



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 12:32 PM UTC

PDB ID : 7QJ5 / pdb_00007qj5
EMDB ID : EMD-14010
Title : Structure of recombinant human gamma-Tubulin Ring Complex (spokes 1-14)
Authors : Zupa, E.; Pfeffer, S.
Deposited on : 2021-12-16
Resolution : 8.70 Å(reported)
Based on initial models : 6X0U, 6L81, 7AS4, 6V6S

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:

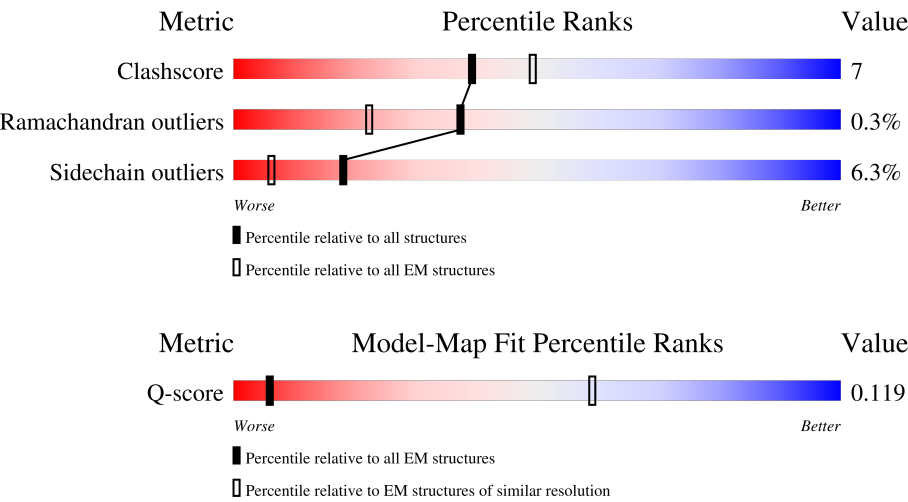
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.70 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	282 (8.20 - 9.20)

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	1	451	57% 61% 28% • 7%
1	2	451	49% 61% 27% 5% 7%
1	O	451	30% 62% 26% 5% 7%
1	P	451	27% 63% 26% 5% 7%

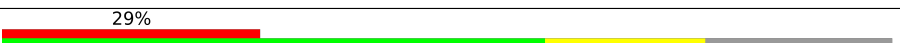
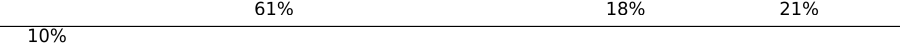
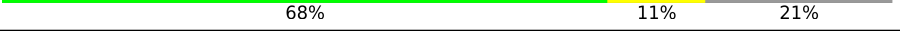
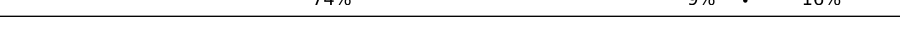
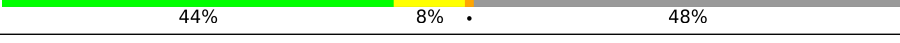
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Mol	Chain	Length	Quality of chain
1	Q	451	
1	R	451	
1	S	451	
1	T	451	
1	U	451	
1	V	451	
1	W	451	
1	X	451	
1	Y	451	
1	Z	451	
2	e	375	
3	A	902	
3	C	902	
3	E	902	
3	G	902	
3	M	902	
4	B	907	
4	D	907	
4	F	907	
4	H	907	
4	N	907	
4	a	907	
4	f	907	
4	h	907	
4	j	907	

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Mol	Chain	Length	Quality of chain
5	b	82	
5	d	82	
5	g	82	
5	i	82	
5	k	82	
5	m	82	
6	I	667	
6	K	667	
7	J	1024	
7	l	1024	
8	L	1819	
8	c	1819	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 126600 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 Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	2	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	O	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	P	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	Q	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	R	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	S	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	T	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	U	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	V	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	W	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	X	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	Y	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		
1	Z	420	Total	C	N	O	S	0	0
			3373	2134	586	638	15		

- Molecule 2 is a protein called actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	364	Total	C	N	O	S	0	0
			2847	1803	476	548	20		

- Molecule 3 is a protein called Gamma-tubulin complex component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	613	Total	C	N	O	S	0	0
			4978	3212	831	903	32		
3	C	620	Total	C	N	O	S	0	0
			5044	3257	845	910	32		
3	G	640	Total	C	N	O	S	0	0
			5216	3359	878	946	33		
3	M	636	Total	C	N	O	S	0	0
			5186	3342	871	940	33		
3	E	640	Total	C	N	O	S	0	0
			5216	3359	878	946	33		

- Molecule 4 is a protein called Gamma-tubulin complex component 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	610	Total	C	N	O	S	0	0
			5029	3203	888	913	25		
4	D	581	Total	C	N	O	S	0	0
			4796	3061	842	868	25		
4	F	599	Total	C	N	O	S	0	0
			4941	3151	871	894	25		
4	H	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
4	N	594	Total	C	N	O	S	0	0
			4907	3130	864	888	25		
4	a	116	Total	C	N	O	S	0	0
			933	591	171	169	2		
4	j	107	Total	C	N	O	S	0	0
			863	545	161	155	2		
4	h	107	Total	C	N	O	S	0	0
			863	545	161	155	2		
4	f	107	Total	C	N	O	S	0	0
			863	545	161	155	2		

- Molecule 5 is a protein called Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	g	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	i	65	Total	C	N	O	S	0	0
			484	299	85	96	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	k	65	Total	C	N	O	S	0	0
			484	299	85	96	4		
5	d	59	Total	C	N	O	S	0	0
			454	281	79	90	4		

- Molecule 6 is a protein called Gamma-tubulin complex component 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	521	Total	C	N	O	S	0	0
			4225	2737	720	750	18		
6	K	562	Total	C	N	O	S	0	0
			4579	2964	781	816	18		

- Molecule 7 is a protein called Gamma-tubulin complex component 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	534	Total	C	N	O	S	0	0
			4429	2893	737	776	23		
7	l	108	Total	C	N	O	S	0	0
			875	556	151	167	1		

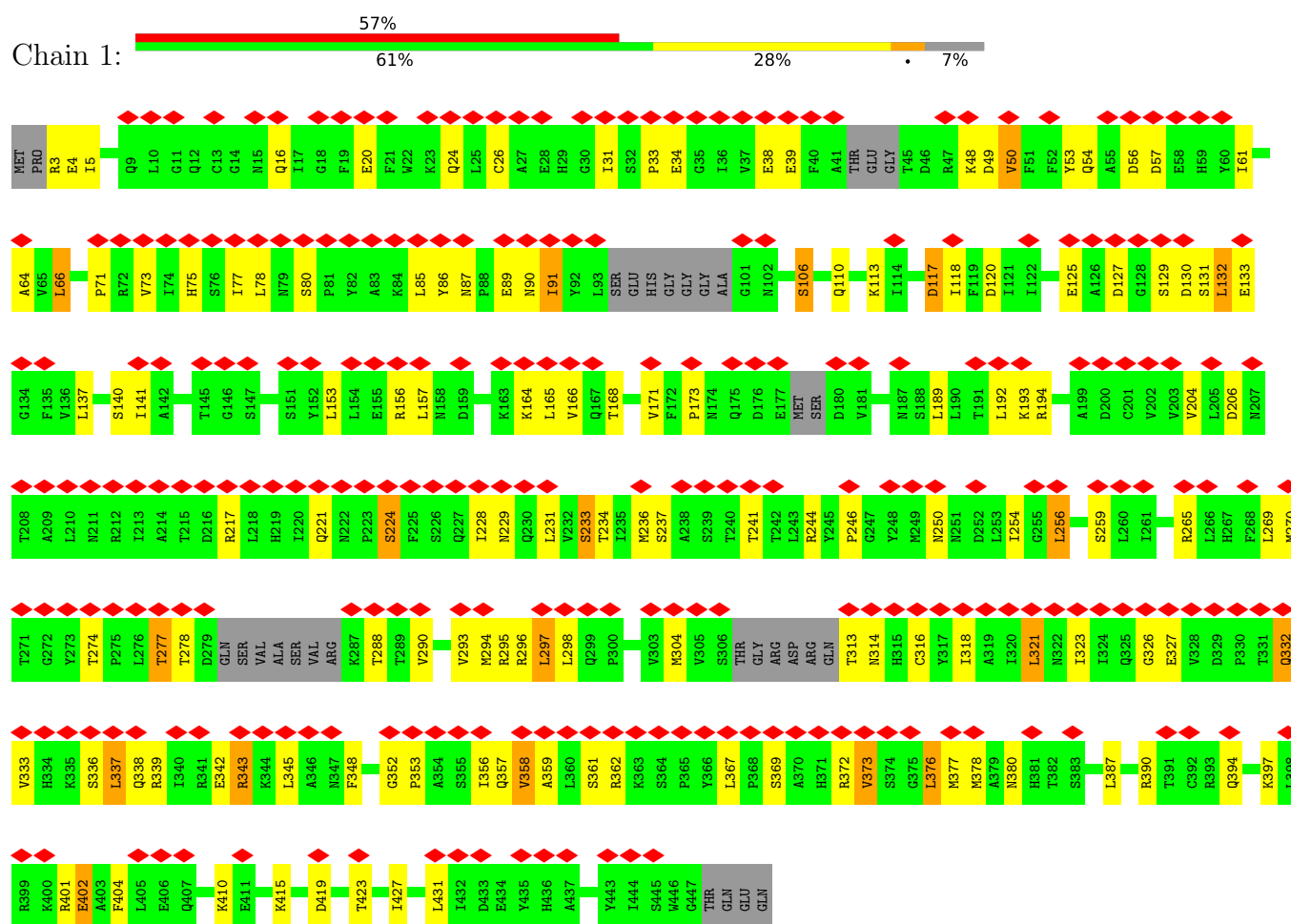
- Molecule 8 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	566	Total	C	N	O	S	0	0
			4587	3000	773	789	25		
8	c	158	Total	C	N	O	S	0	0
			1220	771	209	232	8		

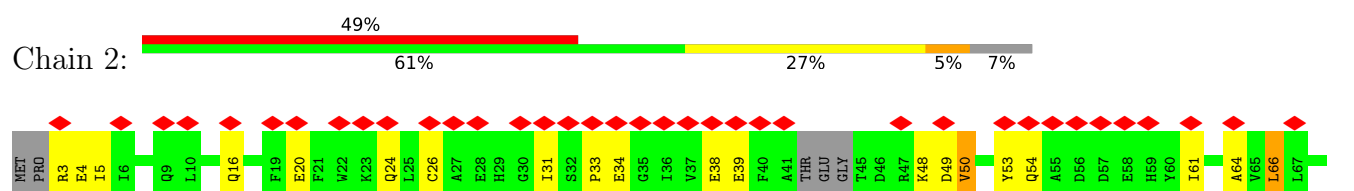
3 Residue-property plots

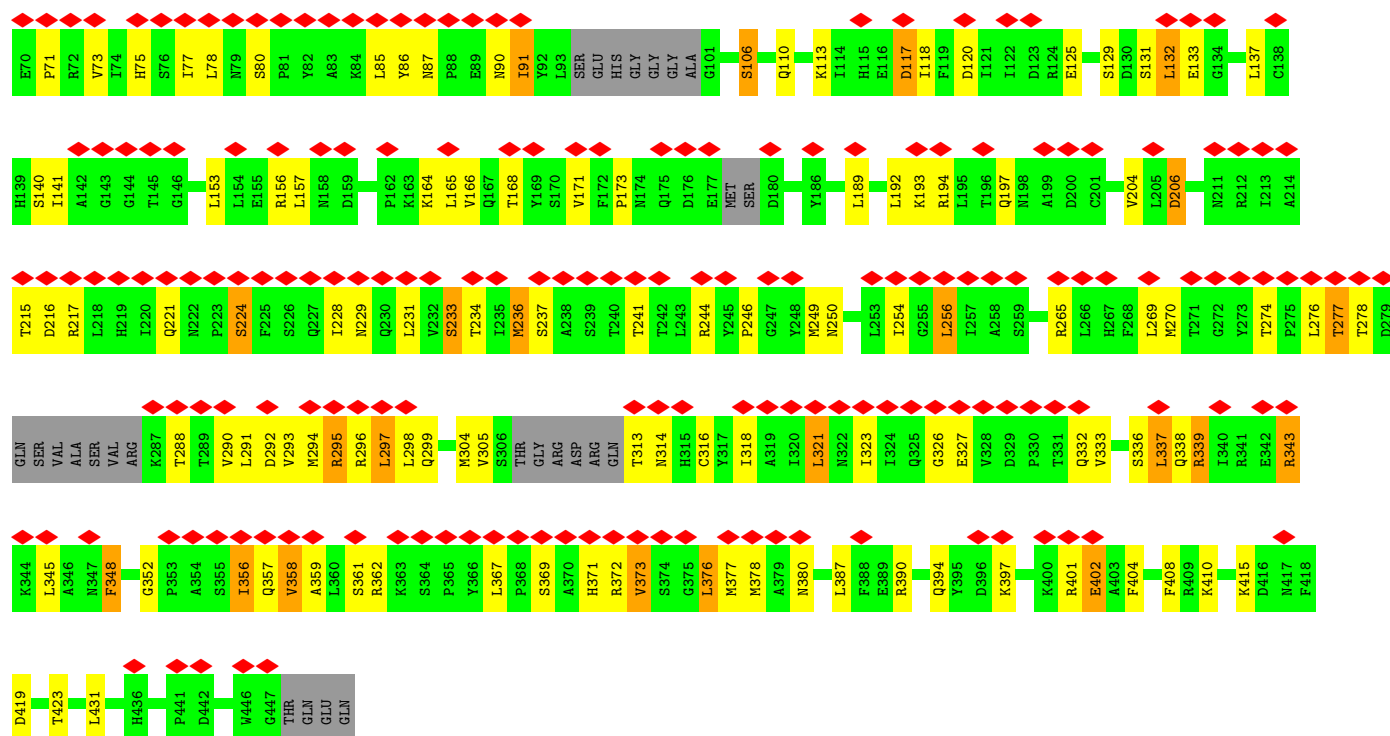
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Tubulin gamma-1 chain

