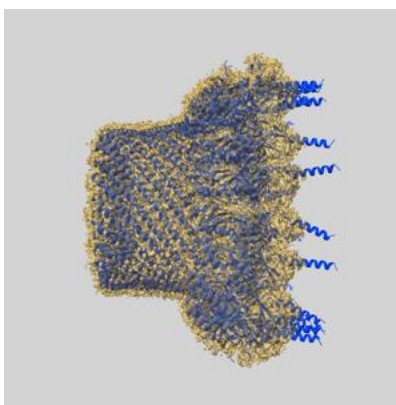
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32002 and PDB model 7VHP. Per-residue inclusion information can be found in section 3 on page 8.

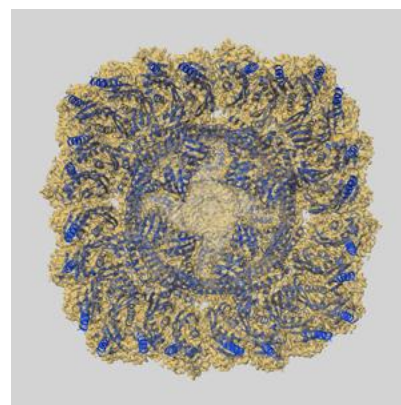
9.1 Map-model overlay [i](#)



X



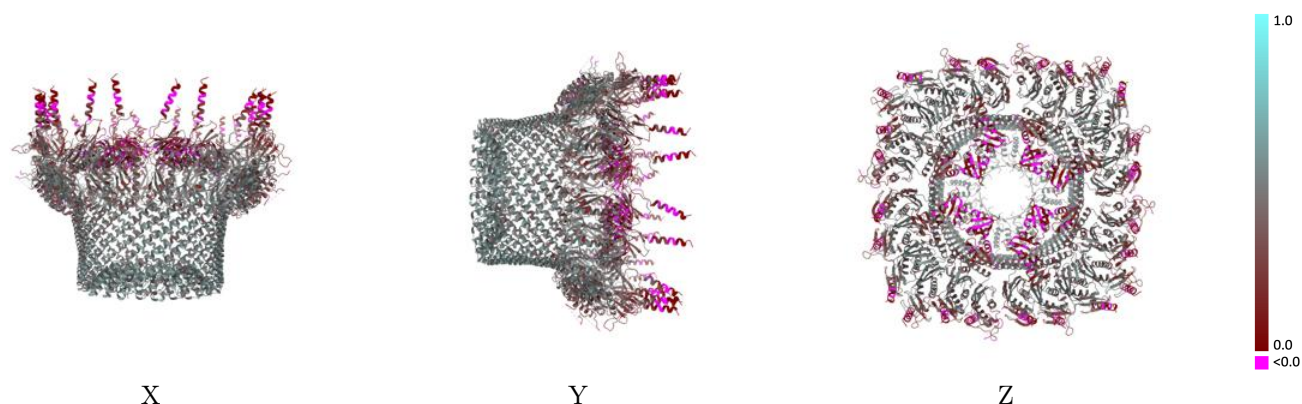
Y



Z

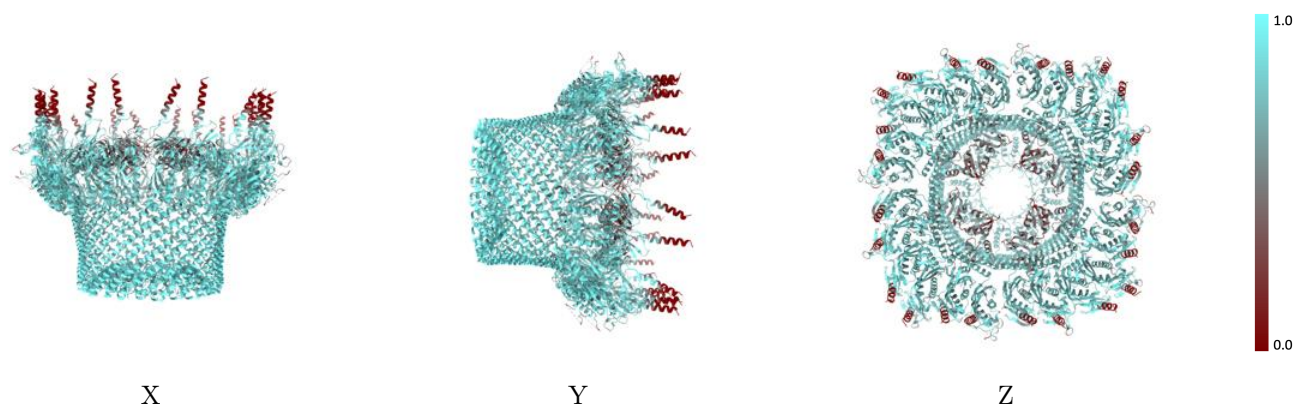
The images above show the 3D surface view of the map at the recommended contour level 0.0146 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