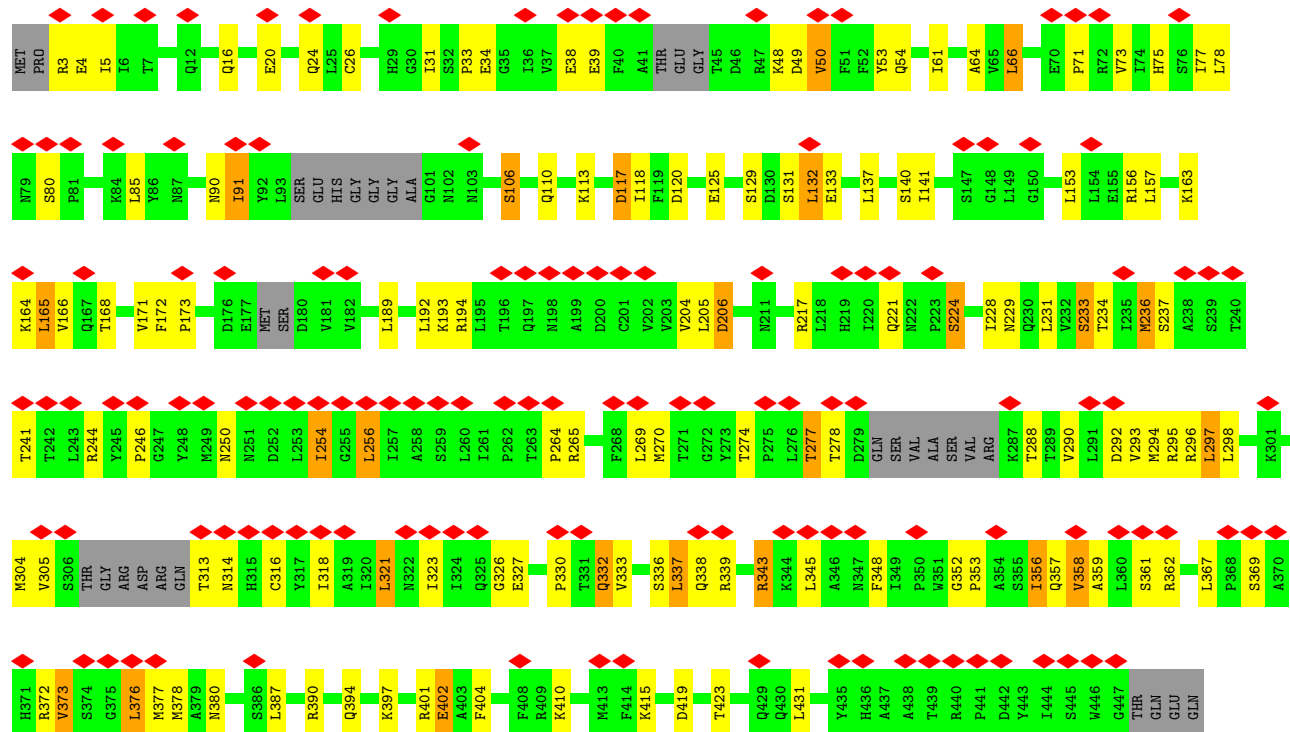


- Molecule 1: Tubulin gamma-1 chain

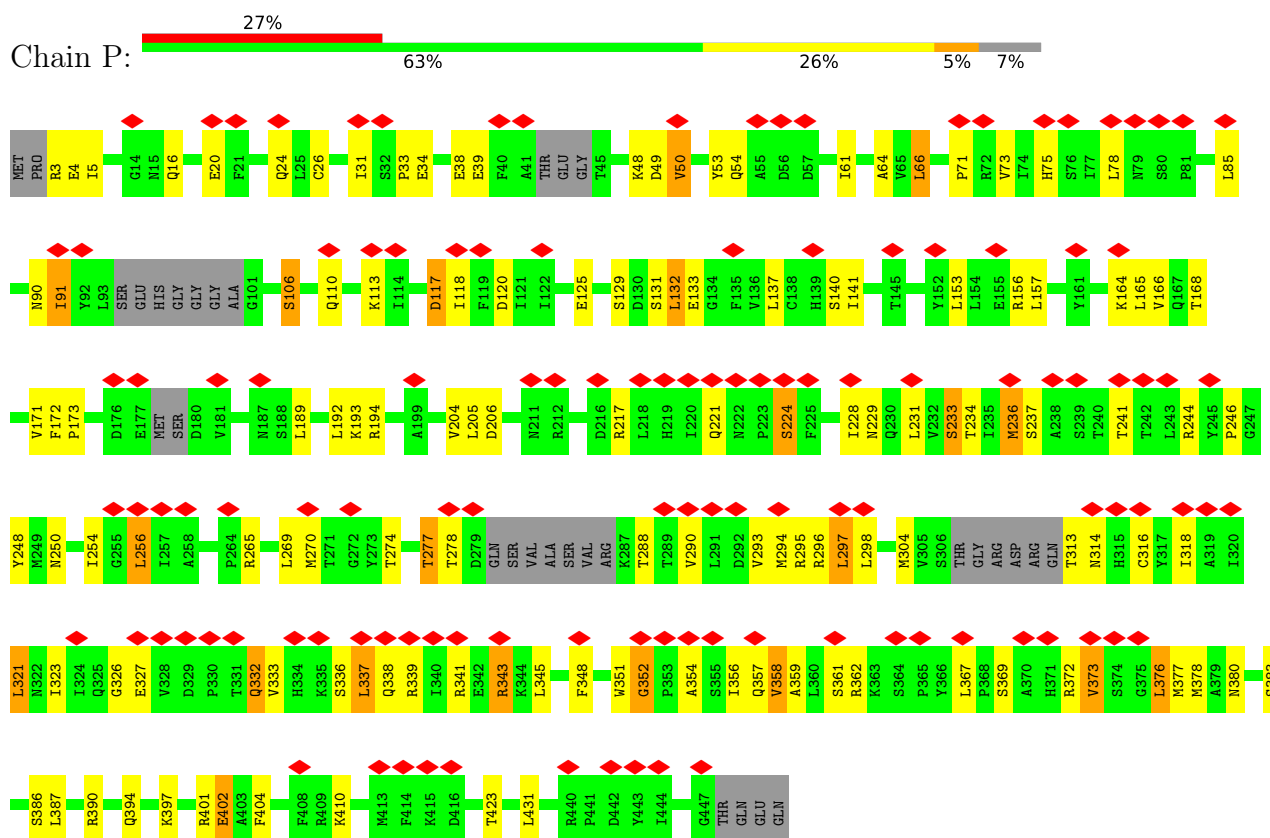




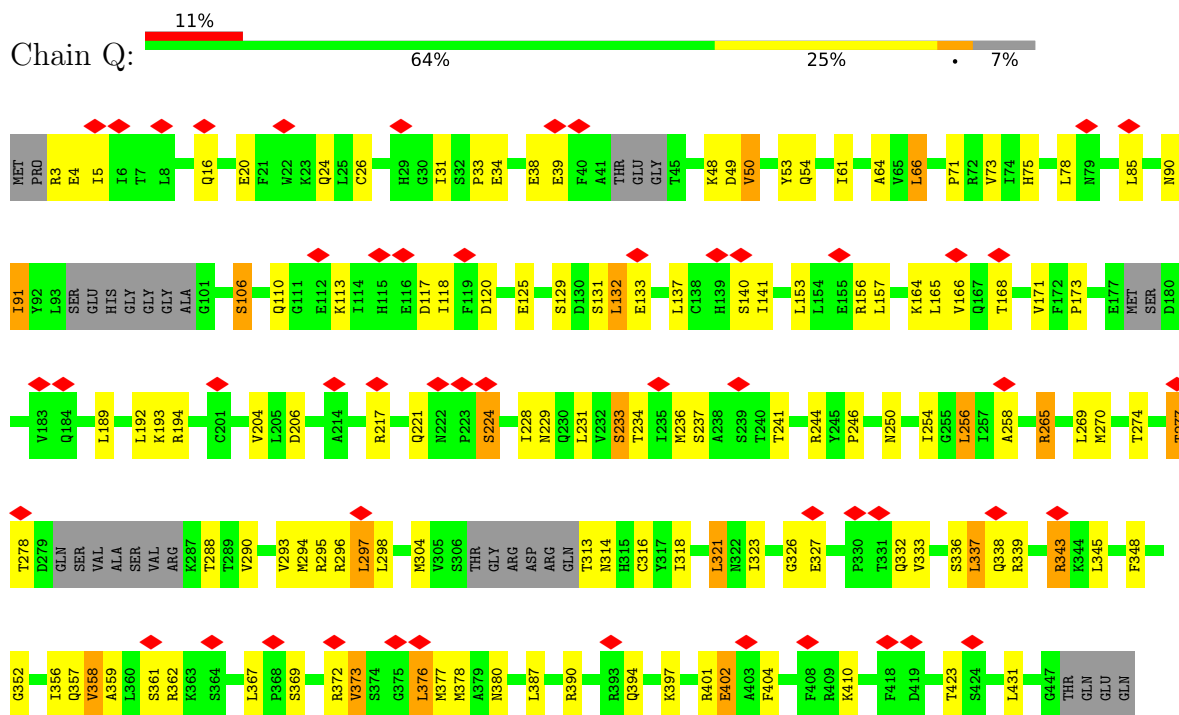
• Molecule 1: Tubulin gamma-1 chain



• Molecule 1: Tubulin gamma-1 chain

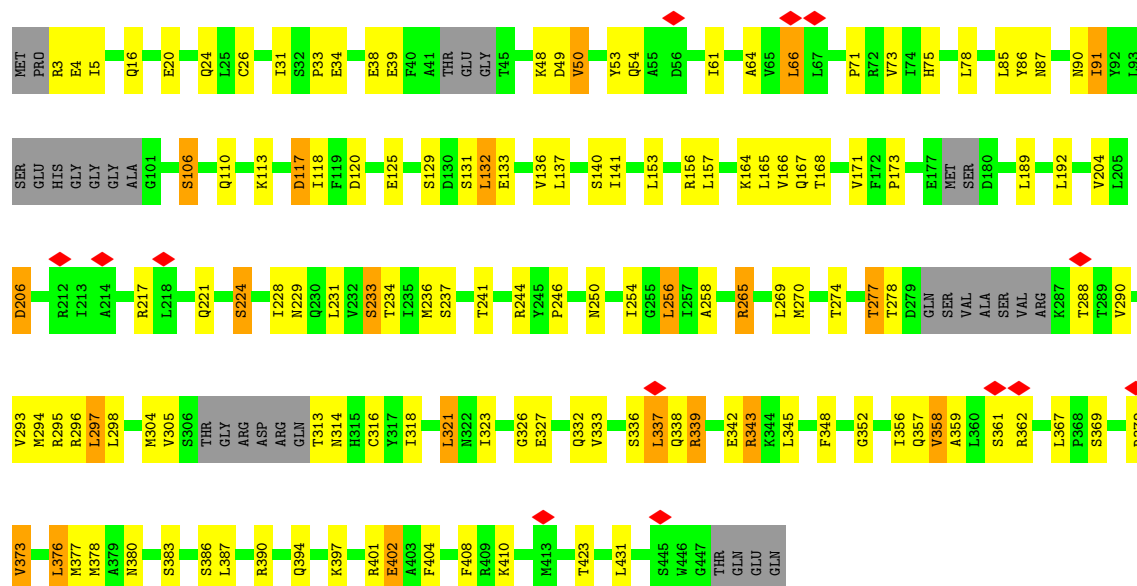


• Molecule 1: Tubulin gamma-1 chain



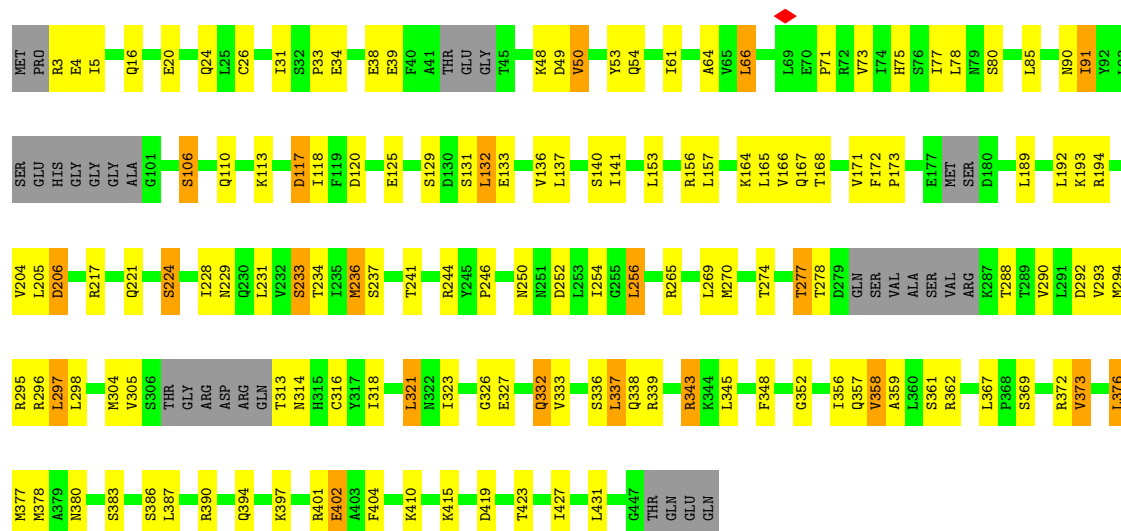
• Molecule 1: Tubulin gamma-1 chain





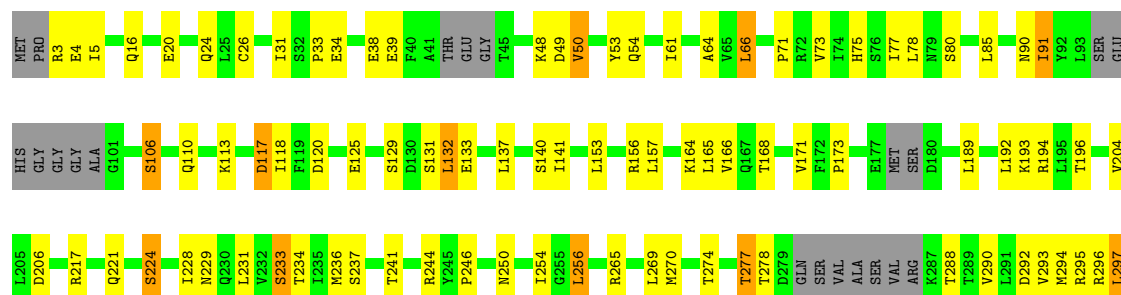
• Molecule 1: Tubulin gamma-1 chain

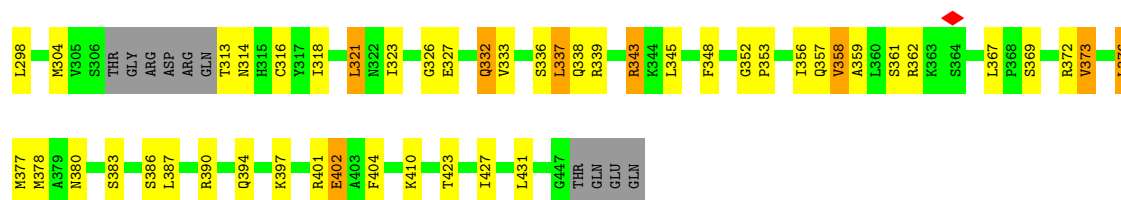
Chain S: 61% 27% 5% 7%



• Molecule 1: Tubulin gamma-1 chain

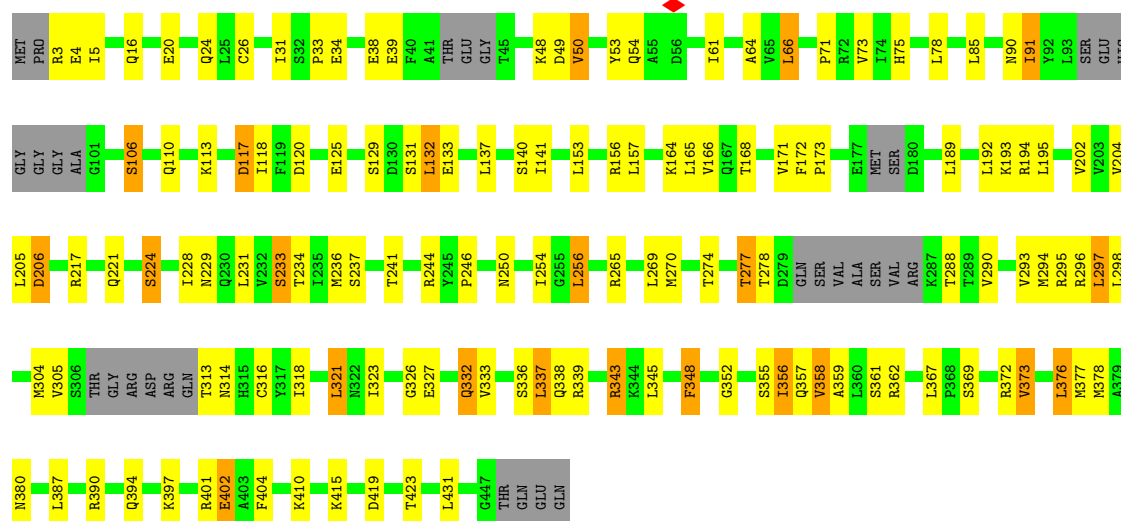
Chain T: 63% 26% 7%





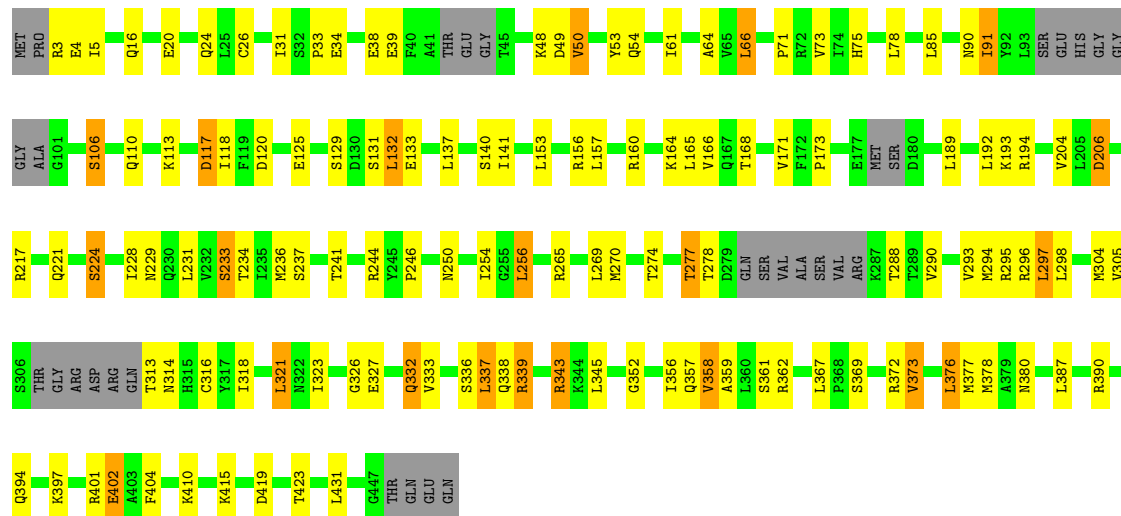
• Molecule 1: Tubulin gamma-1 chain

Chain U: 63% 25% 5% 7%



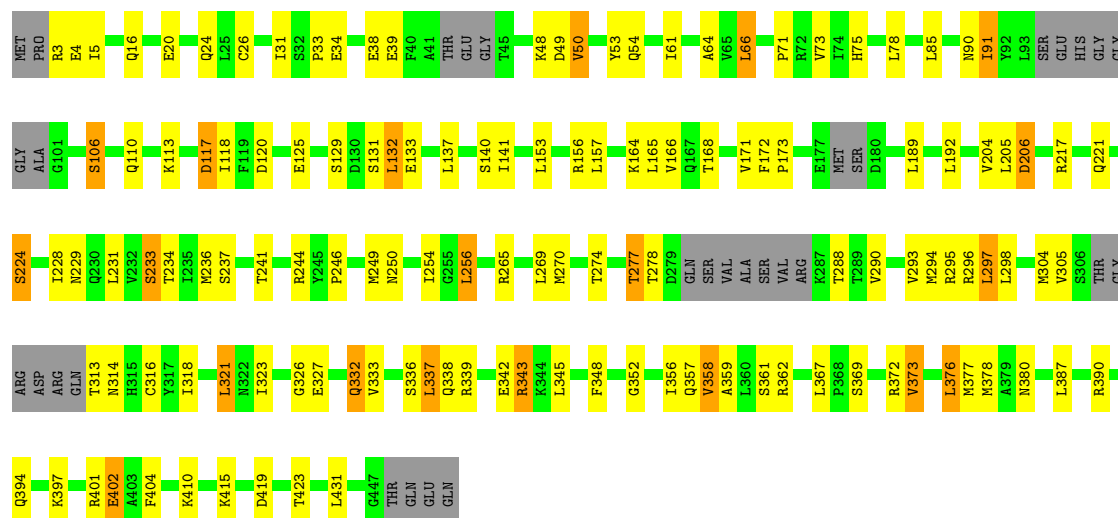
• Molecule 1: Tubulin gamma-1 chain

Chain V: 64% 25% 5% 7%



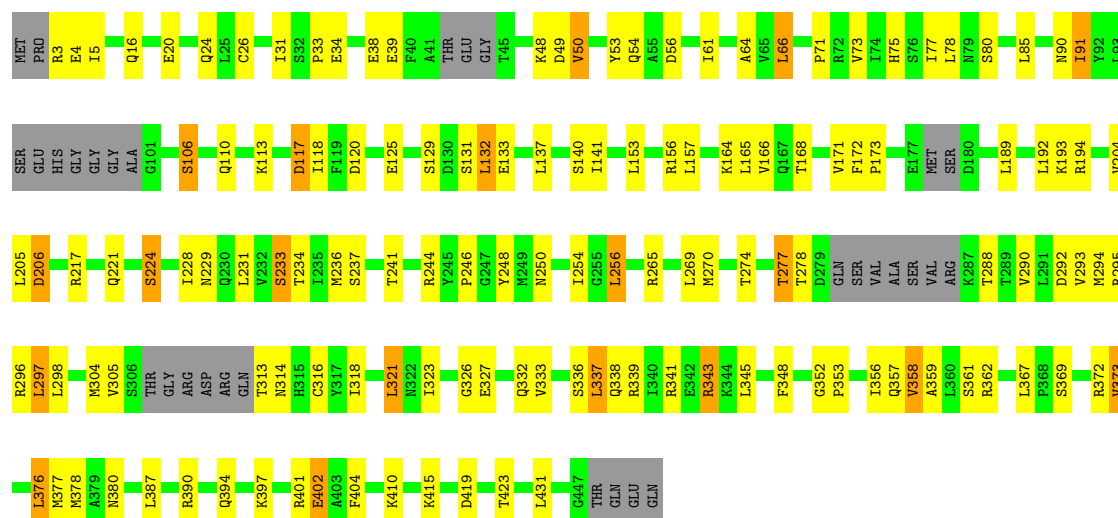
• Molecule 1: Tubulin gamma-1 chain

Chain W: 63% 25% 5% 7%



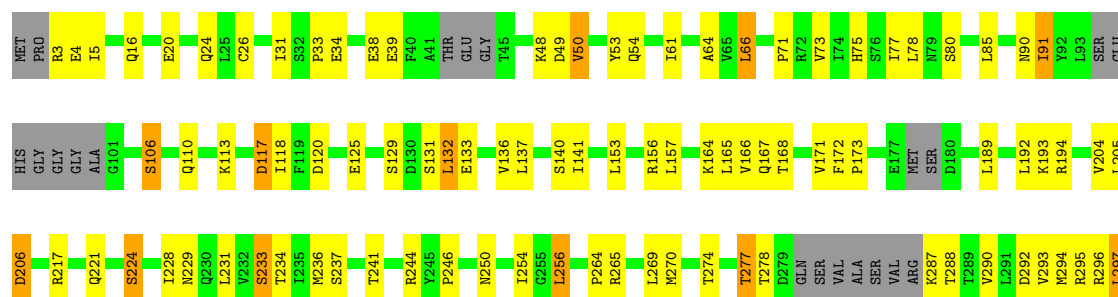
• Molecule 1: Tubulin gamma-1 chain

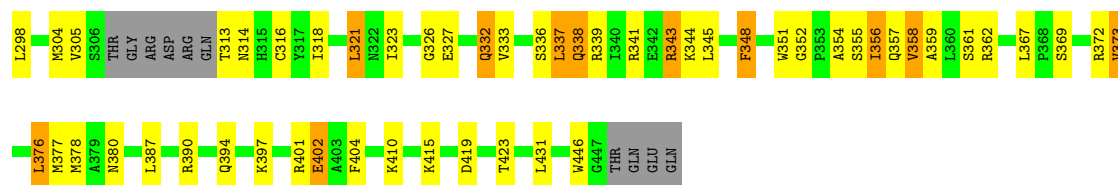
Chain X: 62% 27% 7%



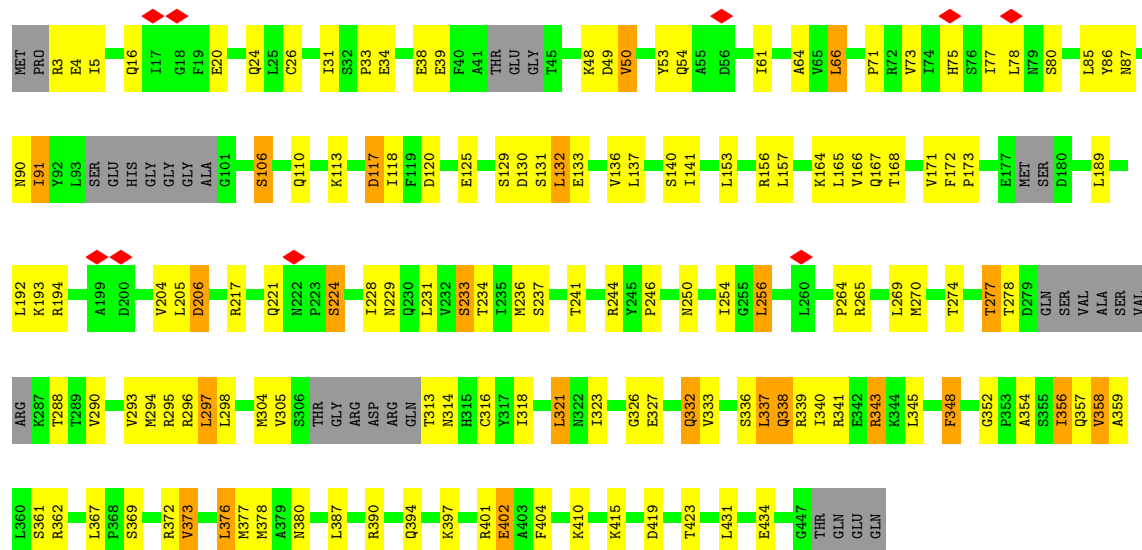
• Molecule 1: Tubulin gamma-1 chain

Chain Y: 61% 27% 5% 7%

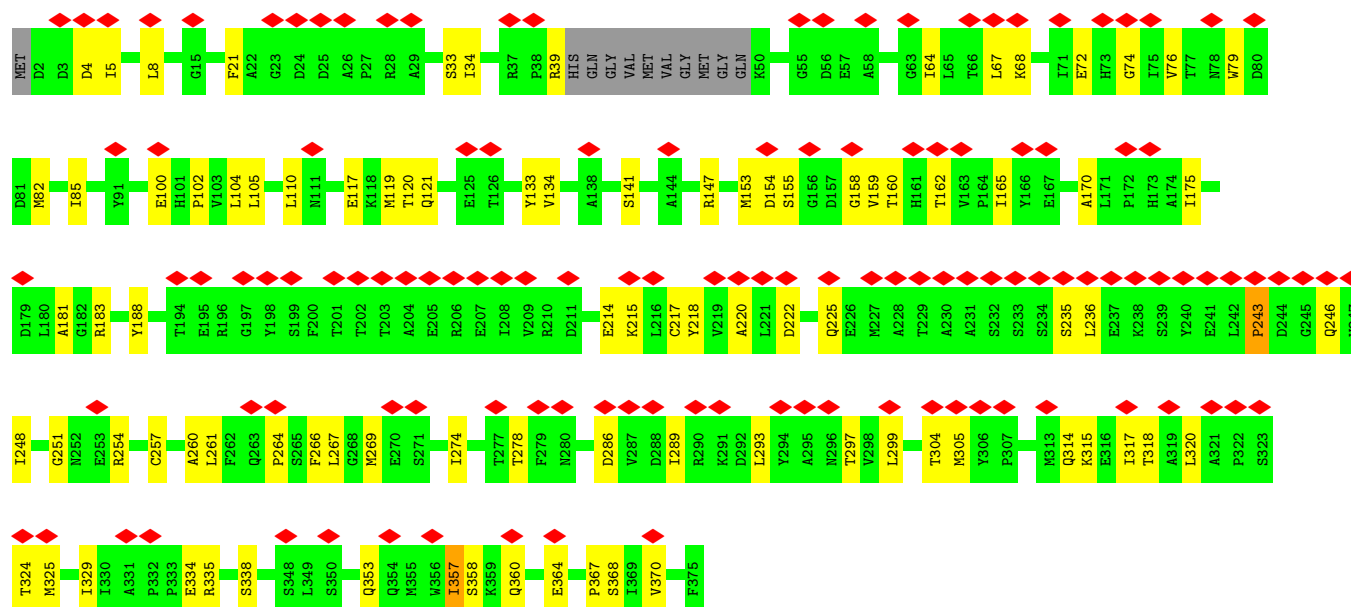




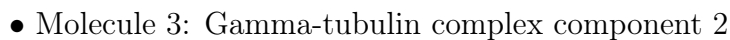
• Molecule 1: Tubulin gamma-1 chain

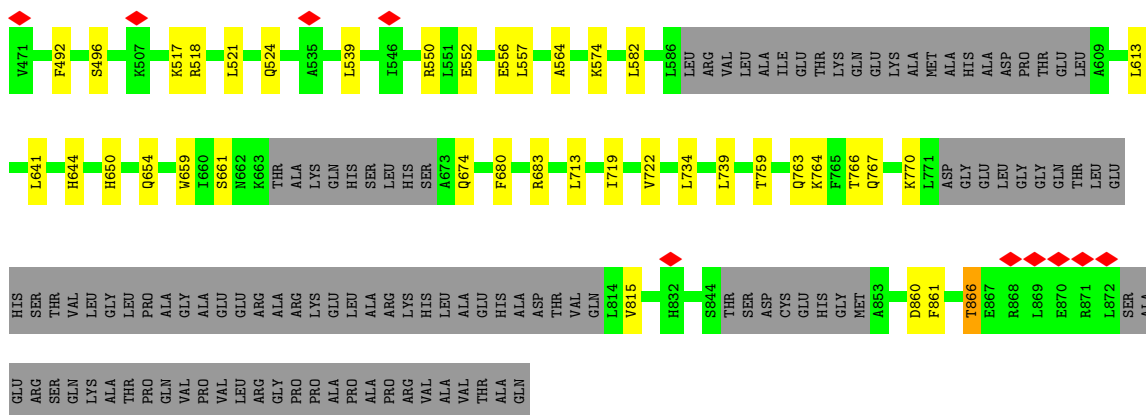


• Molecule 2: actin, cytoplasmic 1

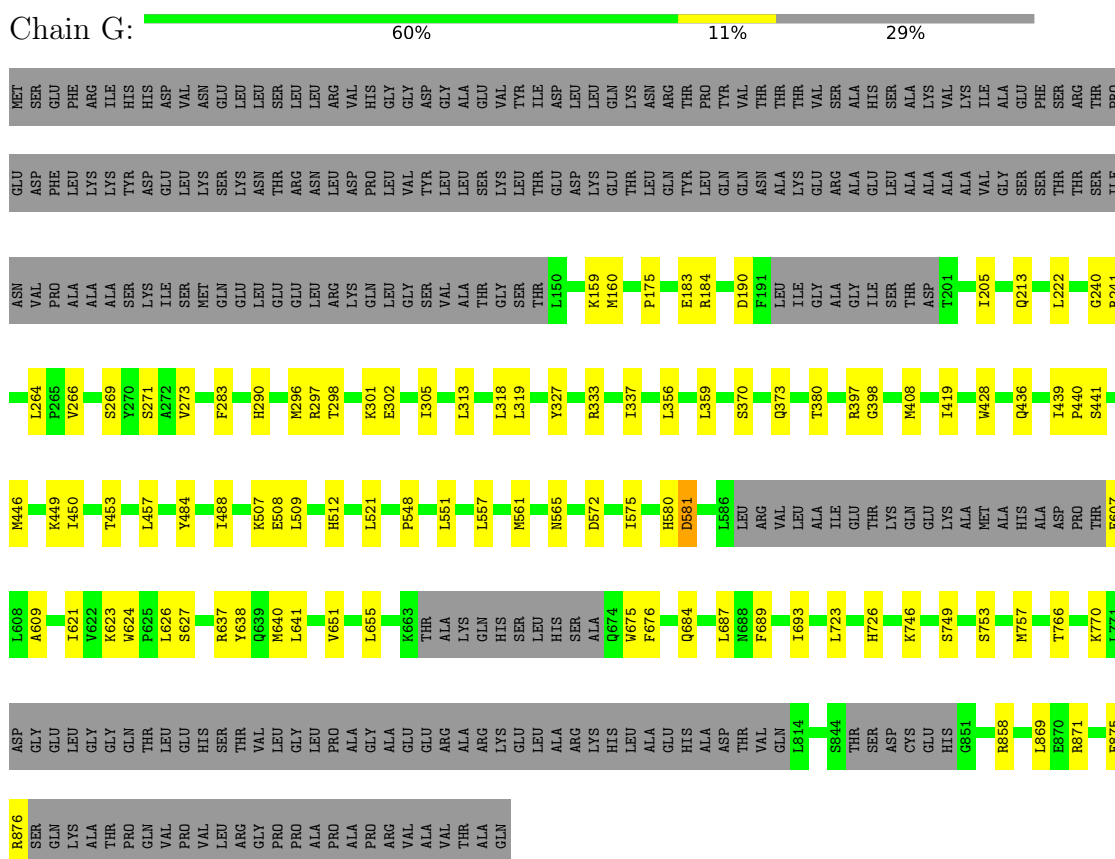


• Molecule 3: Gamma-tubulin complex component 2

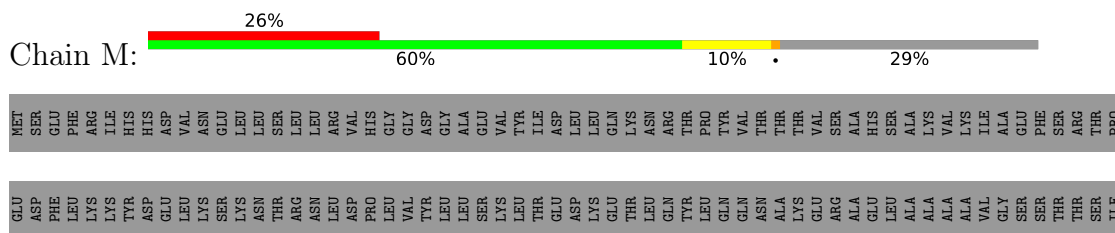




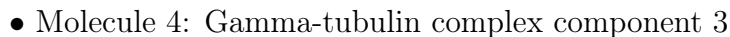
- Molecule 3: Gamma-tubulin complex component 2



- Molecule 3: Gamma-tubulin complex component 2





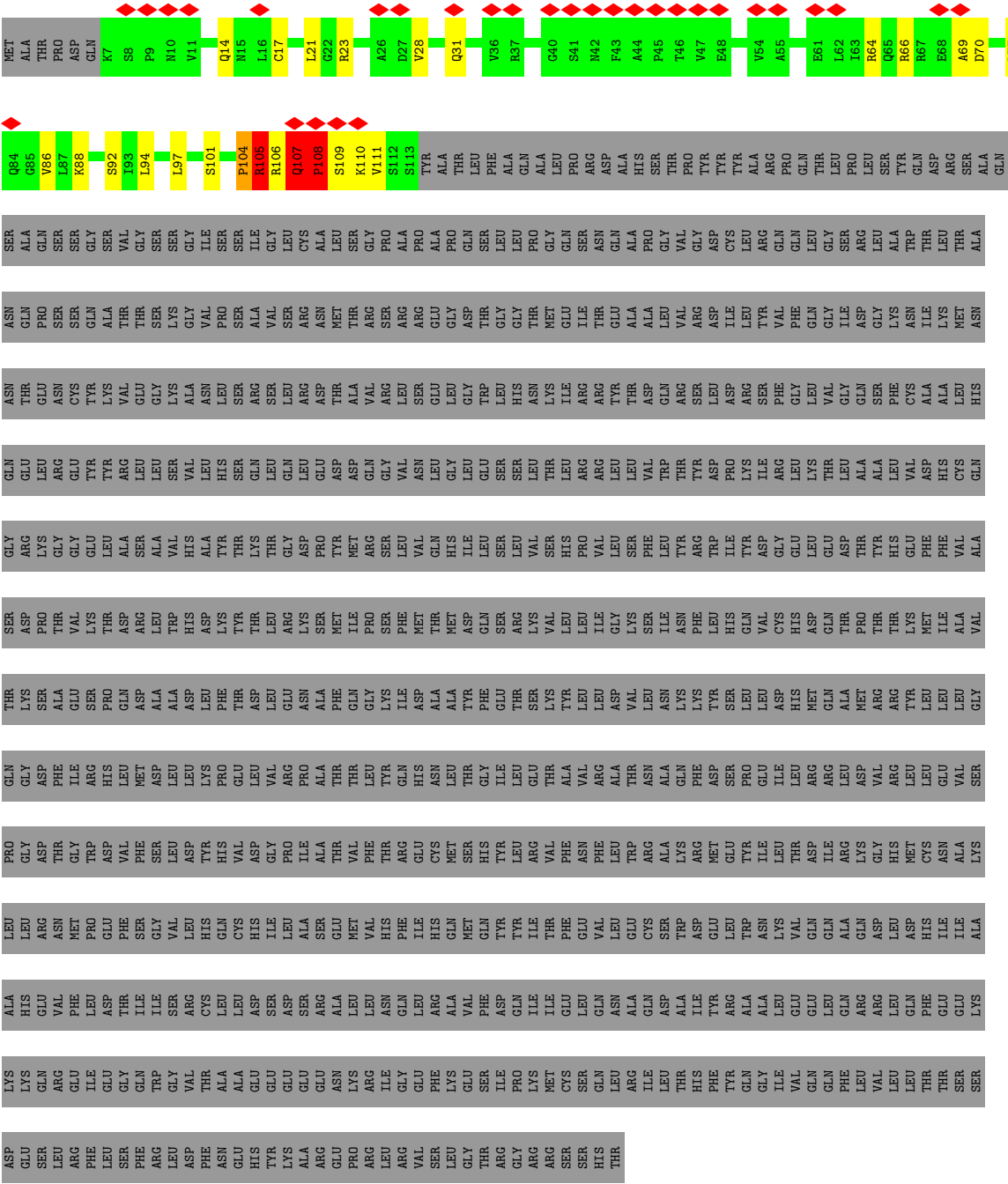


Lys	Ser	Leu	Thr	Ala	Ala	Pro	Met
Ser	Phe	Val	Asp	Ala	Gly	Ala	Ala
Ile	Leu	Trp	Gln	Leu	Gly	Gly	Thr
Asn	Tyr	Thr	Arg	Val	Val	Val	Pro
Phe	Arg	Tyr	Ser	Arg	Gly	Asp	Asp
Leu	Trp	Asp	Leu	Asp	Cys	Gln	Gln
His	Ile	Pro	Asp	Ile	Cys	Ala	K7
Gln	Tyr	Tyr	Arg	Leu	Leu	Arg	Ala
Val	Asp	Ile	Ser	Tyr	Leu	Pro	L12
Cys	Gly	Arg	Phe	Val	Gln	Gln	L13
His	Leu	Leu	Gly	Phe	Gln	Thr	L21
Asp	Leu	Lys	Leu	Gln	Leu	Leu	L21
Gln	Glj	Thr	Val	Gly	Gly	Pro	G22
Thr	Asp	Ala	Gly	Ile	Ser	Leu	R23
Pro	Thr	Leu	Gln	Asp	Arg	Ser	R23
Thr	Tyr	Ala	Ser	Gly	Leu	Tyr	A26
His	His	Leu	Phe	Lys	Ala	Gln	D27
Lys	Glj	Val	Cys	Asn	Trp	Asp	Q31
Met	Phe	Asp	Ala	Ile	Thr	Arg	Q31
Ile	Phe	His	Ala	Lys	Leu	Ser	Q31
Ala	Val	Cys	Leu	Lys	Thr	Ala	A35
Val	Ala	Gln	His	Asn	Ala	Gln	V36
Thr	Ser	Gly	Gln	Asn	Asn	Ser	F52
Lys	Asp	Arg	Glj	Thr	Gln	Ala	F52
Ser	Pro	Lys	Leu	Glj	Pro	Gln	L62
Ala	Thr	Gly	Arg	Asn	Ser	Ser	L62
Glj	Val	Gly	Glj	Cys	Ser	Gly	R67
Ser	Lys	Leu	Tyr	Lys	Ala	Ser	R67
Pro	Thr	Thr	Arg	Val	Thr	Val	L73
Gln	Asp	Ala	Leu	Val	Thr	Gly	L73
Ala	Leu	Ala	Leu	Gly	Ser	Ser	E76
Ala	Trp	Val	Ser	Lys	Lys	Ser	L77
Asp	His	His	Val	Lys	Gly	Gly	H78
Leu	Asp	Ala	Leu	Asn	Val	Ile	R79
Phe	Asp	Ala	Leu	Asn	Val	Ser	R79
Thr	Lys	Tyr	His	Leu	Pro	Ser	K88
Thr	Tyr	Thr	Ser	Ser	Ser	Ser	K88
Asp	Thr	Lys	Gln	Arg	Ala	Ile	N89
Leu	Leu	Thr	Leu	Ser	Val	Gly	N89
Glj	Arg	Gly	Gln	Leu	Ser	Leu	K90
Asn	Lys	Asp	Leu	Arg	Arg	Cys	K90
Ala	Ser	Pro	Glj	Asp	Asn	Leu	I33
Phe	Met	Tyr	Asp	Thr	Met	Ala	L94
Gln	Ile	Met	Asp	Ala	Thr	Ser	L94
Lys	Pro	Arg	Gln	Val	Arg	Ser	L96
Gly	Ser	Ser	Gly	Val	Ser	Gly	L97
Ile	Phe	Leu	Val	Leu	Arg	Pro	L98
Asp	Met	Val	Asn	Ser	Arg	Ala	S99
Ala	Thr	Gln	Leu	Ser	Arg	Pro	S99
Ala	Met	His	Leu	Glj	Ala	Ala	R105
Ala	Thr	Asp	Gly	Leu	Gly	Pro	R105
Tyr	Asp	Ile	Leu	Gly	Asp	Gln	Aln
Phe	Gln	Leu	Glj	Trp	Thr	Ser	Pro
Glj	Ser	Ser	Ser	Leu	Gly	Leu	Ser
Thr	Arg	Leu	Ser	His	Gly	Leu	Lys
Lys	Lys	Val	Leu	Asn	Thr	Pro	Val
Lys	Val	Ser	Thr	Lys	Met	Gly	Val
Tyr	Leu	His	Leu	Lys	Arg	Gln	S113
Leu	Leu	His	Arg	Ile	Glj	Ser	Y114
Ile	Ile	Val	Arg	Arg	Ile	Asn	Y114
Ser	Gly	Leu	Leu	Tyr	Thr	Gln	Ser
Leu	Leu	Leu	Thr	Ala	Ala	Ala	Ser
Asp	Leu	Leu	Leu	Thr	Ala	Gln	Ser

- Molecule 4: Gamma-tubulin complex component 3



GLN	ASP	GLY	LYS	ASP	MET	PRO	THR	ALA	GLN	ASP	ARG	ASP	GLY	LEU	ARG	SER	MET
ASP	LEU	HIS	HIS	ARG	ARG	THR	THR	ALA	LEU	ALA	SER	THR	HIS	GLN	ALA	TYR	ALA
ASP	ASP	MET	GLY	LEU	TYR	LYS	GLU	VAL	GLU	VAL	GLY	ASP	GLN	TRP	ALA	ASP	THR
HIS	HIS	CYS	CYS	LEU	LEU	ILE	PHE	HIS	ALA	HIS	ALA	LEU	ALA	LEU	SER	GLN	GLN
ILE	ILE	ASN	ALA	GLU	VAL	VAL	VAL	CYS	GLN	CYS	GLN	LEU	LEU	THR	ALA	ALA	K7
ILE	ALA	LYS	LYS	SER	GLY	VAL	ALA	VAL	ALA	ALA	GLN	ALA	GLN	ALA	GLN	GLN	R37
ALA	ALA	PRO	GLY	GLY	GLN	THR	SER	ARG	GLY	GLN	GLN	ALA	ASN	ALA	SER	ALA	V38
HIS	LEU	LEU	GLY	GLY	GLN	LYS	ASP	GLY	THR	ASP	LEU	GLN	PRO	GLN	SER	GLN	I39
GLU	GLU	ASP	ASP	PHE	ASP	ALA	THR	GLY	GLY	ARG	GLY	ASN	ASN	SER	SER	SER	G40
VAL	VAL	THR	GLY	ILE	ILE	GLU	VAL	GLY	GLY	GLU	GLU	CYS	SER	SER	SER	SER	S41
PHE	LEU	PRO	PRO	ARG	ARG	SER	LYS	GLU	GLU	THR	TYR	TYR	TYR	GLY	GLY	GLY	M42
ASP	ASP	ASP	ASP	HIS	LEU	PRO	THR	ARG	GLY	TYR	TYR	LYS	ALA	SER	SER	SER	F43
THR	THR	PHE	PHE	VAL	VAL	GLN	ASP	ALA	ALA	ARG	ARG	VAL	VAL	VAL	VAL	VAL	A44
ILE	ILE	PHE	PHE	MET	MET	ASP	ASP	SER	SER	LEU	LEU	GLU	GLY	THR	THR	GLY	E61
ILE	SER	ASP	GLY	ASP	LEU	ALA	LEU	ALA	VAL	SER	SER	LYS	GLY	SER	SER	SER	E61
SER	LEU	LEU	LEU	LEU	LEU	ASP	THR	VAL	HIS	VAL	VAL	ALA	ALA	GLY	GLY	GLY	R64
ARG	ASP	TYR	TYR	LYS	LYS	ASP	ASP	ALA	HIS	VAL	VAL	ALA	ASN	VAL	ILE	ILE	S92
CYS	CYS	HIS	HIS	PRO	PRO	PHE	LEU	LYS	THR	THR	HIS	LEU	LEU	PRO	SER	SER	S92
LEU	LEU	VAL	CYS	GLU	GLU	THR	THR	THR	LYS	GLN	GLN	ARG	ALA	ILE	ILE	ILE	Y96
ASP	ASP	HIS	HIS	VAL	VAL	ASP	THR	THR	LYS	THR	LEU	ARG	ARG	VAL	GLY	GLY	Y96
SER	SER	ILE	ILE	ARG	ARG	LEU	LEU	THR	THR	GLN	GLN	LYS	LEU	SER	SER	SER	R106
ASP	ASP	ALA	ALA	PRO	PRO	ASN	ASN	ASP	GLY	ASP	GLY	LYS	ARG	ARG	CYS	CYS	G107
ARG	ARG	SER	SER	ALA	ALA	PHE	PHE	SER	THR	THR	ASP	ASP	ASN	ALA	ALA	ALA	P108
ALA	ALA	THR	THR	THR	THR	GLN	ILE	MET	THR	THR	ASP	THR	THR	THR	LEU	SER	V111
LEU	LEU	VAL	VAL	THR	THR	GLY	PRO	MET	ILE	ILE	GLN	VAL	VAL	ARG	GLY	GLY	S112
LEU	LEU	ASN	ASN	THR	THR	LYS	THR	SER	PRO	ARG	GLN	ARG	ARG	SER	PRO	PRO	S113
ASN	ASN	HIS	HIS	ILE	ILE	ILE	PHE	LEU	PHE	VAL	VAL	LEU	LEU	ALA	ALA	ALA	TYR
ARG	ARG	GLN	GLN	HIS	LEU	ALA	THR	GLN	THR	GLN	LEU	GLU	GLU	ARG	PRO	ALA	ALA
ALA	ALA	GLN	GLN	LEU	LEU	ALA	MET	HIS	THR	HIS	LEU	GLU	GLY	THR	PRO	PRO	THR
VAL	VAL	ASN	ASN	THR	THR	LYS	VAL	VAL	VAL	VAL	SER	ASN	ASN	THR	GLY	GLY	LEU
THR	THR	THR	THR	THR	THR	LYS	VAL	SER	SER	VAL	SER	LEU	LEU	MET	GLY	GLY	PRO
ILE	ILE	THR	THR	THR	THR	TYR	ASP	HIS	ILE	ILE	THR	ILE	ILE	ILE	GLN	GLN	ARG
GLU	GLU	PHE	PHE	ALA	ALA	TYR	LEU	LEU	LEU	LEU	LEU	ARG	ARG	ILE	SER	SER	ASP
LEU	LEU	VAL	VAL	VAL	VAL	LEU	ILE	VAL	VAL	VAL	VAL	ARG	THR	THR	ASN	ASN	ALA
ASN	ASN	GLY	GLY	GLY	GLY	ASP	GLY	GLY	GLY	GLY							



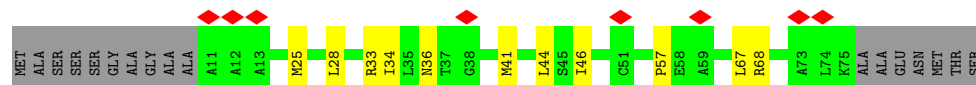
● Molecule 5: Mitotic-spindle organizing protein 1



● Molecule 5: Mitotic-spindle organizing protein 1



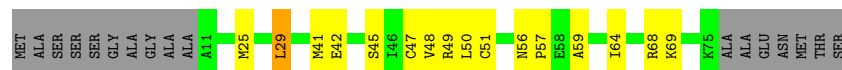
- Molecule 5: Mitotic-spindle organizing protein 1



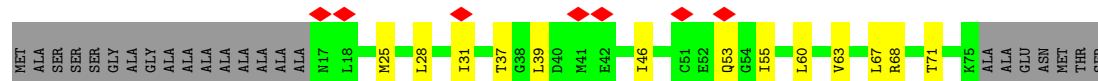
- Molecule 5: Mitotic-spindle organizing protein 1



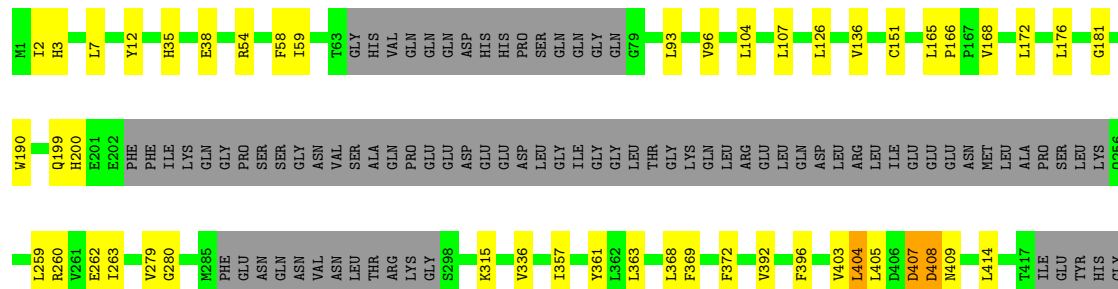
- Molecule 5: Mitotic-spindle organizing protein 1



- Molecule 5: Mitotic-spindle organizing protein 1



- Molecule 6: Gamma-tubulin complex component 4







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

PHE	LEU	LEU	LEU	LEU	LEU
PHE	PHE	PHE	PHE	PHE	PHE
LYS	LYS	LYS	LYS	LYS	LYS
VAL	VAL	VAL	VAL	VAL	VAL
THR	THR	THR	THR	THR	THR
LYS	LYS	LYS	LYS	LYS	LYS
VAL	VAL	VAL	VAL	VAL	VAL
ASN	ASN	ASN	ASN	ASN	ASN
ARG	ARG	ARG	ARG	ARG	ARG
GLY	GLY	GLY	GLY	GLY	GLY
TYR	TYR	TYR	TYR	TYR	TYR
GLN	GLN	GLN	GLN	GLN	GLN
ASP	ASP	ASP	ASP	ASP	ASP
PHE	PHE	PHE	PHE	PHE	PHE
LEU	LEU	LEU	LEU	LEU	LEU
LEU	LEU	LEU	LEU	LEU	LEU
ARG	ARG	ARG	ARG	ARG	ARG
ILE	ILE	ILE	ILE	ILE	ILE
ASN	ASN	ASN	ASN	ASN	ASN
PHE	PHE	PHE	PHE	PHE	PHE
ASN	ASN	ASN	ASN	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN
TYR	TYR	TYR	TYR	TYR	TYR
TYR	TYR	TYR	TYR	TYR	TYR
GLN	GLN	GLN	GLN	GLN	GLN
ASP	ASP	ASP	ASP	ASP	ASP
ALA	ALA	ALA	ALA	ALA	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36881	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.292	Depositor
Minimum map value	-0.125	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0224	Depositor
Map size ($\text{\AA}$)	532.0, 532.0, 532.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.66, 2.66, 2.66	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.30	0/3441	0.71	2/4661 (0.0%)
1	2	0.31	0/3441	0.72	2/4661 (0.0%)
1	O	0.31	0/3441	0.71	2/4661 (0.0%)
1	P	0.31	0/3441	0.72	2/4661 (0.0%)
1	Q	0.31	0/3441	0.72	2/4661 (0.0%)
1	R	0.30	0/3441	0.72	2/4661 (0.0%)
1	S	0.30	0/3441	0.72	2/4661 (0.0%)
1	T	0.30	0/3441	0.72	2/4661 (0.0%)
1	U	0.30	0/3441	0.71	2/4661 (0.0%)
1	V	0.30	0/3441	0.71	2/4661 (0.0%)
1	W	0.30	0/3441	0.72	2/4661 (0.0%)
1	X	0.30	0/3441	0.72	2/4661 (0.0%)
1	Y	0.30	0/3441	0.72	2/4661 (0.0%)
1	Z	0.30	0/3441	0.72	2/4661 (0.0%)
2	e	0.51	2/2908 (0.1%)	0.80	1/3938 (0.0%)
3	A	0.43	0/5085	0.82	4/6866 (0.1%)
3	C	0.36	0/5151	0.81	10/6955 (0.1%)
3	E	0.35	0/5325	0.75	10/7187 (0.1%)
3	G	0.38	0/5325	0.79	4/7187 (0.1%)
3	M	0.48	2/5295 (0.0%)	0.86	5/7147 (0.1%)
4	B	0.40	0/5133	0.81	4/6930 (0.1%)
4	D	0.34	0/4897	0.74	3/6610 (0.0%)
4	F	0.39	0/5044	0.81	15/6809 (0.2%)
4	H	0.40	0/5009	0.77	2/6761 (0.0%)
4	N	0.42	1/5009 (0.0%)	0.82	7/6761 (0.1%)
4	a	0.31	0/948	0.71	1/1277 (0.1%)
4	f	0.33	0/876	0.90	8/1178 (0.7%)
4	h	0.34	0/876	0.89	2/1178 (0.2%)
4	j	0.32	0/876	0.76	2/1178 (0.2%)
5	b	0.40	0/484	0.85	0/653
5	d	0.33	0/454	0.68	0/611
5	g	0.32	0/484	0.73	1/653 (0.2%)
5	i	0.30	0/484	0.61	0/653
5	k	0.30	0/484	0.62	0/653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	m	0.29	0/484	0.60	0/653
6	I	0.41	0/4322	0.76	5/5853 (0.1%)
6	K	0.40	0/4683	0.80	5/6338 (0.1%)
7	J	0.41	0/4525	0.88	13/6119 (0.2%)
7	l	0.37	0/894	0.82	2/1209 (0.2%)
8	L	0.36	0/4697	0.74	2/6348 (0.0%)
8	c	0.34	0/1235	0.72	0/1664
All	All	0.36	5/129161 (0.0%)	0.77	134/174623 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
1	2	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
1	Y	0	1
1	Z	0	1
3	C	0	1
3	E	0	2
3	G	0	2
3	M	0	5
4	B	0	1
4	N	0	4
4	f	0	3
4	h	0	1
6	I	0	2
6	K	0	3
7	J	0	5
8	L	0	1
All	All	0	44