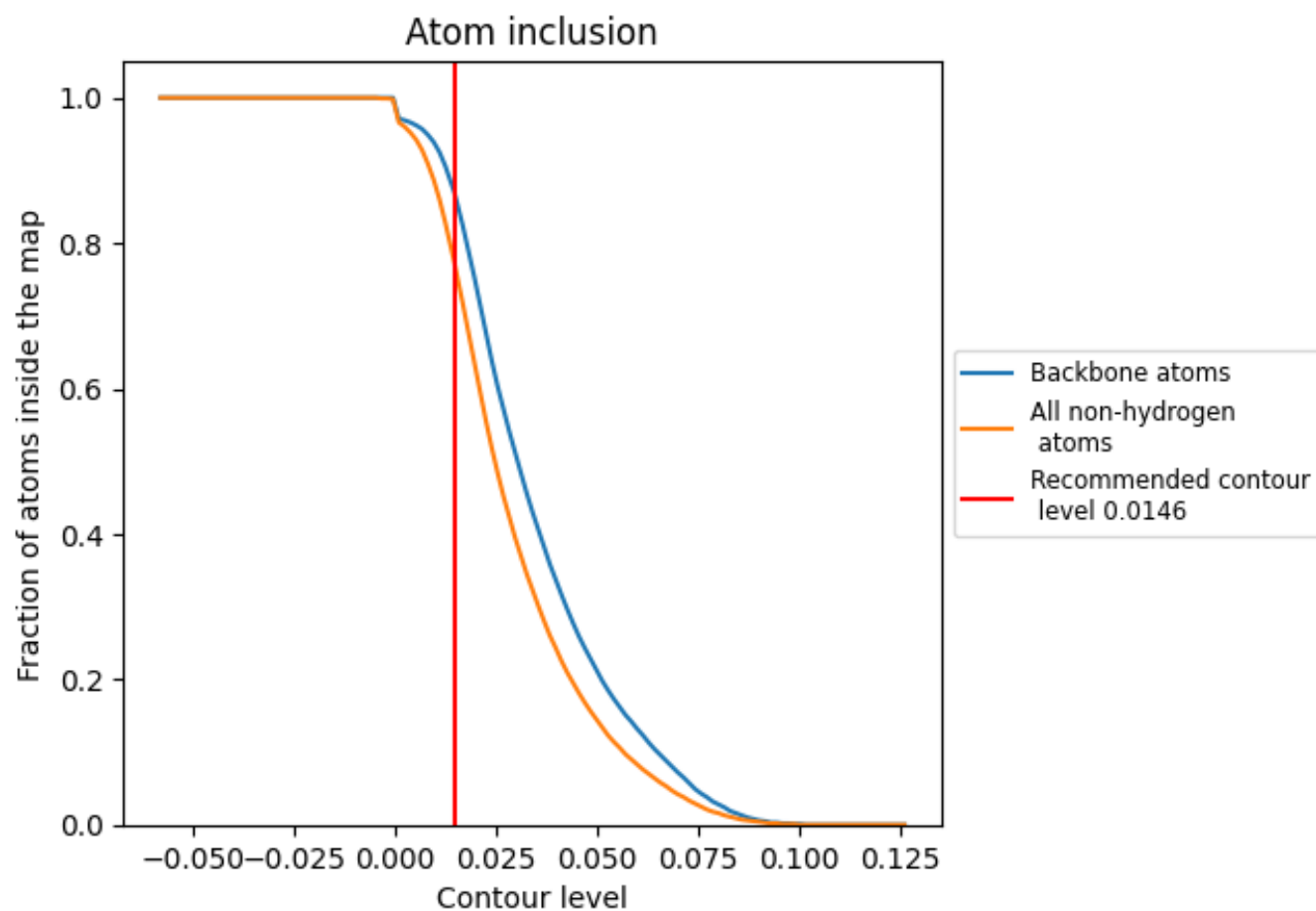
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0146).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 77% 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 (0.0146) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7740	 0.3830
A	 0.4450	 0.1140
B	 0.6500	 0.2300
C	 0.3380	 0.0330
D	 0.5530	 0.1680
E	 0.8540	 0.4470
F	 0.8060	 0.4070
G	 0.8090	 0.4170
H	 0.8000	 0.4100
I	 0.7570	 0.3670
J	 0.4650	 0.1310
K	 0.6540	 0.2480
L	 0.3500	 0.0450
M	 0.5550	 0.1860
N	 0.8640	 0.4580
O	 0.8220	 0.4190
P	 0.8270	 0.4320
Q	 0.8130	 0.4210
R	 0.7730	 0.3840
S	 0.8280	 0.4250
T	 0.7510	 0.3930
U	 0.8230	 0.4140
V	 0.8030	 0.4390
W	 0.4810	 0.1270
X	 0.4470	 0.1230
Y	 0.6480	 0.2440
Z	 0.6540	 0.2480
a	 0.3680	 0.0310
b	 0.3480	 0.0310
c	 0.5450	 0.1710
d	 0.5470	 0.1740
e	 0.7510	 0.3840
f	 0.7930	 0.4270
g	 0.8690	 0.4620
h	 0.8590	 0.4520



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Chain	Atom inclusion	Q-score
i	 0.8110	 0.4050
j	 0.8040	 0.4000
k	 0.8270	 0.4320
l	 0.8170	 0.4290
m	 0.8140	 0.4240
n	 0.8120	 0.4200
o	 0.7740	 0.3790
p	 0.7720	 0.3710
q	 0.8330	 0.4270
r	 0.8290	 0.4250
s	 0.7510	 0.3880
t	 0.7610	 0.3820
u	 0.8070	 0.4450
v	 0.8010	 0.4360