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	e	243	PRO	N-CD	16.99	1.71	1.47
3	M	404	TYR	CD1-CE1	9.59	1.67	1.38
2	e	257	CYS	C-N	7.31	1.39	1.33
3	M	404	TYR	CD2-CE2	5.61	1.55	1.38
4	N	405	LYS	CG-CD	5.23	1.68	1.52

All (134) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	108	PRO	CA-N-CD	-9.93	98.10	112.00
4	D	418	ILE	N-CA-C	-9.68	104.06	111.90
4	j	108	PRO	CA-N-CD	-9.41	98.82	112.00
7	l	121	PRO	CA-N-CD	-8.99	99.41	112.00
4	h	108	PRO	CA-N-CD	-8.66	99.87	112.00
4	F	725	GLU	CA-C-N	-8.52	114.40	122.66
4	F	725	GLU	C-N-CA	-8.52	114.40	122.66
6	K	574	ILE	N-CA-C	-8.45	105.68	113.71
7	l	130	PRO	CA-N-CD	-8.13	100.62	112.00
4	f	107	GLN	C-N-CD	-7.91	92.56	125.00
3	C	468	THR	CA-C-N	7.65	135.47	120.94
3	C	468	THR	C-N-CA	7.65	135.47	120.94
7	J	235	SER	CA-C-N	7.29	135.46	121.54
7	J	235	SER	C-N-CA	7.29	135.46	121.54
4	f	107	GLN	CA-C-N	7.21	128.85	119.84
4	f	107	GLN	C-N-CA	7.21	128.85	119.84
3	M	240	GLY	CA-C-N	7.09	135.09	121.54
3	M	240	GLY	C-N-CA	7.09	135.09	121.54
3	A	483	ALA	N-CA-C	-6.86	104.17	112.54
4	F	269	ASN	CA-C-N	6.81	132.54	122.74
4	F	269	ASN	C-N-CA	6.81	132.54	122.74
4	j	41	SER	N-CA-C	-6.57	107.13	114.62
7	J	237	HIS	CA-C-N	6.45	133.86	121.54
7	J	237	HIS	C-N-CA	6.45	133.86	121.54
7	J	727	PHE	N-CA-C	-6.39	101.07	110.52
3	E	240	GLY	CA-C-N	6.37	133.70	121.54
3	E	240	GLY	C-N-CA	6.37	133.70	121.54
4	N	405	LYS	CB-CG-CD	6.25	125.68	111.30
7	J	840	VAL	N-CA-C	-6.22	107.80	113.71
1	V	339	ARG	CB-CG-CD	-6.12	97.21	111.30
1	Z	339	ARG	CB-CG-CD	-6.12	97.21	111.30
7	J	255	PRO	CA-C-N	6.12	132.72	121.70
7	J	255	PRO	C-N-CA	6.12	132.72	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	339	ARG	CB-CG-CD	-6.12	97.22	111.30
1	Q	339	ARG	CB-CG-CD	-6.12	97.22	111.30
1	1	339	ARG	CB-CG-CD	-6.12	97.23	111.30
1	U	339	ARG	CB-CG-CD	-6.12	97.23	111.30
1	S	339	ARG	CB-CG-CD	-6.11	97.24	111.30
1	Y	339	ARG	CB-CG-CD	-6.11	97.24	111.30
1	O	339	ARG	CB-CG-CD	-6.11	97.24	111.30
1	P	339	ARG	CB-CG-CD	-6.11	97.25	111.30
1	R	339	ARG	CB-CG-CD	-6.11	97.25	111.30
1	W	339	ARG	CB-CG-CD	-6.11	97.25	111.30
1	2	339	ARG	CB-CG-CD	-6.10	97.27	111.30
1	X	339	ARG	CB-CG-CD	-6.09	97.29	111.30
3	C	273	VAL	N-CA-C	-6.02	107.06	112.12
4	F	272	GLU	CA-C-N	5.97	132.95	121.54
4	F	272	GLU	C-N-CA	5.97	132.95	121.54
3	G	264	LEU	N-CA-C	5.96	122.98	109.81
3	E	423	TYR	N-CA-C	-5.91	104.93	114.09
4	D	463	LYS	N-CA-C	-5.90	104.95	114.09
4	H	578	MET	CB-CG-SD	-5.82	95.24	112.70
3	E	431	ARG	N-CA-C	-5.76	108.05	114.62
3	E	173	HIS	CA-C-N	5.72	129.38	120.68
3	E	173	HIS	C-N-CA	5.72	129.38	120.68
3	A	389	GLU	N-CA-C	-5.68	106.06	112.87
4	F	432	ARG	N-CA-C	-5.59	107.11	114.04
4	F	526	LEU	N-CA-C	-5.57	103.65	110.61
4	f	104	PRO	CA-C-O	-5.54	115.45	121.77
4	h	112	SER	N-CA-C	5.53	122.58	110.80
8	L	306	HIS	CA-C-N	5.53	132.10	121.54
8	L	306	HIS	C-N-CA	5.53	132.10	121.54
3	G	581	ASP	N-CA-CB	-5.52	101.16	110.49
3	E	479	LEU	CA-C-N	5.52	132.08	121.54
3	E	479	LEU	C-N-CA	5.52	132.08	121.54
1	X	402	GLU	CA-CB-CG	5.45	124.99	114.10
1	1	402	GLU	CA-CB-CG	5.43	124.96	114.10
1	Z	402	GLU	CA-CB-CG	5.42	124.95	114.10
1	2	402	GLU	CA-CB-CG	5.42	124.95	114.10
3	G	419	ILE	CA-C-N	5.42	131.90	121.54
3	G	419	ILE	C-N-CA	5.42	131.90	121.54
4	f	104	PRO	CA-C-N	5.42	131.89	121.54
4	f	104	PRO	C-N-CA	5.42	131.89	121.54
1	R	402	GLU	CA-CB-CG	5.41	124.92	114.10
1	P	402	GLU	CA-CB-CG	5.41	124.92	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	402	GLU	CA-CB-CG	5.41	124.92	114.10
1	S	402	GLU	CA-CB-CG	5.41	124.91	114.10
1	T	402	GLU	CA-CB-CG	5.40	124.91	114.10
1	Y	402	GLU	CA-CB-CG	5.40	124.91	114.10
3	C	815	VAL	CA-C-N	5.40	132.25	123.93
3	C	815	VAL	C-N-CA	5.40	132.25	123.93
1	U	402	GLU	CA-CB-CG	5.40	124.91	114.10
1	W	402	GLU	CA-CB-CG	5.40	124.90	114.10
1	V	402	GLU	CA-CB-CG	5.39	124.89	114.10
1	Q	402	GLU	CA-CB-CG	5.39	124.88	114.10
4	D	590	THR	N-CA-C	-5.38	106.46	114.64
6	I	504	HIS	CA-C-N	5.37	131.80	121.54
6	I	504	HIS	C-N-CA	5.37	131.80	121.54
6	K	654	TYR	N-CA-C	-5.34	104.75	113.19
4	f	105	ARG	N-CA-C	5.33	122.16	110.80
3	C	564	ALA	N-CA-C	-5.32	105.84	114.09
4	F	697	PHE	CA-C-N	5.30	127.64	120.38
4	F	697	PHE	C-N-CA	5.30	127.64	120.38
4	N	497	CYS	CA-C-N	5.27	131.61	121.54
4	N	497	CYS	C-N-CA	5.27	131.61	121.54
6	K	255	LYS	N-CA-C	-5.25	99.61	110.80
3	E	241	ARG	N-CA-C	5.25	121.99	110.80
6	I	2	ILE	N-CA-C	-5.25	107.24	111.91
3	E	264	LEU	N-CA-C	5.25	120.81	113.57
4	H	454	VAL	CA-C-O	-5.24	115.96	121.41
7	J	302	VAL	N-CA-C	-5.23	102.44	108.82
7	J	256	LEU	CA-C-N	5.22	131.52	121.54
7	J	256	LEU	C-N-CA	5.22	131.52	121.54
3	C	250	PRO	CA-C-N	5.20	131.94	123.93
3	C	250	PRO	C-N-CA	5.20	131.94	123.93
4	B	361	SER	CA-C-N	5.20	130.23	122.74
4	B	361	SER	C-N-CA	5.20	130.23	122.74
6	K	645	LEU	CA-CB-CG	5.19	134.46	116.30
3	A	388	PHE	CA-CB-CG	-5.18	108.61	113.80
4	N	626	LEU	CA-C-N	5.18	128.44	120.82
4	N	626	LEU	C-N-CA	5.18	128.44	120.82
7	J	210	PRO	CA-C-N	5.18	131.44	121.54
7	J	210	PRO	C-N-CA	5.18	131.44	121.54
3	C	861	PHE	CA-C-N	-5.14	115.51	123.17
3	C	861	PHE	C-N-CA	-5.14	115.51	123.17
3	M	561	MET	CB-CG-SD	-5.14	97.28	112.70
4	a	88	LYS	N-CA-C	-5.13	106.95	114.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	K	255	LYS	N-CA-CB	5.13	119.15	110.49
4	N	455	LYS	N-CA-C	5.12	121.70	110.80
4	B	600	ILE	CA-C-N	5.10	127.12	120.28
4	B	600	ILE	C-N-CA	5.10	127.12	120.28
3	A	860	ASP	N-CA-C	5.10	116.59	108.79
4	N	503	THR	CA-CB-CG2	5.07	119.12	110.50
3	M	509	LEU	CD1-CG-CD2	-5.06	99.66	110.80
5	g	71	THR	CB-CA-C	5.06	117.95	109.80
3	M	285	TYR	N-CA-C	-5.05	100.04	110.80
4	F	874	ARG	CA-C-N	5.05	128.68	120.60
4	F	874	ARG	C-N-CA	5.05	128.68	120.60
2	e	243	PRO	CA-N-CD	-5.04	104.94	112.00
4	F	886	TYR	CA-C-N	5.04	131.16	121.54
4	F	886	TYR	C-N-CA	5.04	131.16	121.54
6	I	407	ASP	CA-C-N	5.01	131.12	121.54
6	I	407	ASP	C-N-CA	5.01	131.12	121.54
4	F	726	VAL	N-CA-C	-5.01	107.84	111.90

There are no chirality outliers.

All (44) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	352	GLY	Peptide
1	2	352	GLY	Peptide
4	B	740	GLN	Peptide
3	C	238	LEU	Peptide
3	E	430	GLN	Peptide
3	E	580	HIS	Peptide
3	G	240	GLY	Peptide
3	G	580	HIS	Peptide
6	I	407	ASP	Peptide
6	I	507	SER	Peptide
7	J	235	SER	Peptide
7	J	236	LEU	Mainchain
7	J	237	HIS	Peptide
7	J	256	LEU	Peptide
7	J	726	PHE	Peptide
6	K	408	ASP	Peptide
6	K	409	ASN	Mainchain
6	K	649	LEU	Peptide
8	L	306	HIS	Peptide
3	M	240	GLY	Peptide

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Mol	Chain	Res	Type	Group
3	M	404	TYR	Sidechain
3	M	580	HIS	Peptide
3	M	674	GLN	Mainchain,Peptide
4	N	405	LYS	Peptide
4	N	454	VAL	Peptide
4	N	497	CYS	Peptide
4	N	498	HIS	Mainchain
1	O	352	GLY	Peptide
1	P	352	GLY	Peptide
1	Q	352	GLY	Peptide
1	R	352	GLY	Peptide
1	S	352	GLY	Peptide
1	T	352	GLY	Peptide
1	U	352	GLY	Peptide
1	V	352	GLY	Peptide
1	W	352	GLY	Peptide
1	X	352	GLY	Peptide
1	Y	352	GLY	Peptide
1	Z	352	GLY	Peptide
4	f	104	PRO	Peptide
4	f	107	GLN	Peptide
4	f	108	PRO	Mainchain
4	h	111	VAL	Peptide

5.2 Too-close contacts [i](#)

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	1	3373	0	3325	74	0
1	2	3373	0	3325	78	0
1	O	3373	0	3325	69	0
1	P	3373	0	3325	67	0
1	Q	3373	0	3325	53	0
1	R	3373	0	3325	61	0
1	S	3373	0	3325	62	0
1	T	3373	0	3325	60	0
1	U	3373	0	3325	60	0
1	V	3373	0	3325	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	W	3373	0	3325	58	0
1	X	3373	0	3325	63	0
1	Y	3373	0	3325	73	0
1	Z	3373	0	3325	69	0
2	e	2847	0	2810	68	0
3	A	4978	0	4996	61	0
3	C	5044	0	5081	40	0
3	E	5216	0	5248	48	0
3	G	5216	0	5246	81	0
3	M	5186	0	5219	65	0
4	B	5029	0	5018	74	0
4	D	4796	0	4775	50	0
4	F	4941	0	4935	64	0
4	H	4907	0	4896	50	0
4	N	4907	0	4896	74	0
4	a	933	0	953	16	0
4	f	863	0	896	53	0
4	h	863	0	896	32	0
4	j	863	0	896	27	0
5	b	484	0	512	13	0
5	d	454	0	482	10	0
5	g	484	0	512	13	0
5	i	484	0	512	25	0
5	k	484	0	512	20	0
5	m	484	0	512	18	0
6	I	4225	0	4259	41	0
6	K	4579	0	4586	48	0
7	J	4429	0	4482	46	0
7	l	875	0	842	36	0
8	L	4587	0	4636	36	0
8	c	1220	0	1231	13	0
All	All	126600	0	126389	1819	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 7.

All (1819) 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)
5:i:34:ILE:CG2	4:h:110:LYS:HE2	1.31	1.58
4:f:66:ARG:CD	4:f:106:ARG:HE	1.25	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:876:ARG:HH22	4:j:39:ILE:CA	1.30	1.42
3:G:876:ARG:NH2	4:j:39:ILE:HA	1.36	1.40
5:i:34:ILE:HG21	4:h:110:LYS:CE	1.56	1.32
2:e:243:PRO:CD	2:e:243:PRO:N	1.71	1.31
5:m:35:LEU:HG	7:l:119:ASP:OD1	1.15	1.28
5:i:34:ILE:CG2	4:h:110:LYS:CE	2.10	1.26
3:G:876:ARG:NH2	4:j:38:VAL:O	1.74	1.20
4:f:66:ARG:HD3	4:f:106:ARG:NE	1.53	1.19
3:G:876:ARG:CD	4:j:42:ASN:HB2	1.74	1.18
4:f:66:ARG:CD	4:f:106:ARG:NE	2.04	1.15
5:m:35:LEU:HD11	7:l:119:ASP:OD2	1.41	1.14
3:G:876:ARG:HD2	4:j:42:ASN:CB	1.77	1.12
5:m:35:LEU:CG	7:l:119:ASP:OD1	1.97	1.11
2:e:153:MET:CE	2:e:278:THR:OG1	2.00	1.09
7:l:129:THR:H	7:l:130:PRO:HD3	1.13	1.07
7:l:127:VAL:HG11	7:l:130:PRO:C	1.79	1.07
3:G:876:ARG:CZ	4:j:38:VAL:O	2.03	1.05
7:l:127:VAL:CG1	7:l:130:PRO:HD2	1.85	1.05
3:G:876:ARG:NE	5:k:59:ALA:HB2	1.70	1.05
4:f:66:ARG:HB2	4:f:106:ARG:HG2	1.07	1.05
3:G:875:GLU:OE2	4:j:37:ARG:NH1	1.89	1.05
3:G:876:ARG:NH2	4:j:38:VAL:C	2.15	1.05
2:e:5:ILE:HG23	2:e:102:PRO:CD	1.89	1.03
4:f:66:ARG:HD3	4:f:106:ARG:HE	0.84	1.00
7:l:127:VAL:HG12	7:l:130:PRO:HD2	1.43	0.98
5:i:34:ILE:HG22	4:h:110:LYS:CE	1.91	0.98
5:m:35:LEU:HG	7:l:119:ASP:CG	1.88	0.98
4:h:73:LEU:HD22	4:h:110:LYS:HD3	1.43	0.97
3:G:876:ARG:NE	5:k:59:ALA:CB	2.28	0.96
4:f:66:ARG:CB	4:f:106:ARG:HG2	1.95	0.96
4:f:66:ARG:NE	4:f:106:ARG:HH21	1.64	0.95
3:G:876:ARG:CZ	5:k:59:ALA:CB	2.44	0.95
7:l:129:THR:N	7:l:130:PRO:HD3	1.79	0.95
5:g:30:GLU:CD	4:f:111:VAL:HG11	1.93	0.93
3:G:876:ARG:NH2	4:j:39:ILE:CA	2.08	0.92
4:f:66:ARG:HB2	4:f:106:ARG:CG	1.99	0.91
1:l:130:ASP:CG	1:2:295:ARG:HH22	1.79	0.90
5:m:35:LEU:CD1	7:l:119:ASP:OD2	2.20	0.88
7:l:127:VAL:CG1	7:l:130:PRO:C	2.45	0.88
3:G:876:ARG:CZ	5:k:59:ALA:HB1	2.04	0.87
4:f:66:ARG:CG	4:f:106:ARG:NE	2.37	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:i:36:ASN:CA	4:h:107:GLN:HE22	1.88	0.86
4:j:111:VAL:O	4:j:111:VAL:HG12	1.73	0.86
3:M:696:TYR:O	3:M:700:GLU:HB2	1.75	0.86
7:l:129:THR:N	7:l:130:PRO:CD	2.39	0.86
2:e:153:MET:HE3	2:e:278:THR:OG1	1.75	0.86
5:i:34:ILE:HG22	4:h:110:LYS:HE3	1.57	0.85
4:f:69:ALA:HB1	4:f:110:LYS:HG3	1.58	0.84
7:l:129:THR:H	7:l:130:PRO:CD	1.91	0.84
5:m:35:LEU:CG	7:l:119:ASP:CG	2.49	0.84
3:G:876:ARG:NH2	5:k:59:ALA:HB1	1.92	0.83
7:l:118:SER:O	7:l:119:ASP:OD1	1.97	0.82
3:G:876:ARG:HD2	4:j:42:ASN:HB2	0.87	0.82
4:f:66:ARG:NE	4:f:106:ARG:HE	1.77	0.82
6:I:361:TYR:HE2	6:I:475:TYR:HB3	1.45	0.81
2:e:5:ILE:CG2	2:e:102:PRO:HD3	2.10	0.81
3:G:876:ARG:CZ	5:k:59:ALA:HB2	2.08	0.81
4:f:69:ALA:HB1	4:f:110:LYS:CG	2.12	0.80
4:F:780:ASP:CG	4:j:106:ARG:NH2	2.38	0.80
4:f:66:ARG:HE	4:f:106:ARG:HH21	1.26	0.80
4:f:66:ARG:HD3	4:f:106:ARG:CG	2.12	0.80
4:B:684:HIS:HE2	4:B:704:CYS:HG	1.27	0.80
4:h:73:LEU:CD2	4:h:110:LYS:HD3	2.11	0.79
2:e:4:ASP:OD2	2:e:353:GLN:HB2	1.83	0.79
7:l:127:VAL:HG13	7:l:130:PRO:HD2	1.65	0.79
4:f:66:ARG:HG2	4:f:106:ARG:NE	1.97	0.79
3:G:876:ARG:HD3	5:k:56:ASN:HD22	1.47	0.78
2:e:5:ILE:HG23	2:e:102:PRO:HD3	1.66	0.78
2:e:5:ILE:CG2	2:e:102:PRO:CD	2.61	0.78
3:G:876:ARG:NH2	4:j:39:ILE:N	2.31	0.78
2:e:154:ASP:O	2:e:160:THR:HG23	1.84	0.78
3:G:875:GLU:OE2	4:j:37:ARG:CZ	2.31	0.77
4:h:104:PRO:HG3	4:h:107:GLN:OE1	1.86	0.76
1:2:358:VAL:HG13	4:N:879:ARG:HH12	1.50	0.75
1:1:56:ASP:OD2	1:2:277:THR:N	2.19	0.75
2:e:153:MET:HE2	2:e:278:THR:OG1	1.85	0.74
4:B:323:SER:HB3	4:B:421:LEU:HG	1.69	0.74
5:i:33:ARG:CZ	4:h:109:SER:OG	2.36	0.74
4:h:111:VAL:O	4:h:111:VAL:HG12	1.87	0.74
4:f:66:ARG:HD3	4:f:106:ARG:CD	2.17	0.74
3:C:763:GLN:HG3	3:C:766:THR:H	1.53	0.73
3:G:507:LYS:HE2	3:G:623:LYS:HE3	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:f:111:VAL:HG12	4:f:111:VAL:O	1.86	0.73
5:i:36:ASN:CB	4:h:107:GLN:HE22	2.01	0.73
6:K:649:LEU:O	1:Y:344:LYS:NZ	2.23	0.72
3:E:242:GLN:HE21	3:E:343:THR:HA	1.54	0.72
4:f:66:ARG:NE	4:f:106:ARG:NH2	2.36	0.72
3:A:186:ALA:HB1	4:B:293:ARG:HA	1.71	0.72
1:l:353:PRO:HA	3:M:862:ASN:HD22	1.54	0.72
3:G:876:ARG:HH21	4:j:38:VAL:C	1.98	0.71
4:h:109:SER:O	4:h:111:VAL:HG23	1.90	0.71
3:G:876:ARG:CD	5:k:59:ALA:HB2	2.20	0.71
4:N:589:ALA:HA	4:N:592:LEU:HG	1.70	0.71
4:B:884:GLU:OE2	1:P:341:ARG:NH2	2.23	0.71
4:D:624:ARG:O	4:D:639:SER:HB2	1.92	0.70
6:K:9:LEU:HD22	6:K:104:LEU:HD13	1.73	0.70
3:A:259:LEU:HD23	3:A:262:ARG:HH12	1.56	0.70
3:G:876:ARG:HH22	4:j:39:ILE:HA	0.57	0.70
5:i:36:ASN:HA	4:h:107:GLN:HE22	1.55	0.69
3:G:876:ARG:HD3	5:k:56:ASN:ND2	2.05	0.69
1:l:343:ARG:NH1	1:Z:130:ASP:OD1	2.20	0.69
4:B:409:PRO:HA	4:B:412:ARG:HG3	1.72	0.69
5:i:57:PRO:HB3	4:h:96:LEU:HG	1.75	0.69
4:N:586:VAL:HG13	4:N:587:ARG:HE	1.58	0.69
2:e:5:ILE:HG23	2:e:102:PRO:HD2	1.73	0.69
6:K:358:LYS:HZ3	6:K:362:LEU:HB2	1.57	0.69
3:G:572:ASP:HB3	3:G:621:ILE:H	1.58	0.69
6:I:361:TYR:CE2	6:I:475:TYR:HB3	2.28	0.68
8:L:1590:VAL:HG11	8:L:1733:PHE:HB3	1.76	0.68
3:M:304:LEU:HD11	4:N:364:LEU:HB3	1.75	0.68
4:B:720:TYR:OH	1:P:250:ASN:ND2	2.27	0.68
3:G:875:GLU:OE2	4:j:37:ARG:NH2	2.27	0.68
4:B:479:GLN:HG2	4:B:482:LYS:HE2	1.76	0.67
4:H:630:PRO:HD2	7:l:119:ASP:HB2	1.76	0.67
5:m:35:LEU:CD1	7:l:119:ASP:CG	2.68	0.66
3:G:607:GLU:HG3	3:G:609:ALA:H	1.61	0.66
5:i:68:ARG:HH12	4:h:100:LEU:HD11	1.60	0.66
5:g:30:GLU:OE2	4:f:111:VAL:HG11	1.94	0.66
8:L:1800:LEU:HB2	1:Z:341:ARG:HG3	1.77	0.65
4:H:703:GLN:HE21	4:H:847:LEU:HD13	1.62	0.65
1:V:323:ILE:HG12	1:V:359:ALA:HB3	1.79	0.65
1:2:323:ILE:HG12	1:2:359:ALA:HB3	1.79	0.65
8:L:409:ARG:HA	8:L:412:HIS:HB3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:780:ASP:CG	4:j:106:ARG:HH22	2.03	0.65
2:e:4:ASP:OD1	2:e:353:GLN:HG3	1.96	0.65
6:K:358:LYS:O	6:K:358:LYS:NZ	2.29	0.65
7:J:889:LYS:HA	1:X:353:PRO:HD2	1.79	0.65
1:S:323:ILE:HG12	1:S:359:ALA:HB3	1.79	0.65
1:1:130:ASP:OD1	1:2:295:ARG:NH2	2.30	0.65
1:Z:323:ILE:HG12	1:Z:359:ALA:HB3	1.79	0.65
1:U:323:ILE:HG12	1:U:359:ALA:HB3	1.79	0.64
1:1:127:ASP:O	1:2:299:GLN:NE2	2.31	0.64
1:1:323:ILE:HG12	1:1:359:ALA:HB3	1.79	0.64
3:C:557:LEU:HB2	1:R:339:ARG:HH11	1.63	0.64
6:K:358:LYS:HE2	6:K:537:LEU:HD21	1.79	0.64
1:W:323:ILE:HG12	1:W:359:ALA:HB3	1.79	0.64
1:O:323:ILE:HG12	1:O:359:ALA:HB3	1.79	0.64
1:T:323:ILE:HG12	1:T:359:ALA:HB3	1.79	0.64
5:g:47:CYS:HA	5:g:50:LEU:HD12	1.80	0.64
4:F:601:LEU:HD22	4:F:623:VAL:HG23	1.79	0.64
5:m:35:LEU:CD2	7:l:119:ASP:OD1	2.46	0.64
1:P:323:ILE:HG12	1:P:359:ALA:HB3	1.79	0.64
1:R:323:ILE:HG12	1:R:359:ALA:HB3	1.79	0.64
5:b:47:CYS:HA	5:b:50:LEU:HD12	1.80	0.64
1:X:323:ILE:HG12	1:X:359:ALA:HB3	1.79	0.63
1:Q:323:ILE:HG12	1:Q:359:ALA:HB3	1.79	0.63
4:B:776:ARG:NH1	4:f:106:ARG:O	2.31	0.63
6:K:579:VAL:HA	6:K:626:LEU:HD21	1.81	0.63
4:D:862:LEU:HD21	4:D:880:LEU:HD22	1.81	0.63
1:Y:323:ILE:HG12	1:Y:359:ALA:HB3	1.79	0.63
3:C:310:LEU:HB3	3:C:319:LEU:HD11	1.81	0.63
4:F:259:GLN:HE21	4:F:339:LEU:HD13	1.62	0.62
4:j:111:VAL:O	4:j:111:VAL:CG1	2.43	0.62
6:K:499:GLN:HB3	6:K:516:ARG:HE	1.62	0.62
3:M:181:VAL:HG13	3:M:186:ALA:HB3	1.81	0.62
5:b:46:ILE:HA	5:b:49:ARG:HE	1.63	0.62
3:M:224:VAL:HG21	3:M:233:VAL:HB	1.82	0.62
4:D:703:GLN:HG2	4:D:847:LEU:HD22	1.82	0.62
4:N:563:ARG:NH2	4:N:660:TYR:OH	2.33	0.62
5:i:36:ASN:CB	4:h:107:GLN:NE2	2.62	0.62
3:E:734:LEU:HB2	3:E:739:LEU:HD11	1.80	0.62
4:F:486:ILE:HD11	4:F:538:TYR:HD1	1.65	0.62
3:M:509:LEU:HD23	3:M:629:ILE:HD13	1.82	0.62
4:N:564:ARG:HB3	4:N:570:GLN:HB2	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:J:562:ALA:HB2	7:J:699:TYR:HD1	1.65	0.62
8:L:1656:ARG:NH1	1:Z:434:GLU:OE2	2.30	0.61
5:m:35:LEU:HD11	7:l:119:ASP:CG	2.22	0.61
5:g:30:GLU:OE1	4:f:111:VAL:HG11	2.00	0.61
5:m:47:CYS:HA	5:m:50:LEU:HD12	1.82	0.61
4:f:86:VAL:O	4:f:88:LYS:NZ	2.33	0.61
3:E:710:GLU:HB2	3:E:711:LYS:HZ2	1.63	0.61
1:l:56:ASP:OD2	1:2:276:LEU:N	2.32	0.61
2:e:79:TRP:HH2	2:e:119:MET:HG2	1.66	0.61
3:A:388:PHE:CE1	3:A:391:LEU:HD22	2.35	0.61
1:U:64:ALA:O	1:U:90:ASN:ND2	2.34	0.61
5:m:39:LEU:HD11	7:l:117:LEU:HD13	1.82	0.61
3:E:223:TYR:HB3	3:E:228:VAL:HG23	1.81	0.61
3:A:168:LYS:HD3	3:A:403:PRO:HB3	1.83	0.61
4:N:391:ARG:HB3	4:N:395:GLU:HG3	1.83	0.61
3:E:559:LEU:HD21	3:E:570:LYS:HB2	1.83	0.61
6:K:510:THR:HG1	1:Y:446:TRP:CD1	2.19	0.61
1:X:64:ALA:O	1:X:90:ASN:ND2	2.34	0.61
4:F:317:PHE:HB3	4:F:322:GLN:HE22	1.66	0.60
3:A:388:PHE:CZ	3:A:391:LEU:HD22	2.36	0.60
1:T:64:ALA:O	1:T:90:ASN:ND2	2.34	0.60
1:W:64:ALA:O	1:W:90:ASN:ND2	2.34	0.60
2:e:155:SER:HA	2:e:160:THR:HG23	1.83	0.60
6:I:544:LEU:HD12	6:I:547:GLN:HE21	1.66	0.60
3:C:277:ILE:HD11	3:C:296:MET:HG2	1.84	0.60
1:V:64:ALA:O	1:V:90:ASN:ND2	2.34	0.60
6:K:90:CYS:HA	6:K:93:LEU:HD12	1.84	0.60
1:Q:64:ALA:O	1:Q:90:ASN:ND2	2.34	0.60
3:G:370:SER:HA	3:G:373:GLN:HB3	1.83	0.60
3:G:557:LEU:HA	1:V:339:ARG:HG2	1.84	0.60
3:M:834:LEU:HD11	3:M:869:LEU:H	1.67	0.60
1:P:64:ALA:O	1:P:90:ASN:ND2	2.34	0.60
5:i:34:ILE:HG21	4:h:110:LYS:HE2	0.63	0.60
3:C:680:PHE:HD2	3:C:683:ARG:HH21	1.50	0.60
1:O:64:ALA:O	1:O:90:ASN:ND2	2.34	0.60
4:N:765:ASP:O	4:N:769:ARG:NH1	2.35	0.59
4:N:763:LEU:O	4:N:769:ARG:NH2	2.35	0.59
1:l:64:ALA:O	1:l:90:ASN:ND2	2.34	0.59
4:D:859:GLN:HE22	4:D:887:LYS:H	1.51	0.59
4:F:561:ALA:HA	4:F:564:ARG:HE	1.67	0.59
6:K:651:TYR:CE1	1:Y:355:SER:HA	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:64:ALA:O	1:Z:90:ASN:ND2	2.34	0.59
3:A:693:ILE:HG21	3:A:738:MET:HE1	1.83	0.59
1:S:64:ALA:O	1:S:90:ASN:ND2	2.34	0.59
4:F:586:VAL:HG12	4:F:635:TRP:HE1	1.66	0.59
6:I:357:ILE:O	6:I:361:TYR:HB3	2.02	0.59
3:M:164:LYS:HA	3:M:167:LYS:HG2	1.85	0.59
1:Y:64:ALA:O	1:Y:90:ASN:ND2	2.34	0.59
4:N:626:LEU:HD21	4:N:661:LEU:HD11	1.84	0.59
1:2:249:MET:SD	4:N:575:ARG:NH2	2.76	0.59
3:E:428:TRP:HE1	3:E:723:LEU:HD22	1.68	0.59
1:2:64:ALA:O	1:2:90:ASN:ND2	2.34	0.59
8:L:496:PRO:HB3	8:L:500:LYS:HG3	1.85	0.59
5:d:28:LEU:HD23	5:d:31:ILE:HD11	1.84	0.59
6:I:530:TYR:CE1	1:W:249:MET:HE3	2.38	0.58
4:f:105:ARG:O	4:f:107:GLN:HG3	2.02	0.58
3:G:509:LEU:HD13	3:G:626:LEU:HD22	1.85	0.58
5:k:29:LEU:HD13	5:k:41:MET:HE2	1.83	0.58
2:e:110:LEU:HD23	2:e:175:ILE:HD13	1.84	0.58
2:e:214:GLU:HG2	2:e:215:LYS:HD3	1.84	0.58
4:a:94:LEU:HA	4:a:97:LEU:HG	1.85	0.58
1:1:130:ASP:CG	1:2:295:ARG:NH2	2.58	0.58
3:M:164:LYS:HG2	3:M:404:TYR:HE1	1.68	0.58
4:h:111:VAL:O	4:h:111:VAL:CG1	2.50	0.58
4:B:524:THR:HG22	4:B:526:LEU:H	1.68	0.58
4:B:879:ARG:HE	1:P:337:LEU:HD22	1.69	0.58
1:R:64:ALA:O	1:R:90:ASN:ND2	2.34	0.58
5:k:47:CYS:HA	5:k:50:LEU:HD12	1.85	0.58
4:N:269:ASN:HD22	4:N:276:LYS:HD2	1.68	0.58
4:f:111:VAL:O	4:f:111:VAL:CG1	2.51	0.58
3:E:418:ARG:HB2	3:E:426:LYS:HD3	1.86	0.58
1:2:16:GLN:HE21	1:2:73:VAL:HG11	1.69	0.58
4:B:289:ASP:HB3	4:B:293:ARG:HH21	1.69	0.58
4:B:546:LEU:HD21	4:B:744:LEU:HG	1.84	0.58
1:Y:16:GLN:HE21	1:Y:73:VAL:HG11	1.69	0.58
3:A:704:PRO:HG3	1:O:330:PRO:HG2	1.86	0.58
1:Q:217:ARG:HB2	1:Q:277:THR:HG23	1.86	0.58
1:T:217:ARG:HB2	1:T:277:THR:HG23	1.86	0.58
1:V:16:GLN:HE21	1:V:73:VAL:HG11	1.69	0.58
2:e:120:THR:HG21	2:e:370:VAL:HG21	1.86	0.58
3:A:547:THR:HG22	3:A:549:PRO:HD2	1.83	0.58
1:2:217:ARG:HB2	1:2:277:THR:HG23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:885:HIS:CE1	1:P:352:GLY:HA2	2.39	0.57
4:D:734:LEU:HD11	4:D:751:HIS:HD2	1.68	0.57
4:F:578:MET:HE1	4:F:671:LYS:HB2	1.85	0.57
1:P:217:ARG:HB2	1:P:277:THR:HG23	1.86	0.57
4:N:252:ARG:HG2	4:N:346:LEU:HD21	1.87	0.57
6:I:497:ALA:HA	6:I:500:MET:HE3	1.85	0.57
1:T:16:GLN:HE21	1:T:73:VAL:HG11	1.69	0.57
1:U:117:ASP:OD1	1:U:117:ASP:N	2.36	0.57
1:Z:16:GLN:HE21	1:Z:73:VAL:HG11	1.69	0.57
7:l:121:PRO:HD2	7:l:121:PRO:O	2.04	0.57
1:1:16:GLN:HE21	1:1:73:VAL:HG11	1.69	0.57
1:1:89:GLU:HB2	1:2:215:THR:O	2.04	0.57
1:O:16:GLN:HE21	1:O:73:VAL:HG11	1.69	0.57
1:S:217:ARG:HB2	1:S:277:THR:HG23	1.86	0.57
1:2:229:ASN:O	1:2:233:SER:OG	2.21	0.57
1:O:217:ARG:HB2	1:O:277:THR:HG23	1.86	0.57
1:P:16:GLN:HE21	1:P:73:VAL:HG11	1.69	0.57
1:Q:16:GLN:HE21	1:Q:73:VAL:HG11	1.69	0.57
1:R:16:GLN:HE21	1:R:73:VAL:HG11	1.69	0.57
1:W:16:GLN:HE21	1:W:73:VAL:HG11	1.69	0.57
1:W:217:ARG:HB2	1:W:277:THR:HG23	1.86	0.57
1:X:16:GLN:HE21	1:X:73:VAL:HG11	1.69	0.57
1:1:217:ARG:HB2	1:1:277:THR:HG23	1.86	0.57
6:K:118:SER:O	6:K:121:HIS:ND1	2.37	0.57
1:O:217:ARG:HH21	1:O:278:THR:H	1.53	0.57
1:U:16:GLN:HE21	1:U:73:VAL:HG11	1.69	0.57
1:W:117:ASP:OD1	1:W:117:ASP:N	2.36	0.57
1:O:229:ASN:O	1:O:233:SER:OG	2.21	0.57
1:R:229:ASN:O	1:R:233:SER:OG	2.21	0.57
1:V:217:ARG:HB2	1:V:277:THR:HG23	1.86	0.57
1:Y:217:ARG:HB2	1:Y:277:THR:HG23	1.86	0.57
4:f:66:ARG:CZ	4:f:106:ARG:HH21	2.17	0.57
1:1:217:ARG:HH21	1:1:278:THR:H	1.53	0.57
8:L:1676:ILE:HG23	8:L:1680:ILE:HD12	1.87	0.57
5:i:36:ASN:HA	4:h:107:GLN:NE2	2.20	0.57
1:2:117:ASP:OD1	1:2:117:ASP:N	2.36	0.57
1:1:229:ASN:O	1:1:233:SER:OG	2.21	0.56
4:B:677:LEU:HA	4:B:680:ILE:HD12	1.86	0.56
6:K:630:LEU:HB3	6:K:645:LEU:HD21	1.87	0.56
4:N:247:GLU:HG2	4:N:366:ARG:HH11	1.69	0.56
1:Z:217:ARG:HH21	1:Z:278:THR:H	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:619:ASP:N	3:A:619:ASP:OD2	2.34	0.56
4:B:297:LEU:HD21	4:B:375:LYS:HA	1.87	0.56
3:G:297:ARG:HG2	3:G:301:LYS:HE3	1.87	0.56
5:i:33:ARG:O	4:h:107:GLN:CD	2.48	0.56
3:E:150:LEU:HD12	3:E:240:GLY:H	1.69	0.56
3:E:183:GLU:HB2	3:E:184:ARG:HH11	1.70	0.56
4:D:659:HIS:HB2	4:D:755:LEU:HD11	1.88	0.56
6:I:403:VAL:HG22	6:I:404:LEU:HG	1.88	0.56
3:M:450:ILE:O	3:M:453:THR:OG1	2.23	0.56
1:Q:217:ARG:HH21	1:Q:278:THR:H	1.53	0.56
1:R:217:ARG:HB2	1:R:277:THR:HG23	1.86	0.56
1:S:16:GLN:HE21	1:S:73:VAL:HG11	1.69	0.56
1:V:217:ARG:HH21	1:V:278:THR:H	1.53	0.56
1:X:290:VAL:HG21	1:X:333:VAL:HG12	1.88	0.56
1:1:290:VAL:HG21	1:1:333:VAL:HG12	1.88	0.56
1:1:337:LEU:HD11	1:1:358:VAL:HG11	1.88	0.56
4:H:416:GLN:O	4:H:420:SER:OG	2.23	0.56
1:U:337:LEU:HD11	1:U:358:VAL:HG11	1.88	0.56
1:1:343:ARG:HH11	1:Z:130:ASP:CG	2.12	0.56
2:e:5:ILE:HG21	2:e:102:PRO:HD3	1.86	0.56
4:H:625:LEU:HD12	4:H:637:VAL:HG12	1.88	0.56
4:H:869:SER:H	4:H:873:LEU:HD12	1.71	0.56
1:O:337:LEU:HD11	1:O:358:VAL:HG11	1.88	0.56
1:R:290:VAL:HG21	1:R:333:VAL:HG12	1.88	0.56
1:R:337:LEU:HD11	1:R:358:VAL:HG11	1.88	0.56
1:S:217:ARG:HH21	1:S:278:THR:H	1.53	0.56
1:T:290:VAL:HG21	1:T:333:VAL:HG12	1.88	0.56
4:F:430:LEU:HD11	4:F:483:VAL:HG21	1.87	0.56
1:S:337:LEU:HD11	1:S:358:VAL:HG11	1.88	0.56
1:W:290:VAL:HG21	1:W:333:VAL:HG12	1.88	0.56
4:f:69:ALA:HB1	4:f:110:LYS:HG2	1.88	0.56
2:e:141:SER:O	2:e:335:ARG:NH1	2.39	0.56
4:F:581:LEU:HG	4:F:585:LEU:HG	1.88	0.56
4:F:780:ASP:OD2	4:j:106:ARG:NH2	2.39	0.56
1:T:229:ASN:O	1:T:233:SER:OG	2.21	0.56
1:Y:217:ARG:HH21	1:Y:278:THR:H	1.53	0.56
1:Y:290:VAL:HG21	1:Y:333:VAL:HG12	1.88	0.56
4:B:723:THR:HG22	1:P:248:TYR:HD2	1.71	0.56
1:O:290:VAL:HG21	1:O:333:VAL:HG12	1.88	0.56
1:Y:337:LEU:HD11	1:Y:358:VAL:HG11	1.88	0.56
1:2:290:VAL:HG21	1:2:333:VAL:HG12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:e:34:ILE:HG13	2:e:67:LEU:HA	1.87	0.56
6:I:392:VAL:HG22	6:I:414:LEU:HD13	1.87	0.56
1:U:217:ARG:HB2	1:U:277:THR:HG23	1.86	0.56
4:j:108:PRO:O	4:j:108:PRO:HD2	2.05	0.56
4:f:94:LEU:HD23	4:f:97:LEU:HD21	1.87	0.56
2:e:5:ILE:CG2	2:e:102:PRO:HG3	2.36	0.56
3:G:439:ILE:HG22	3:G:441:SER:H	1.69	0.56
1:S:290:VAL:HG21	1:S:333:VAL:HG12	1.88	0.56
1:T:337:LEU:HD11	1:T:358:VAL:HG11	1.88	0.56
5:m:64:ILE:HD12	7:l:26:VAL:HG21	1.87	0.56
4:B:284:SER:OG	4:B:285:ARG:NH2	2.39	0.55
1:P:229:ASN:O	1:P:233:SER:OG	2.21	0.55
1:I:294:MET:SD	1:I:336:SER:OG	2.64	0.55
7:J:276:TRP:O	7:J:279:SER:OG	2.24	0.55
1:R:217:ARG:HH21	1:R:278:THR:H	1.53	0.55
1:R:294:MET:SD	1:R:336:SER:OG	2.64	0.55
1:X:217:ARG:HB2	1:X:277:THR:HG23	1.86	0.55
4:B:291:ALA:O	4:B:295:SER:HB2	2.05	0.55
8:L:1663:HIS:O	8:L:1666:GLN:NE2	2.39	0.55
1:P:294:MET:SD	1:P:336:SER:OG	2.64	0.55
1:U:290:VAL:HG21	1:U:333:VAL:HG12	1.88	0.55
1:Z:290:VAL:HG21	1:Z:333:VAL:HG12	1.88	0.55
4:D:681:ARG:HG2	1:R:258:ALA:HB1	1.89	0.55
1:P:290:VAL:HG21	1:P:333:VAL:HG12	1.88	0.55
1:T:217:ARG:HH21	1:T:278:THR:H	1.53	0.55
1:Z:217:ARG:HB2	1:Z:277:THR:HG23	1.86	0.55
1:P:337:LEU:HD11	1:P:358:VAL:HG11	1.88	0.55
1:Z:229:ASN:O	1:Z:233:SER:OG	2.21	0.55
1:2:337:LEU:HD11	1:2:358:VAL:HG11	1.88	0.55
2:e:165:ILE:HA	2:e:170:ALA:HA	1.89	0.55
8:L:499:VAL:HG21	8:L:553:MET:HE3	1.89	0.55
1:Q:50:VAL:HG21	1:Q:244:ARG:HG2	1.89	0.55
1:Q:337:LEU:HD11	1:Q:358:VAL:HG11	1.88	0.55
1:V:337:LEU:HD11	1:V:358:VAL:HG11	1.88	0.55
1:X:337:LEU:HD11	1:X:358:VAL:HG11	1.88	0.55
1:2:217:ARG:HH21	1:2:278:THR:H	1.53	0.55
1:T:50:VAL:HG21	1:T:244:ARG:HG2	1.89	0.55
1:T:294:MET:SD	1:T:336:SER:OG	2.64	0.55
1:U:217:ARG:HH21	1:U:278:THR:H	1.53	0.55
1:V:50:VAL:HG21	1:V:244:ARG:HG2	1.89	0.55
1:W:50:VAL:HG21	1:W:244:ARG:HG2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:638:TYR:HA	3:G:641:LEU:HD12	1.87	0.55
3:M:233:VAL:HG22	3:M:248:VAL:HG23	1.89	0.55
3:M:578:MET:SD	3:M:639:GLN:NE2	2.79	0.55
1:O:50:VAL:HG21	1:O:244:ARG:HG2	1.89	0.55
1:U:50:VAL:HG21	1:U:244:ARG:HG2	1.89	0.55
2:e:72:GLU:HG2	2:e:183:ARG:HH22	1.72	0.55
1:Q:290:VAL:HG21	1:Q:333:VAL:HG12	1.88	0.55
1:V:290:VAL:HG21	1:V:333:VAL:HG12	1.88	0.55
1:V:343:ARG:HG3	1:V:345:LEU:HB2	1.89	0.55
1:W:229:ASN:O	1:W:233:SER:OG	2.21	0.55
1:Y:50:VAL:HG21	1:Y:244:ARG:HG2	1.89	0.55
1:1:50:VAL:HG21	1:1:244:ARG:HG2	1.89	0.55
4:F:567:LEU:HD23	4:F:727:LEU:HD22	1.88	0.55
8:L:461:PHE:HA	8:L:464:LYS:HD3	1.88	0.55
1:W:337:LEU:HD11	1:W:358:VAL:HG11	1.88	0.55
1:X:343:ARG:HG3	1:X:345:LEU:HB2	1.89	0.55
1:Z:337:LEU:HD11	1:Z:358:VAL:HG11	1.88	0.55
4:f:66:ARG:HE	4:f:106:ARG:NH2	1.98	0.55
1:2:50:VAL:HG21	1:2:244:ARG:HG2	1.89	0.54
3:G:159:LYS:HB2	3:G:160:MET:HE2	1.89	0.54
7:J:275:LEU:HD23	7:J:278:LEU:HD12	1.89	0.54
8:L:1553:VAL:HA	8:L:1556:LYS:HG2	1.89	0.54
1:P:217:ARG:HH21	1:P:278:THR:H	1.53	0.54
2:e:5:ILE:HG23	2:e:102:PRO:CG	2.36	0.54
4:N:482:LYS:HG3	4:N:534:ILE:HG21	1.89	0.54
1:Y:343:ARG:HG3	1:Y:345:LEU:HB2	1.89	0.54
4:D:714:PHE:HD1	4:D:880:LEU:HD21	1.72	0.54
1:Q:343:ARG:HG3	1:Q:345:LEU:HB2	1.89	0.54
1:R:343:ARG:HG3	1:R:345:LEU:HB2	1.89	0.54
1:S:229:ASN:O	1:S:233:SER:OG	2.21	0.54
1:U:229:ASN:O	1:U:233:SER:OG	2.21	0.54
1:X:50:VAL:HG21	1:X:244:ARG:HG2	1.89	0.54
1:P:343:ARG:HG3	1:P:345:LEU:HB2	1.89	0.54
4:a:76:GLU:OE2	4:a:79:ARG:NH2	2.39	0.54
4:F:707:LEU:HD22	4:F:851:THR:HG22	1.90	0.54
3:G:359:LEU:HB3	3:G:380:THR:HG22	1.89	0.54
6:K:500:MET:HA	1:Y:264:PRO:HB3	1.90	0.54
5:b:49:ARG:HB2	4:a:12:LEU:HD21	1.90	0.54
4:F:734:LEU:HD11	4:F:751:HIS:HD2	1.72	0.54
3:G:175:PRO:HB3	4:H:403:TYR:HE1	1.72	0.54
8:L:1659:GLN:HA	8:L:1662:LYS:HG3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:89:GLU:HG2	1:2:215:THR:HB	1.89	0.54
6:I:612:LEU:HA	6:I:615:LEU:HD12	1.90	0.54
1:P:50:VAL:HG21	1:P:244:ARG:HG2	1.89	0.54
1:S:343:ARG:HG3	1:S:345:LEU:HB2	1.89	0.54
1:T:343:ARG:HG3	1:T:345:LEU:HB2	1.89	0.54
1:X:217:ARG:HH21	1:X:278:THR:H	1.53	0.54
1:Y:294:MET:SD	1:Y:336:SER:OG	2.64	0.54
3:C:187:LEU:HD23	4:D:379:LYS:HG3	1.89	0.54
4:D:594:GLN:HG2	4:D:623:VAL:HG13	1.90	0.54
6:K:131:LEU:HD12	6:K:165:LEU:HD23	1.89	0.54
1:W:217:ARG:HH21	1:W:278:THR:H	1.53	0.54
1:X:229:ASN:O	1:X:233:SER:OG	2.21	0.54
1:Z:343:ARG:HG3	1:Z:345:LEU:HB2	1.89	0.54
7:J:437:LEU:HD22	7:J:549:VAL:HG11	1.90	0.54
3:M:691:GLN:O	3:M:694:GLN:NE2	2.41	0.54
1:2:343:ARG:HG3	1:2:345:LEU:HB2	1.89	0.54
4:F:490:ILE:HG13	4:F:494:HIS:HE1	1.73	0.54
4:H:388:CYS:HB2	4:H:396:LEU:HD13	1.90	0.54
1:R:50:VAL:HG21	1:R:244:ARG:HG2	1.89	0.54
1:S:50:VAL:HG21	1:S:244:ARG:HG2	1.89	0.54
1:U:343:ARG:HG3	1:U:345:LEU:HB2	1.89	0.54
8:c:46:PHE:HA	8:c:49:LEU:HD12	1.90	0.54
4:F:807:GLU:HG3	4:F:811:LYS:HE2	1.90	0.53
4:F:847:LEU:HA	4:F:850:LEU:HD12	1.90	0.53
4:N:626:LEU:HG	4:N:639:SER:HB2	1.90	0.53
1:W:231:LEU:O	1:W:234:THR:OG1	2.26	0.53
1:W:294:MET:SD	1:W:336:SER:OG	2.64	0.53
1:Z:50:VAL:HG21	1:Z:244:ARG:HG2	1.89	0.53
3:M:494:TYR:HA	3:M:497:LYS:HG2	1.90	0.53
2:e:39:ARG:HB3	2:e:64:ILE:HD12	1.91	0.53
4:F:364:LEU:HD12	4:F:370:TRP:HE1	1.74	0.53
3:G:509:LEU:HD21	3:G:726:HIS:HE1	1.72	0.53
1:Q:229:ASN:O	1:Q:233:SER:OG	2.21	0.53
4:a:93:ILE:HA	4:a:96:LEU:HD12	1.90	0.53
4:N:245:ILE:HD13	4:N:265:ASN:HD21	1.74	0.53
4:N:680:ILE:HD11	4:N:786:GLN:HA	1.91	0.53
7:J:716:LEU:HD11	7:J:812:VAL:HG21	1.91	0.53
6:K:518:ARG:HH12	6:K:589:LEU:HD13	1.72	0.53
3:M:377:LEU:HD11	3:M:479:LEU:HD22	1.91	0.53
1:R:321:LEU:HA	1:R:357:GLN:HB2	1.90	0.53
1:Z:321:LEU:HA	1:Z:357:GLN:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:356:LEU:HG	3:E:440:PRO:HB3	1.90	0.53
4:F:490:ILE:O	4:F:494:HIS:ND1	2.29	0.53
6:K:143:ILE:HD13	6:K:148:ILE:HD12	1.91	0.53
1:V:321:LEU:HA	1:V:357:GLN:HB2	1.91	0.53
5:m:35:LEU:CG	7:l:119:ASP:OD2	2.53	0.53
3:M:821:THR:HG23	3:M:822:ILE:HD13	1.89	0.53
1:S:294:MET:SD	1:S:336:SER:OG	2.64	0.53
1:Y:321:LEU:HA	1:Y:357:GLN:HB2	1.91	0.53
4:f:66:ARG:NE	4:f:106:ARG:NE	2.47	0.53
1:X:321:LEU:HA	1:X:357:GLN:HB2	1.90	0.53
4:B:714:PHE:HA	4:B:717:GLN:HE21	1.74	0.53
4:D:326:ALA:HB2	3:E:333:ARG:HH22	1.74	0.53
7:J:225:TRP:CD1	7:J:226:THR:HG1	2.26	0.53
4:N:717:GLN:HB2	4:N:880:LEU:HD23	1.91	0.53
1:P:321:LEU:HA	1:P:357:GLN:HB2	1.90	0.53
1:R:231:LEU:O	1:R:234:THR:OG1	2.26	0.53
1:U:321:LEU:HA	1:U:357:GLN:HB2	1.91	0.53
1:W:343:ARG:HG3	1:W:345:LEU:HB2	1.89	0.53
1:X:294:MET:SD	1:X:336:SER:OG	2.64	0.53
1:1:48:LYS:O	1:1:54:GLN:NE2	2.42	0.53
1:2:321:LEU:HA	1:2:357:GLN:HB2	1.90	0.53
3:G:273:VAL:HG13	3:G:296:MET:HE2	1.91	0.53
8:L:1590:VAL:HG13	8:L:1628:LEU:HD22	1.89	0.53
1:O:343:ARG:HG3	1:O:345:LEU:HB2	1.89	0.53
1:2:48:LYS:O	1:2:54:GLN:NE2	2.42	0.52
6:K:119:ILE:HB	8:L:313:THR:HG21	1.91	0.52
1:T:48:LYS:O	1:T:54:GLN:NE2	2.42	0.52
1:U:48:LYS:O	1:U:54:GLN:NE2	2.43	0.52
1:V:229:ASN:O	1:V:233:SER:OG	2.21	0.52
1:W:48:LYS:O	1:W:54:GLN:NE2	2.42	0.52
4:B:832:ARG:NH1	4:B:835:GLU:OE2	2.40	0.52
1:R:318:ILE:HB	1:R:380:ASN:HB3	1.92	0.52
1:W:250:ASN:HB3	1:W:256:LEU:HB2	1.92	0.52
4:F:677:LEU:HD21	4:F:712:VAL:HG22	1.90	0.52
6:I:7:LEU:HG	6:I:12:TYR:HB2	1.91	0.52
3:M:244:ARG:HB2	3:M:275:ARG:HH22	1.74	0.52
1:P:250:ASN:HB3	1:P:256:LEU:HB2	1.92	0.52
1:Z:48:LYS:O	1:Z:54:GLN:NE2	2.42	0.52
1:Z:318:ILE:HB	1:Z:380:ASN:HB3	1.92	0.52
1:2:318:ILE:HB	1:2:380:ASN:HB3	1.92	0.52
2:e:105:LEU:HB3	2:e:134:VAL:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:K:117:LEU:HB3	6:K:121:HIS:CE1	2.45	0.52
1:P:318:ILE:HB	1:P:380:ASN:HB3	1.92	0.52
1:U:318:ILE:HB	1:U:380:ASN:HB3	1.92	0.52
1:V:48:LYS:O	1:V:54:GLN:NE2	2.42	0.52
1:W:321:LEU:HA	1:W:357:GLN:HB2	1.90	0.52
1:Z:250:ASN:HB3	1:Z:256:LEU:HB2	1.92	0.52
1:1:117:ASP:OD1	1:1:117:ASP:N	2.36	0.52
1:Q:321:LEU:HA	1:Q:357:GLN:HB2	1.90	0.52
1:S:321:LEU:HA	1:S:357:GLN:HB2	1.91	0.52
1:U:294:MET:SD	1:U:336:SER:OG	2.64	0.52
4:F:734:LEU:HD11	4:F:751:HIS:CD2	2.44	0.52
3:G:302:GLU:HA	3:G:305:ILE:HD12	1.90	0.52
3:M:326:PHE:HA	3:M:329:GLN:HE21	1.74	0.52
1:O:48:LYS:O	1:O:54:GLN:NE2	2.42	0.52
1:O:321:LEU:HA	1:O:357:GLN:HB2	1.91	0.52
1:R:250:ASN:HB3	1:R:256:LEU:HB2	1.92	0.52
1:T:250:ASN:HB3	1:T:256:LEU:HB2	1.92	0.52
1:Y:48:LYS:O	1:Y:54:GLN:NE2	2.42	0.52
1:1:250:ASN:HB3	1:1:256:LEU:HB2	1.92	0.52
3:A:307:VAL:HG12	4:B:365:ARG:HD2	1.92	0.52
3:C:181:VAL:HG13	3:C:187:LEU:HD22	1.92	0.52
1:O:132:LEU:HD23	1:O:164:LYS:HG3	1.92	0.52
1:R:48:LYS:O	1:R:54:GLN:NE2	2.42	0.52
1:S:132:LEU:HD23	1:S:164:LYS:HG3	1.92	0.52
1:V:250:ASN:HB3	1:V:256:LEU:HB2	1.92	0.52
1:Y:318:ILE:HB	1:Y:380:ASN:HB3	1.92	0.52
1:1:321:LEU:HA	1:1:357:GLN:HB2	1.90	0.52
3:G:175:PRO:HB3	4:H:403:TYR:CE1	2.44	0.52
1:T:321:LEU:HA	1:T:357:GLN:HB2	1.91	0.52
1:U:132:LEU:HD23	1:U:164:LYS:HG3	1.92	0.52
1:W:318:ILE:HB	1:W:380:ASN:HB3	1.92	0.52
4:H:565:TYR:OH	4:H:613:ASP:OD2	2.24	0.52
7:J:243:ALA:HA	7:J:306:THR:HG22	1.91	0.52
7:J:358:PHE:HD2	7:J:361:TYR:H	1.58	0.52
8:L:454:LEU:HD22	8:L:458:THR:HG21	1.92	0.52
3:M:559:LEU:HD21	3:M:570:LYS:HE2	1.92	0.52
1:P:48:LYS:O	1:P:54:GLN:NE2	2.43	0.52
1:R:117:ASP:OD1	1:R:117:ASP:N	2.36	0.52
1:S:48:LYS:O	1:S:54:GLN:NE2	2.42	0.52
1:V:231:LEU:O	1:V:234:THR:OG1	2.26	0.52
1:Y:132:LEU:HD23	1:Y:164:LYS:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:318:ILE:HB	1:1:380:ASN:HB3	1.92	0.52
1:2:132:LEU:HD23	1:2:164:LYS:HG3	1.92	0.52
2:e:121:GLN:HE21	2:e:367:PRO:HG2	1.75	0.52
1:O:231:LEU:O	1:O:234:THR:OG1	2.26	0.52
1:Q:48:LYS:O	1:Q:54:GLN:NE2	2.42	0.52
1:Q:250:ASN:HB3	1:Q:256:LEU:HB2	1.92	0.52
1:T:231:LEU:O	1:T:234:THR:OG1	2.26	0.52
1:U:250:ASN:HB3	1:U:256:LEU:HB2	1.92	0.52
1:X:48:LYS:O	1:X:54:GLN:NE2	2.42	0.51
1:X:250:ASN:HB3	1:X:256:LEU:HB2	1.92	0.51
1:Y:117:ASP:OD1	1:Y:117:ASP:N	2.36	0.51
1:Z:132:LEU:HD23	1:Z:164:LYS:HG3	1.92	0.51
3:E:150:LEU:HD21	3:E:275:ARG:HD2	1.91	0.51
1:S:318:ILE:HB	1:S:380:ASN:HB3	1.92	0.51
1:W:132:LEU:HD23	1:W:164:LYS:HG3	1.92	0.51
1:1:132:LEU:HD23	1:1:164:LYS:HG3	1.92	0.51
2:e:218:TYR:H	2:e:254:ARG:HE	1.58	0.51
3:C:641:LEU:HG	3:C:734:LEU:HD13	1.93	0.51
4:D:400:VAL:HG21	4:D:422:VAL:HG21	1.92	0.51
6:I:529:GLN:HE22	6:I:533:GLN:HE21	1.59	0.51
3:M:164:LYS:HG2	3:M:404:TYR:CE1	2.45	0.51
1:O:318:ILE:HB	1:O:380:ASN:HB3	1.92	0.51
1:Q:237:SER:O	1:Q:244:ARG:NH2	2.44	0.51
1:S:250:ASN:HB3	1:S:256:LEU:HB2	1.92	0.51
2:e:5:ILE:CG2	2:e:102:PRO:CG	2.89	0.51
3:A:191:PHE:HE2	4:B:293:ARG:HH12	1.58	0.51
1:R:237:SER:O	1:R:244:ARG:NH2	2.44	0.51
1:T:132:LEU:HD23	1:T:164:LYS:HG3	1.92	0.51
1:V:237:SER:O	1:V:244:ARG:NH2	2.44	0.51
1:Z:237:SER:O	1:Z:244:ARG:NH2	2.44	0.51
1:1:237:SER:O	1:1:244:ARG:NH2	2.44	0.51
3:A:156:LEU:HA	3:A:159:LYS:HG2	1.92	0.51
4:B:590:THR:HA	4:B:628:VAL:HG21	1.92	0.51
4:B:680:ILE:HD13	4:B:785:LEU:HD23	1.92	0.51
3:C:713:LEU:HD22	3:C:722:VAL:HG23	1.93	0.51
3:G:876:ARG:NE	5:k:59:ALA:HB1	2.14	0.51
1:W:237:SER:O	1:W:244:ARG:NH2	2.44	0.51
1:X:56:ASP:O	1:Y:287:LYS:HD3	2.10	0.51
7:J:222:HIS:HA	7:J:225:TRP:NE1	2.26	0.51
7:J:1015:LEU:HD11	1:X:341:ARG:HG3	1.92	0.51
3:M:674:GLN:HG2	3:M:769:MET:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:237:SER:O	1:T:244:ARG:NH2	2.44	0.51
1:Z:231:LEU:O	1:Z:234:THR:OG1	2.26	0.51
1:1:57:ASP:HA	1:2:371:HIS:CD2	2.45	0.51
7:J:902:MET:HG3	1:X:248:TYR:HD2	1.76	0.51
1:O:237:SER:O	1:O:244:ARG:NH2	2.44	0.51
1:Q:313:THR:OG1	1:Q:314:ASN:N	2.44	0.51
1:S:237:SER:O	1:S:244:ARG:NH2	2.44	0.51
5:i:36:ASN:HB2	4:h:107:GLN:NE2	2.26	0.51
3:A:408:MET:HA	3:A:435:VAL:HG22	1.92	0.51
4:D:563:ARG:HD2	4:D:731:TRP:CD1	2.46	0.51
4:D:782:ILE:O	4:D:785:LEU:HB2	2.11	0.51
3:G:684:GLN:HE22	3:G:687:LEU:HD22	1.75	0.51
4:H:677:LEU:HD21	4:H:712:VAL:HG22	1.93	0.51
4:N:769:ARG:HH21	4:N:772:LEU:HB2	1.76	0.51
1:U:237:SER:O	1:U:244:ARG:NH2	2.44	0.51
1:X:313:THR:OG1	1:X:314:ASN:N	2.44	0.51
1:2:237:SER:O	1:2:244:ARG:NH2	2.44	0.51
2:e:215:LYS:HD2	2:e:305:MET:HG2	1.92	0.51
3:A:765:PHE:HZ	1:O:163:LYS:HE3	1.74	0.51
4:B:479:GLN:HA	4:B:482:LYS:HG2	1.93	0.51
6:I:564:PHE:HD2	6:I:565:LEU:HD12	1.75	0.51
4:N:576:HIS:HD2	4:N:604:ALA:HA	1.75	0.51
4:N:763:LEU:C	4:N:769:ARG:HH22	2.19	0.51
1:Q:125:GLU:O	1:Q:129:SER:N	2.42	0.51
1:Q:318:ILE:HB	1:Q:380:ASN:HB3	1.92	0.51
1:R:313:THR:OG1	1:R:314:ASN:N	2.44	0.51
1:V:132:LEU:HD23	1:V:164:LYS:HG3	1.92	0.51
3:A:221:LEU:HD11	3:A:260:VAL:HG23	1.93	0.51
3:A:388:PHE:C	3:A:390:VAL:N	2.69	0.51
4:B:713:HIS:NE2	1:P:354:ALA:HA	2.26	0.51
4:F:276:LYS:NZ	4:F:277:VAL:O	2.41	0.51
3:G:869:LEU:HG	3:G:871:ARG:H	1.75	0.51
6:K:530:TYR:O	6:K:534:VAL:HG23	2.10	0.51
4:N:485:LEU:HA	4:N:488:LYS:HE2	1.93	0.51
1:O:250:ASN:HB3	1:O:256:LEU:HB2	1.92	0.51
1:P:231:LEU:O	1:P:234:THR:OG1	2.26	0.51
1:P:237:SER:O	1:P:244:ARG:NH2	2.44	0.51
1:1:313:THR:OG1	1:1:314:ASN:N	2.44	0.50
3:A:552:GLU:HG2	3:A:575:ILE:HB	1.94	0.50
4:H:697:PHE:HB3	4:H:701:LEU:HD23	1.93	0.50
6:I:59:ILE:HD11	6:I:93:LEU:HG	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L:1481:THR:HA	8:L:1484:LEU:HD12	1.93	0.50
1:Q:132:LEU:HD23	1:Q:164:LYS:HG3	1.92	0.50
1:X:237:SER:O	1:X:244:ARG:NH2	2.44	0.50
1:Y:237:SER:O	1:Y:244:ARG:NH2	2.44	0.50
1:Y:250:ASN:HB3	1:Y:256:LEU:HB2	1.92	0.50
1:2:197:GLN:HB2	4:N:689:LYS:HE3	1.93	0.50
2:e:5:ILE:HG22	2:e:102:PRO:HG3	1.93	0.50
4:N:608:THR:HG23	4:N:610:ALA:H	1.76	0.50
1:O:313:THR:OG1	1:O:314:ASN:N	2.44	0.50
1:R:132:LEU:HD23	1:R:164:LYS:HG3	1.92	0.50
1:V:318:ILE:HB	1:V:380:ASN:HB3	1.92	0.50
1:X:132:LEU:HD23	1:X:164:LYS:HG3	1.92	0.50
1:X:318:ILE:HB	1:X:380:ASN:HB3	1.92	0.50
3:C:539:LEU:HB3	3:C:613:LEU:HD23	1.93	0.50
8:L:1667:HIS:CE1	1:Z:354:ALA:HA	2.46	0.50
4:N:297:LEU:HB3	4:N:378:LEU:HD13	1.92	0.50
1:S:117:ASP:OD1	1:S:117:ASP:N	2.36	0.50
5:g:74:LEU:HB3	4:f:23:ARG:HH12	1.75	0.50
3:C:241:ARG:HH12	3:C:245:THR:H	1.58	0.50
4:H:694:MET:HE1	4:H:701:LEU:HG	1.93	0.50
1:O:125:GLU:O	1:O:129:SER:N	2.42	0.50
1:P:132:LEU:HD23	1:P:164:LYS:HG3	1.92	0.50
1:S:125:GLU:O	1:S:129:SER:N	2.42	0.50
5:d:46:ILE:HG21	8:c:11:LEU:HG	1.93	0.50
4:f:66:ARG:CD	4:f:106:ARG:CG	2.88	0.50
1:1:259:SER:O	3:M:684:GLN:NE2	2.44	0.50
6:I:35:HIS:HB3	6:I:38:GLU:HG2	1.93	0.50
8:L:296:CYS:SG	8:L:297:TRP:N	2.84	0.50
4:N:493:LEU:HD21	4:N:545:LEU:HA	1.94	0.50
1:P:394:GLN:HA	1:P:397:LYS:HE2	1.94	0.50
1:V:313:THR:OG1	1:V:314:ASN:N	2.44	0.50
1:W:394:GLN:HA	1:W:397:LYS:HE2	1.94	0.50
5:d:46:ILE:HG23	8:c:7:LEU:HD22	1.94	0.50
3:E:617:SER:HB2	3:E:639:GLN:HE21	1.76	0.50
2:e:315:LYS:O	2:e:318:THR:OG1	2.25	0.50
3:G:446:MET:HG3	3:G:450:ILE:HG13	1.93	0.50
1:T:318:ILE:HB	1:T:380:ASN:HB3	1.92	0.50
1:Y:313:THR:OG1	1:Y:314:ASN:N	2.44	0.50
5:i:68:ARG:HG2	4:h:20:ILE:HD11	1.93	0.50
1:2:250:ASN:HB3	1:2:256:LEU:HB2	1.92	0.50
2:e:188:TYR:OH	2:e:266:PHE:O	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:559:LEU:HD11	3:A:570:LYS:HB2	1.93	0.50
1:Z:294:MET:SD	1:Z:336:SER:OG	2.64	0.50
3:A:469:CYS:HB2	3:A:471:VAL:HG22	1.93	0.50
6:K:639:ASN:O	6:K:643:ALA:HB2	2.12	0.50
1:Y:394:GLN:HA	1:Y:397:LYS:HE2	1.94	0.50
3:M:158:ARG:HE	3:M:159:LYS:HE3	1.77	0.50
1:V:125:GLU:O	1:V:129:SER:N	2.42	0.50
5:d:67:LEU:HD11	8:c:41:ALA:HA	1.94	0.50
3:A:738:MET:HG3	3:A:745:LEU:HD12	1.94	0.49
4:F:430:LEU:HD13	4:F:446:PHE:HZ	1.77	0.49
6:I:481:TYR:O	6:I:484:SER:OG	2.27	0.49
1:W:125:GLU:O	1:W:129:SER:N	2.42	0.49
1:X:394:GLN:HA	1:X:397:LYS:HE2	1.94	0.49
7:l:110:ILE:HD12	7:l:113:LEU:HD23	1.94	0.49
4:B:304:ILE:HD11	4:B:382:ALA:HA	1.94	0.49
4:B:376:ILE:HA	4:B:379:LYS:HZ3	1.78	0.49
4:B:861:PHE:HD2	4:B:862:LEU:HD22	1.77	0.49
4:H:689:LYS:HA	4:H:692:ARG:HH21	1.76	0.49
4:N:649:ALA:HB1	4:N:654:ARG:HH22	1.78	0.49
1:T:313:THR:OG1	1:T:314:ASN:N	2.44	0.49
1:U:313:THR:OG1	1:U:314:ASN:N	2.44	0.49
3:A:519:TYR:CD2	3:A:573:LEU:HD11	2.47	0.49
1:U:125:GLU:O	1:U:129:SER:N	2.42	0.49
3:C:659:TRP:CZ2	1:Q:258:ALA:HA	2.48	0.49
5:b:22:ARG:HH12	5:b:41:MET:HE3	1.77	0.49
7:J:935:SER:O	7:J:944:ARG:NH1	2.45	0.49
6:K:653:LYS:HE3	1:Y:351:TRP:HA	1.94	0.49
1:S:394:GLN:HA	1:S:397:LYS:HE2	1.94	0.49
3:A:551:LEU:HD22	3:A:575:ILE:HG13	1.94	0.49
4:F:568:LEU:HD23	4:F:574:ILE:HG21	1.93	0.49
4:N:573:PHE:HA	4:N:608:THR:HG21	1.95	0.49
4:N:589:ALA:HB2	4:N:634:GLY:HA2	1.93	0.49
1:S:66:LEU:HB3	1:S:91:ILE:HA	1.95	0.49
1:Y:66:LEU:HB3	1:Y:91:ILE:HA	1.95	0.49
3:C:308:SER:HB2	4:D:369:VAL:HG21	1.95	0.49
4:N:500:GLN:HG2	4:N:502:PRO:HD3	1.94	0.49
1:Q:5:ILE:HG12	1:Q:133:GLU:HB3	1.95	0.49
1:Q:394:GLN:HA	1:Q:397:LYS:HE2	1.94	0.49
1:T:394:GLN:HA	1:T:397:LYS:HE2	1.94	0.49
1:V:5:ILE:HG12	1:V:133:GLU:HB3	1.95	0.49
1:V:394:GLN:HA	1:V:397:LYS:HE2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:66:LEU:HB3	1:Z:91:ILE:HA	1.95	0.49
5:g:67:LEU:HD22	4:f:21:LEU:HD21	1.94	0.49
3:E:871:ARG:HH21	3:E:872:LEU:HD23	1.78	0.49
4:f:77:LEU:HA	4:f:80:LYS:HG3	1.93	0.49
4:H:778:VAL:HA	4:H:781:GLN:HE22	1.78	0.49
1:S:4:GLU:HG3	1:S:131:SER:H	1.78	0.49
1:U:5:ILE:HG12	1:U:133:GLU:HB3	1.95	0.49
5:i:28:LEU:HB2	5:i:44:LEU:HD21	1.95	0.49
7:J:909:THR:HA	7:J:912:GLU:HG3	1.93	0.49
6:K:648:ARG:HG3	6:K:649:LEU:HD12	1.95	0.49
1:W:5:ILE:HG12	1:W:133:GLU:HB3	1.95	0.49
4:f:70:ASP:OD2	4:f:111:VAL:HG23	2.13	0.49
4:F:799:GLU:HG3	4:F:836:PHE:HZ	1.78	0.49
3:M:734:LEU:HB2	3:M:739:LEU:HD22	1.95	0.49
1:O:66:LEU:HB3	1:O:91:ILE:HA	1.95	0.49
1:O:394:GLN:HA	1:O:397:LYS:HE2	1.94	0.49
1:T:66:LEU:HB3	1:T:91:ILE:HA	1.95	0.49
1:U:4:GLU:HG3	1:U:131:SER:H	1.78	0.49
1:U:66:LEU:HB3	1:U:91:ILE:HA	1.95	0.49
1:X:4:GLU:HG3	1:X:131:SER:H	1.78	0.49
5:g:57:PRO:HA	5:g:60:LEU:HB2	1.95	0.49
7:l:119:ASP:HB3	7:l:121:PRO:HD3	1.94	0.49
3:E:205:ILE:HD12	3:E:208:LEU:HD12	1.95	0.49
3:A:412:HIS:HE1	3:A:433:THR:HG22	1.78	0.48
4:F:365:ARG:HG2	3:E:308:SER:HB3	1.95	0.48
6:K:649:LEU:HB2	1:Y:341:ARG:NH2	2.28	0.48
1:V:4:GLU:HG3	1:V:131:SER:H	1.78	0.48
1:X:231:LEU:O	1:X:234:THR:OG1	2.26	0.48
1:Z:5:ILE:HG12	1:Z:133:GLU:HB3	1.95	0.48
1:2:5:ILE:HG12	1:2:133:GLU:HB3	1.95	0.48
1:2:394:GLN:HA	1:2:397:LYS:HE2	1.94	0.48
3:G:183:GLU:OE2	3:G:184:ARG:NH1	2.46	0.48
3:M:693:ILE:HD13	3:M:858:ARG:HH12	1.78	0.48
1:P:66:LEU:HB3	1:P:91:ILE:HA	1.95	0.48
1:S:231:LEU:O	1:S:234:THR:OG1	2.26	0.48
1:W:313:THR:OG1	1:W:314:ASN:N	2.44	0.48
1:1:394:GLN:HA	1:1:397:LYS:HE2	1.94	0.48
2:e:324:THR:OG1	2:e:325:MET:SD	2.71	0.48
4:N:862:LEU:HD11	4:N:886:TYR:HD2	1.78	0.48
1:O:5:ILE:HG12	1:O:133:GLU:HB3	1.95	0.48
1:P:5:ILE:HG12	1:P:133:GLU:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:5:ILE:HG12	1:R:133:GLU:HB3	1.95	0.48
1:R:125:GLU:O	1:R:129:SER:N	2.42	0.48
1:W:66:LEU:HB3	1:W:91:ILE:HA	1.95	0.48
1:Y:229:ASN:O	1:Y:233:SER:OG	2.21	0.48
3:A:695:TYR:HA	3:A:698:MET:HE3	1.96	0.48
4:F:555:LEU:HG	4:F:559:MET:HE3	1.94	0.48
1:Q:4:GLU:HG3	1:Q:131:SER:H	1.78	0.48
1:U:394:GLN:HA	1:U:397:LYS:HE2	1.94	0.48
1:W:4:GLU:HG3	1:W:131:SER:H	1.78	0.48
1:Z:125:GLU:O	1:Z:129:SER:N	2.42	0.48
3:E:449:LYS:O	3:E:453:THR:OG1	2.31	0.48
2:e:147:ARG:HG3	8:c:49:LEU:HD13	1.95	0.48
8:L:347:VAL:HG21	8:L:352:LEU:HD13	1.96	0.48
1:R:293:VAL:HA	1:R:296:ARG:HD2	1.96	0.48
1:T:4:GLU:HG3	1:T:131:SER:H	1.78	0.48
3:E:319:LEU:HD13	3:E:324:LEU:HD21	1.95	0.48
4:h:112:SER:O	4:h:113:SER:OG	2.28	0.48
4:B:578:MET:HE1	4:B:585:LEU:HD11	1.95	0.48
4:D:319:LEU:N	4:D:445:GLU:OE2	2.47	0.48
3:M:304:LEU:HD21	4:N:364:LEU:HD13	1.96	0.48
1:P:4:GLU:HG3	1:P:131:SER:H	1.78	0.48
1:R:4:GLU:HG3	1:R:131:SER:H	1.78	0.48
1:Y:4:GLU:HG3	1:Y:131:SER:H	1.78	0.48
1:Z:293:VAL:HA	1:Z:296:ARG:HD2	1.96	0.48
1:1:66:LEU:HB3	1:1:91:ILE:HA	1.95	0.48
1:2:4:GLU:HG3	1:2:131:SER:H	1.78	0.48
1:2:231:LEU:O	1:2:234:THR:OG1	2.26	0.48
1:2:294:MET:SD	1:2:336:SER:OG	2.64	0.48
3:A:656:CYS:HB3	1:O:254:ILE:HG12	1.96	0.48
1:O:332:GLN:H	1:O:332:GLN:HG3	1.53	0.48
1:Q:66:LEU:HB3	1:Q:91:ILE:HA	1.95	0.48
1:T:125:GLU:O	1:T:129:SER:N	2.42	0.48
1:X:5:ILE:HG12	1:X:133:GLU:HB3	1.95	0.48
3:A:163:ASP:O	3:A:167:LYS:NZ	2.46	0.48
3:G:637:ARG:NH2	3:G:640:MET:SD	2.86	0.48
7:J:223:GLN:HB3	7:J:228:ARG:HH21	1.77	0.48
1:P:125:GLU:O	1:P:129:SER:N	2.42	0.48
1:R:241:THR:OG1	1:R:244:ARG:NH2	2.47	0.48
1:V:326:GLY:HA3	1:V:373:VAL:HA	1.96	0.48
1:Z:394:GLN:HA	1:Z:397:LYS:HE2	1.94	0.48
1:1:4:GLU:HG3	1:1:131:SER:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:277:VAL:HG21	4:F:291:ALA:HB3	1.95	0.48
8:L:1800:LEU:HD22	1:Z:338:GLN:OE1	2.14	0.48
4:N:718:MET:HE2	4:N:775:LEU:HD11	1.96	0.48
1:S:332:GLN:H	1:S:332:GLN:HG3	1.53	0.48
1:T:293:VAL:HA	1:T:296:ARG:HD2	1.96	0.48
1:T:326:GLY:HA3	1:T:373:VAL:HA	1.96	0.48
1:W:241:THR:OG1	1:W:244:ARG:NH2	2.47	0.48
7:l:118:SER:O	7:l:119:ASP:CG	2.56	0.48
1:1:5:ILE:HG12	1:1:133:GLU:HB3	1.95	0.48
1:1:415:LYS:HZ2	1:1:419:ASP:H	1.62	0.48
3:C:719:ILE:HA	3:C:722:VAL:HG12	1.95	0.48
3:C:764:LYS:HD3	3:C:767:GLN:HA	1.96	0.48
4:F:554:SER:O	4:F:554:SER:OG	2.31	0.48
7:J:712:LYS:HG3	7:J:715:ARG:HH11	1.79	0.48
6:K:339:HIS:HA	6:K:342:LYS:HE2	1.95	0.48
1:V:66:LEU:HB3	1:V:91:ILE:HA	1.95	0.48
1:V:241:THR:OG1	1:V:244:ARG:NH2	2.47	0.48
1:1:241:THR:OG1	1:1:244:ARG:NH2	2.47	0.47
4:D:847:LEU:O	4:D:850:LEU:HB3	2.13	0.47
3:G:428:TRP:HZ2	3:G:723:LEU:HD23	1.79	0.47
8:L:1804:PHE:HZ	1:Z:340:ILE:HG22	1.79	0.47
1:R:66:LEU:HB3	1:R:91:ILE:HA	1.95	0.47
1:R:394:GLN:HA	1:R:397:LYS:HE2	1.94	0.47
1:S:313:THR:OG1	1:S:314:ASN:N	2.44	0.47
1:V:294:MET:SD	1:V:336:SER:OG	2.64	0.47
1:X:377:MET:HE2	1:X:377:MET:HB3	1.78	0.47
5:g:27:VAL:HG13	4:f:77:LEU:HD22	1.96	0.47
5:k:49:ARG:HB3	4:j:7:LYS:HE3	1.96	0.47
1:2:66:LEU:HB3	1:2:91:ILE:HA	1.95	0.47
4:D:714:PHE:CD1	4:D:880:LEU:HD21	2.49	0.47
8:L:1636:VAL:O	8:L:1662:LYS:NZ	2.44	0.47
1:O:294:MET:SD	1:O:336:SER:OG	2.64	0.47
1:Q:293:VAL:HA	1:Q:296:ARG:HD2	1.96	0.47
1:S:293:VAL:O	1:S:297:LEU:HB3	2.14	0.47
1:S:326:GLY:HA3	1:S:373:VAL:HA	1.96	0.47
1:V:293:VAL:HA	1:V:296:ARG:HD2	1.96	0.47
3:A:814:LEU:HG	3:A:815:VAL:H	1.80	0.47
4:B:588:PRO:HA	4:B:633:THR:HA	1.96	0.47
3:C:492:PHE:O	3:C:496:SER:OG	2.32	0.47
7:J:294:VAL:HG23	7:J:318:ALA:HB1	1.96	0.47
7:J:419:GLY:HA2	7:J:436:LEU:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:K:653:LYS:HD2	6:K:653:LYS:HA	1.65	0.47
1:P:293:VAL:HA	1:P:296:ARG:HD2	1.96	0.47
1:S:415:LYS:HZ2	1:S:419:ASP:H	1.61	0.47
1:X:241:THR:OG1	1:X:244:ARG:NH2	2.47	0.47
3:E:242:GLN:HE22	3:E:346:ASP:HB3	1.78	0.47
1:1:3:ARG:NH1	1:1:131:SER:OG	2.48	0.47
1:2:241:THR:OG1	1:2:244:ARG:NH2	2.47	0.47
4:B:581:LEU:HD11	4:B:597:LEU:HD13	1.95	0.47
6:I:199:GLN:HE21	6:I:200:HIS:CD2	2.32	0.47
3:M:315:ARG:HH12	4:N:363:THR:HG22	1.79	0.47
3:M:321:LEU:HD12	3:M:324:LEU:HD22	1.95	0.47
3:M:701:VAL:O	3:M:705:THR:OG1	2.31	0.47
1:O:241:THR:OG1	1:O:244:ARG:NH2	2.47	0.47
1:R:110:GLN:HA	1:R:113:LYS:HE3	1.97	0.47
1:X:3:ARG:NH1	1:X:131:SER:OG	2.48	0.47
1:Y:231:LEU:O	1:Y:234:THR:OG1	2.26	0.47
1:Z:326:GLY:HA3	1:Z:373:VAL:HA	1.96	0.47
4:f:14:GLN:NE2	4:f:17:CYS:SG	2.87	0.47
1:1:110:GLN:HA	1:1:113:LYS:HE3	1.97	0.47
2:e:74:GLY:HA2	2:e:159:VAL:HG22	1.94	0.47
2:e:260:ALA:HA	2:e:264:PRO:HA	1.97	0.47
4:H:377:ARG:CZ	4:H:414:LEU:HB2	2.44	0.47
6:I:621:ARG:O	6:I:624:SER:OG	2.31	0.47
1:O:293:VAL:O	1:O:297:LEU:HB3	2.15	0.47
1:P:326:GLY:HA3	1:P:373:VAL:HA	1.96	0.47
1:U:241:THR:OG1	1:U:244:ARG:NH2	2.47	0.47
1:U:293:VAL:HA	1:U:296:ARG:HD2	1.96	0.47
1:U:332:GLN:H	1:U:332:GLN:HG3	1.53	0.47
1:W:110:GLN:HA	1:W:113:LYS:HE3	1.97	0.47
1:X:326:GLY:HA3	1:X:373:VAL:HA	1.96	0.47
1:Z:241:THR:OG1	1:Z:244:ARG:NH2	2.47	0.47
1:Z:293:VAL:O	1:Z:297:LEU:HB3	2.15	0.47
4:j:61:GLU:OE1	4:j:64:ARG:NH2	2.47	0.47
3:E:617:SER:HB2	3:E:639:GLN:NE2	2.29	0.47
1:1:231:LEU:O	1:1:234:THR:OG1	2.26	0.47
1:1:326:GLY:HA3	1:1:373:VAL:HA	1.96	0.47
1:2:326:GLY:HA3	1:2:373:VAL:HA	1.96	0.47
3:C:644:HIS:HB2	3:C:739:LEU:HD21	1.96	0.47
4:H:317:PHE:HD1	4:H:392:LYS:HZ3	1.63	0.47
6:K:379:MET:HE2	6:K:391:ASP:HB2	1.96	0.47
6:K:651:TYR:CE2	1:Y:354:ALA:HB3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:568:LEU:HD22	4:N:574:ILE:HD12	1.96	0.47
1:O:293:VAL:HA	1:O:296:ARG:HD2	1.96	0.47
1:R:293:VAL:O	1:R:297:LEU:HB3	2.15	0.47
1:S:5:ILE:HG12	1:S:133:GLU:HB3	1.95	0.47
1:T:5:ILE:HG12	1:T:133:GLU:HB3	1.95	0.47
1:Y:3:ARG:NH1	1:Y:131:SER:OG	2.48	0.47
1:Y:5:ILE:HG12	1:Y:133:GLU:HB3	1.95	0.47
1:2:110:GLN:HA	1:2:113:LYS:HE3	1.97	0.47
2:e:335:ARG:HG3	2:e:338:SER:HB3	1.97	0.47
3:A:233:VAL:HA	3:A:247:LEU:O	2.15	0.47
3:A:521:LEU:HD23	3:A:702:MET:HE2	1.97	0.47
4:B:773:ASN:OD1	4:f:108:PRO:CG	2.62	0.47
4:D:685:MET:O	4:D:689:LYS:NZ	2.40	0.47
4:F:780:ASP:OD1	4:j:106:ARG:NH2	2.46	0.47
4:H:375:LYS:HG3	4:H:376:ILE:HG12	1.96	0.47
4:N:706:ILE:O	4:N:709:SER:OG	2.30	0.47
1:O:4:GLU:HG3	1:O:131:SER:H	1.78	0.47
1:O:326:GLY:HA3	1:O:373:VAL:HA	1.96	0.47
1:Q:293:VAL:O	1:Q:297:LEU:HB3	2.15	0.47
1:R:3:ARG:NH1	1:R:131:SER:OG	2.48	0.47
1:S:293:VAL:HA	1:S:296:ARG:HD2	1.96	0.47
1:T:3:ARG:NH1	1:T:131:SER:OG	2.48	0.47
1:T:241:THR:OG1	1:T:244:ARG:NH2	2.47	0.47
1:V:293:VAL:O	1:V:297:LEU:HB3	2.15	0.47
1:W:293:VAL:O	1:W:297:LEU:HB3	2.15	0.47
1:W:323:ILE:HD12	1:W:376:LEU:HD11	1.97	0.47
1:X:66:LEU:HB3	1:X:91:ILE:HA	1.95	0.47
1:X:293:VAL:HA	1:X:296:ARG:HD2	1.96	0.47
1:Y:293:VAL:HA	1:Y:296:ARG:HD2	1.96	0.47
7:l:127:VAL:HG13	7:l:130:PRO:CD	2.42	0.47
1:1:71:PRO:O	1:1:75:HIS:NE2	2.48	0.47
1:1:293:VAL:HA	1:1:296:ARG:HD2	1.96	0.47
1:2:293:VAL:HA	1:2:296:ARG:HD2	1.96	0.47
1:2:415:LYS:HZ2	1:2:419:ASP:H	1.63	0.47
3:C:154:LEU:O	3:C:158:ARG:HG2	2.14	0.47
4:D:848:ARG:HB3	4:D:852:HIS:CE1	2.50	0.47
4:H:376:ILE:HG22	4:H:411:MET:HE3	1.97	0.47
1:P:241:THR:OG1	1:P:244:ARG:NH2	2.47	0.47
1:P:293:VAL:O	1:P:297:LEU:HB3	2.15	0.47
1:Q:3:ARG:NH1	1:Q:131:SER:OG	2.48	0.47
1:Q:71:PRO:O	1:Q:75:HIS:NE2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:241:THR:OG1	1:Q:244:ARG:NH2	2.47	0.47
1:R:297:LEU:HD13	1:R:377:MET:HB2	1.97	0.47
1:T:293:VAL:O	1:T:297:LEU:HB3	2.15	0.47
1:T:323:ILE:HD12	1:T:376:LEU:HD11	1.97	0.47
1:V:71:PRO:O	1:V:75:HIS:NE2	2.48	0.47
1:X:110:GLN:HA	1:X:113:LYS:HE3	1.97	0.47
1:Z:53:TYR:HD1	1:Z:61:ILE:HB	1.80	0.47
1:Z:71:PRO:O	1:Z:75:HIS:NE2	2.48	0.47
1:1:297:LEU:HD13	1:1:377:MET:HB2	1.97	0.47
1:2:297:LEU:HD13	1:2:377:MET:HB2	1.97	0.47
2:e:267:LEU:HD22	2:e:269:MET:HB2	1.97	0.47
3:A:485:VAL:O	3:A:489:GLU:HG2	2.15	0.47
4:B:773:ASN:CG	4:f:108:PRO:HD3	2.40	0.47
6:I:369:PHE:HA	6:I:372:PHE:HB3	1.97	0.47
3:M:413:GLU:OE2	3:M:416:LYS:NZ	2.48	0.47
3:M:689:PHE:O	3:M:693:ILE:HG12	2.15	0.47
1:S:3:ARG:NH1	1:S:131:SER:OG	2.48	0.47
1:X:293:VAL:O	1:X:297:LEU:HB3	2.15	0.47
1:2:71:PRO:O	1:2:75:HIS:NE2	2.48	0.47
3:A:865:TYR:CZ	1:O:353:PRO:HG3	2.50	0.47
1:O:71:PRO:O	1:O:75:HIS:NE2	2.48	0.47
1:O:297:LEU:HD13	1:O:377:MET:HB2	1.97	0.47
1:Q:53:TYR:HD1	1:Q:61:ILE:HB	1.80	0.47
1:Q:323:ILE:HD12	1:Q:376:LEU:HD11	1.97	0.47
1:Q:326:GLY:HA3	1:Q:373:VAL:HA	1.96	0.47
1:T:297:LEU:HD13	1:T:377:MET:HB2	1.97	0.47
1:V:297:LEU:HD13	1:V:377:MET:HB2	1.97	0.47
1:X:297:LEU:HD13	1:X:377:MET:HB2	1.97	0.47
1:Z:3:ARG:NH1	1:Z:131:SER:OG	2.48	0.47
1:Z:4:GLU:HG3	1:Z:131:SER:H	1.78	0.47
5:g:66:GLU:HA	5:g:69:LYS:HG2	1.97	0.47
4:f:66:ARG:CG	4:f:106:ARG:CD	2.93	0.47
1:1:130:ASP:OD2	1:2:295:ARG:NH2	2.35	0.46
1:1:293:VAL:O	1:1:297:LEU:HB3	2.15	0.46
4:B:706:ILE:HD11	1:P:351:TRP:CZ3	2.49	0.46
4:F:365:ARG:HA	4:F:365:ARG:HD2	1.71	0.46
3:G:876:ARG:HD3	5:k:59:ALA:HB2	1.94	0.46
6:I:363:LEU:HD12	6:I:482:LEU:HB2	1.97	0.46
7:J:283:LYS:HD2	7:J:283:LYS:HA	1.68	0.46
7:J:432:ARG:O	7:J:436:LEU:HD13	2.15	0.46
1:P:3:ARG:NH1	1:P:131:SER:OG	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:110:GLN:HA	1:P:113:LYS:HE3	1.97	0.46
1:S:53:TYR:HD1	1:S:61:ILE:HB	1.80	0.46
1:X:71:PRO:O	1:X:75:HIS:NE2	2.48	0.46
1:Y:110:GLN:HA	1:Y:113:LYS:HE3	1.97	0.46
1:Y:241:THR:OG1	1:Y:244:ARG:NH2	2.47	0.46
1:Z:323:ILE:HD12	1:Z:376:LEU:HD11	1.97	0.46
1:2:53:TYR:HD1	1:2:61:ILE:HB	1.80	0.46
1:2:293:VAL:O	1:2:297:LEU:HB3	2.15	0.46
4:B:846:GLN:O	4:B:850:LEU:HG	2.16	0.46
4:D:247:GLU:HB2	4:D:366:ARG:CZ	2.46	0.46
6:I:262:GLU:HG3	6:I:263:ILE:HG23	1.97	0.46
4:N:771:LEU:HD11	4:N:873:LEU:HD13	1.97	0.46
1:T:164:LYS:HD3	1:T:164:LYS:HA	1.71	0.46
1:U:71:PRO:O	1:U:75:HIS:NE2	2.48	0.46
1:U:164:LYS:HA	1:U:164:LYS:HD3	1.71	0.46
1:V:3:ARG:NH1	1:V:131:SER:OG	2.48	0.46
1:W:3:ARG:NH1	1:W:131:SER:OG	2.48	0.46
1:W:293:VAL:HA	1:W:296:ARG:HD2	1.96	0.46
7:I:127:VAL:CG1	7:I:130:PRO:CD	2.77	0.46
6:I:279:VAL:HG13	6:I:336:VAL:HG11	1.98	0.46
3:M:403:PRO:HD2	4:N:412:ARG:HH22	1.80	0.46
1:O:53:TYR:HD1	1:O:61:ILE:HB	1.80	0.46
1:Y:293:VAL:O	1:Y:297:LEU:HB3	2.15	0.46
1:Y:387:LEU:HD13	1:Y:390:ARG:HD3	1.98	0.46
3:E:695:TYR:HA	3:E:698:MET:HG2	1.98	0.46
1:2:3:ARG:NH1	1:2:131:SER:OG	2.48	0.46
1:2:323:ILE:HD12	1:2:376:LEU:HD11	1.97	0.46
2:e:317:ILE:HD12	2:e:320:LEU:HD13	1.96	0.46
4:B:689:LYS:HA	4:B:689:LYS:HD2	1.46	0.46
6:I:151:CYS:SG	6:I:260:ARG:NH2	2.88	0.46
6:K:626:LEU:HD23	6:K:626:LEU:HA	1.74	0.46
1:O:3:ARG:NH1	1:O:131:SER:OG	2.48	0.46
1:O:110:GLN:HA	1:O:113:LYS:HE3	1.97	0.46
1:P:71:PRO:O	1:P:75:HIS:NE2	2.48	0.46
1:Q:297:LEU:HD13	1:Q:377:MET:HB2	1.97	0.46
1:Q:387:LEU:HD13	1:Q:390:ARG:HD3	1.98	0.46
1:R:71:PRO:O	1:R:75:HIS:NE2	2.48	0.46
1:W:297:LEU:HD13	1:W:377:MET:HB2	1.97	0.46
1:W:326:GLY:HA3	1:W:373:VAL:HA	1.96	0.46
1:Y:326:GLY:HA3	1:Y:373:VAL:HA	1.96	0.46
4:f:66:ARG:HG2	4:f:106:ARG:CZ	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:387:LEU:HD13	1:1:390:ARG:HD3	1.98	0.46
3:A:517:LYS:HE2	3:A:521:LEU:HD22	1.96	0.46
3:M:161:LEU:HG	3:M:174:LEU:HD12	1.97	0.46
1:O:323:ILE:HD12	1:O:376:LEU:HD11	1.97	0.46
1:Q:110:GLN:HA	1:Q:113:LYS:HE3	1.97	0.46
1:R:53:TYR:HD1	1:R:61:ILE:HB	1.80	0.46
1:R:387:LEU:HD13	1:R:390:ARG:HD3	1.98	0.46
1:S:241:THR:OG1	1:S:244:ARG:NH2	2.47	0.46
1:U:323:ILE:HD12	1:U:376:LEU:HD11	1.97	0.46
1:Z:297:LEU:HD13	1:Z:377:MET:HB2	1.97	0.46
1:Z:415:LYS:HZ2	1:Z:419:ASP:H	1.62	0.46
2:e:222:ASP:H	2:e:225:GLN:HE21	1.64	0.46
4:B:683:GLY:O	4:B:687:ASN:ND2	2.49	0.46
3:C:306:LEU:HB2	8:c:190:LEU:HD21	1.96	0.46
3:C:412:HIS:HB2	3:C:431:ARG:HA	1.97	0.46
4:H:589:ALA:HB3	4:H:632:ASP:HB3	1.97	0.46
3:M:557:LEU:HD11	3:M:561:MET:HE2	1.98	0.46
4:N:453:THR:HG23	4:N:455:LYS:HE2	1.97	0.46
1:P:297:LEU:HD13	1:P:377:MET:HB2	1.97	0.46
1:R:326:GLY:HA3	1:R:373:VAL:HA	1.96	0.46
1:S:71:PRO:O	1:S:75:HIS:NE2	2.48	0.46
1:S:110:GLN:HA	1:S:113:LYS:HE3	1.97	0.46
1:T:71:PRO:O	1:T:75:HIS:NE2	2.48	0.46
1:T:387:LEU:HD13	1:T:390:ARG:HD3	1.98	0.46
1:U:326:GLY:HA3	1:U:373:VAL:HA	1.96	0.46
1:U:387:LEU:HD13	1:U:390:ARG:HD3	1.98	0.46
1:Y:71:PRO:O	1:Y:75:HIS:NE2	2.48	0.46
5:g:50:LEU:HD23	5:g:53:GLN:HE22	1.80	0.46
5:k:57:PRO:HB2	4:j:95:TYR:HD1	1.81	0.46
1:1:125:GLU:O	1:1:129:SER:N	2.42	0.46
2:e:236:LEU:HG	2:e:251:GLY:HA3	1.97	0.46
6:I:136:VAL:HG22	6:I:172:LEU:HD21	1.97	0.46
4:N:692:ARG:HH11	4:N:701:LEU:HD21	1.81	0.46
1:T:110:GLN:HA	1:T:113:LYS:HE3	1.97	0.46
4:f:28:VAL:HG21	4:f:31:GLN:HG2	1.98	0.46
1:1:53:TYR:HD1	1:1:61:ILE:HB	1.80	0.46
1:1:89:GLU:HB2	1:2:216:ASP:HA	1.97	0.46
3:A:660:ILE:HG13	1:O:165:LEU:HD12	1.98	0.46
3:C:582:LEU:HD13	3:C:739:LEU:HD11	1.98	0.46
6:I:54:ARG:HG3	6:I:58:PHE:CZ	2.50	0.46
1:Q:377:MET:HE2	1:Q:377:MET:HB3	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:293:VAL:O	1:U:297:LEU:HB3	2.15	0.46
1:U:297:LEU:HD13	1:U:377:MET:HB2	1.97	0.46
1:U:415:LYS:HZ2	1:U:419:ASP:H	1.63	0.46
1:X:125:GLU:O	1:X:129:SER:N	2.42	0.46
3:E:331:ALA:O	3:E:335:MET:HG3	2.16	0.46
4:f:66:ARG:NE	4:f:106:ARG:CZ	2.78	0.46
3:A:285:TYR:O	3:A:289:ASN:ND2	2.40	0.46
3:A:304:LEU:HD22	4:B:365:ARG:HH22	1.81	0.46
3:G:222:LEU:HD11	4:H:365:ARG:HH22	1.81	0.46
6:K:639:ASN:O	6:K:643:ALA:CB	2.63	0.46
3:M:315:ARG:NH1	4:N:363:THR:HG22	2.31	0.46
3:M:405:SER:O	3:M:405:SER:OG	2.22	0.46
3:M:834:LEU:HD13	3:M:867:GLU:HA	1.98	0.46
4:N:468:LYS:HG2	4:N:471:ILE:HD12	1.98	0.46
1:S:387:LEU:HD13	1:S:390:ARG:HD3	1.98	0.46
1:U:3:ARG:NH1	1:U:131:SER:OG	2.48	0.46
1:U:53:TYR:HD1	1:U:61:ILE:HB	1.80	0.46
1:U:323:ILE:HB	1:U:376:LEU:HG	1.98	0.46
1:V:110:GLN:HA	1:V:113:LYS:HE3	1.97	0.46
1:X:53:TYR:HD1	1:X:61:ILE:HB	1.80	0.46
1:X:323:ILE:HD12	1:X:376:LEU:HD11	1.97	0.46
5:i:25:MET:HG3	5:i:41:MET:HE1	1.98	0.46
1:2:291:LEU:HD11	3:M:557:LEU:HA	1.98	0.46
3:A:231:ARG:NH2	4:B:285:ARG:HB2	2.31	0.46
4:B:361:SER:OG	4:B:362:LEU:N	2.47	0.46
4:H:589:ALA:HA	4:H:592:LEU:HG	1.98	0.46
4:H:723:THR:HA	4:H:727:LEU:HG	1.98	0.46
1:U:110:GLN:HA	1:U:113:LYS:HE3	1.97	0.46
1:Z:323:ILE:HB	1:Z:376:LEU:HG	1.98	0.46
2:e:314:GLN:HA	2:e:317:ILE:HG22	1.97	0.45
4:B:283:LEU:HD12	4:B:287:LEU:HD23	1.98	0.45
4:B:578:MET:HE2	4:B:578:MET:HA	1.98	0.45
3:G:222:LEU:HG	4:H:365:ARG:HH12	1.80	0.45
4:H:568:LEU:HD23	4:H:667:LEU:HD13	1.98	0.45
4:H:783:ILE:O	4:H:786:GLN:HG2	2.16	0.45
6:I:450:TRP:HD1	6:I:453:LEU:HD22	1.81	0.45
8:L:348:LYS:HG2	8:L:349:GLU:H	1.80	0.45
8:L:1659:GLN:HE21	1:Z:264:PRO:HD3	1.81	0.45
1:P:323:ILE:HB	1:P:376:LEU:HG	1.98	0.45
1:Q:323:ILE:HB	1:Q:376:LEU:HG	1.98	0.45
1:T:53:TYR:HD1	1:T:61:ILE:HB	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:323:ILE:HD12	1:V:376:LEU:HD11	1.97	0.45
1:W:156:ARG:HD3	1:W:156:ARG:HA	1.75	0.45
1:W:415:LYS:HZ2	1:W:419:ASP:H	1.63	0.45
1:Y:323:ILE:HD12	1:Y:376:LEU:HD11	1.97	0.45
1:Z:110:GLN:HA	1:Z:113:LYS:HE3	1.97	0.45
4:a:96:LEU:O	4:a:99:SER:OG	2.29	0.45
4:D:341:VAL:O	4:D:344:SER:OG	2.34	0.45
5:b:60:LEU:HA	5:b:63:VAL:HG12	1.99	0.45
6:I:7:LEU:HD12	6:I:7:LEU:HA	1.83	0.45
4:N:451:ASP:O	4:N:463:LYS:NZ	2.49	0.45
1:R:323:ILE:HB	1:R:376:LEU:HG	1.98	0.45
1:R:323:ILE:HD12	1:R:376:LEU:HD11	1.97	0.45
1:T:117:ASP:OD1	1:T:117:ASP:N	2.36	0.45
1:W:71:PRO:O	1:W:75:HIS:NE2	2.48	0.45
1:Z:313:THR:OG1	1:Z:314:ASN:N	2.44	0.45
4:f:108:PRO:O	4:f:109:SER:OG	2.29	0.45
1:2:125:GLU:O	1:2:129:SER:N	2.42	0.45
1:2:164:LYS:HA	1:2:164:LYS:HD3	1.71	0.45
4:B:425:PRO:O	4:B:428:SER:OG	2.33	0.45
4:B:718:MET:HG3	4:B:880:LEU:HD11	1.98	0.45
3:C:550:ARG:HG3	1:R:342:GLU:HB3	1.98	0.45
1:O:387:LEU:HD13	1:O:390:ARG:HD3	1.98	0.45
1:V:117:ASP:OD1	1:V:117:ASP:N	2.36	0.45
1:W:323:ILE:HB	1:W:376:LEU:HG	1.98	0.45
1:W:332:GLN:H	1:W:332:GLN:HG3	1.53	0.45
1:Y:53:TYR:HD1	1:Y:61:ILE:HB	1.80	0.45
5:g:35:LEU:HD12	4:f:101:SER:HB2	1.98	0.45
1:1:323:ILE:HB	1:1:376:LEU:HG	1.98	0.45
3:A:478:THR:OG1	3:A:479:LEU:N	2.50	0.45
4:H:364:LEU:HD13	4:H:364:LEU:HA	1.77	0.45
6:I:190:TRP:CE2	6:I:280:GLY:HA3	2.51	0.45
7:J:723:MET:HE3	7:J:723:MET:HB3	1.84	0.45
4:N:576:HIS:CD2	4:N:604:ALA:HA	2.51	0.45
1:Q:231:LEU:O	1:Q:234:THR:OG1	2.26	0.45
1:S:297:LEU:HD13	1:S:377:MET:HB2	1.97	0.45
1:V:53:TYR:HD1	1:V:61:ILE:HB	1.80	0.45
1:X:117:ASP:OD1	1:X:117:ASP:N	2.36	0.45
3:E:370:SER:HA	3:E:373:GLN:HB3	1.98	0.45
1:2:323:ILE:HB	1:2:376:LEU:HG	1.98	0.45
3:A:184:ARG:HG3	3:A:186:ALA:H	1.79	0.45
6:I:181:GLY:HA3	6:I:315:LYS:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:164:LYS:HD3	1:O:164:LYS:HA	1.71	0.45
1:P:53:TYR:HD1	1:P:61:ILE:HB	1.80	0.45
1:S:323:ILE:HB	1:S:376:LEU:HG	1.98	0.45
3:E:655:LEU:HD22	3:E:687:LEU:HD13	1.98	0.45
4:f:66:ARG:CD	4:f:106:ARG:HG2	2.46	0.45
1:1:323:ILE:HD12	1:1:376:LEU:HD11	1.97	0.45
1:1:332:GLN:H	1:1:332:GLN:HG3	1.53	0.45
1:2:348:PHE:HZ	1:2:356:ILE:CD1	2.29	0.45
4:F:490:ILE:HG13	4:F:494:HIS:CE1	2.52	0.45
4:H:377:ARG:HH12	4:H:410:TYR:C	2.25	0.45
1:O:323:ILE:HB	1:O:376:LEU:HG	1.98	0.45
1:R:383:SER:O	1:R:386:SER:OG	2.32	0.45
1:V:332:GLN:H	1:V:332:GLN:HG3	1.53	0.45
1:V:415:LYS:HZ2	1:V:419:ASP:H	1.63	0.45
1:X:323:ILE:HB	1:X:376:LEU:HG	1.98	0.45
1:Y:323:ILE:HB	1:Y:376:LEU:HG	1.98	0.45
1:Z:164:LYS:HD3	1:Z:164:LYS:HA	1.71	0.45
7:l:114:LEU:HA	7:l:117:LEU:HD12	1.99	0.45
3:A:542:PRO:HA	3:A:611:SER:HA	1.98	0.45
3:A:623:LYS:H	3:A:626:LEU:HB2	1.81	0.45
4:D:433:TRP:HE1	4:D:484:LEU:HA	1.81	0.45
4:D:684:HIS:HE1	4:D:708:ALA:HB2	1.81	0.45
4:F:391:ARG:HB2	4:F:396:LEU:HD13	1.98	0.45
7:J:902:MET:HG3	1:X:248:TYR:CD2	2.51	0.45
3:M:454:GLY:O	3:M:458:ASN:ND2	2.50	0.45
3:M:693:ILE:HA	3:M:858:ARG:HH12	1.81	0.45
4:B:297:LEU:HD22	4:B:378:LEU:HD23	1.98	0.45
3:G:551:LEU:HD13	3:G:575:ILE:HB	1.99	0.45
3:G:858:ARG:O	1:U:355:SER:OG	2.28	0.45
4:H:621:LEU:HD11	4:H:640:LEU:HD13	1.99	0.45
4:N:375:LYS:O	4:N:379:LYS:HG3	2.17	0.45
1:Q:294:MET:SD	1:Q:336:SER:OG	2.64	0.45
1:U:231:LEU:O	1:U:234:THR:OG1	2.26	0.45
1:W:387:LEU:HD13	1:W:390:ARG:HD3	1.98	0.45
1:Y:297:LEU:HD13	1:Y:377:MET:HB2	1.97	0.45
5:i:46:ILE:HD13	4:h:19:ARG:HG3	1.98	0.45
2:e:4:ASP:CG	2:e:353:GLN:HB2	2.41	0.45
3:G:356:LEU:HB2	3:G:440:PRO:HB3	1.99	0.45
4:N:297:LEU:HD23	4:N:300:LEU:HD12	1.99	0.45
1:P:323:ILE:HD12	1:P:376:LEU:HD11	1.97	0.45
1:P:387:LEU:HD13	1:P:390:ARG:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:156:ARG:HA	1:S:156:ARG:HD3	1.75	0.45
1:V:387:LEU:HD13	1:V:390:ARG:HD3	1.98	0.45
1:W:53:TYR:HD1	1:W:61:ILE:HB	1.80	0.45
1:X:387:LEU:HD13	1:X:390:ARG:HD3	1.98	0.45
1:X:415:LYS:HZ2	1:X:419:ASP:H	1.65	0.45
8:c:93:VAL:HA	8:c:96:LEU:HD12	1.98	0.45
3:E:547:THR:HG23	3:E:550:ARG:HB2	1.99	0.45
3:E:696:TYR:CZ	3:E:855:VAL:HB	2.52	0.45
2:e:82:MET:HA	2:e:85:ILE:HG22	1.99	0.45
2:e:246:GLN:HE21	2:e:248:ILE:HG22	1.82	0.45
3:C:306:LEU:O	3:C:310:LEU:HG	2.17	0.45
4:H:644:VAL:H	4:H:654:ARG:HH22	1.65	0.45
6:I:368:LEU:HD21	6:I:396:PHE:CE1	2.52	0.45
7:J:565:SER:HA	7:J:568:LEU:HD12	1.99	0.45
3:M:201:THR:OG1	3:M:202:ALA:N	2.41	0.45
1:S:252:ASP:HB3	3:E:529:VAL:HG21	1.98	0.45
1:U:156:ARG:HA	1:U:156:ARG:HD3	1.75	0.45
1:Z:387:LEU:HD13	1:Z:390:ARG:HD3	1.98	0.45
1:2:387:LEU:HD13	1:2:390:ARG:HD3	1.98	0.44
3:C:334:THR:HG23	3:C:375:LEU:HD22	1.99	0.44
1:S:323:ILE:HD12	1:S:376:LEU:HD11	1.97	0.44
1:V:323:ILE:HB	1:V:376:LEU:HG	1.98	0.44
3:E:219:GLU:O	3:E:222:LEU:HG	2.17	0.44
3:E:840:LEU:HG	3:E:856:ILE:HG12	1.99	0.44
2:e:299:LEU:HD21	2:e:329:ILE:HD11	1.99	0.44
3:A:381:LYS:HE2	3:A:478:THR:HG22	1.98	0.44
3:A:521:LEU:HA	3:A:645:MET:HE1	2.00	0.44
4:B:690:LEU:HD21	4:B:800:LEU:HD22	1.99	0.44
3:C:654:GLN:HB3	3:C:759:THR:HG21	1.98	0.44
4:F:493:LEU:HG	4:F:545:LEU:HD13	1.99	0.44
3:G:561:MET:HB2	1:V:339:ARG:HH11	1.82	0.44
6:I:478:VAL:O	6:I:482:LEU:HG	2.16	0.44
6:K:255:LYS:HD2	6:K:255:LYS:HA	1.86	0.44
6:K:649:LEU:HD22	1:Y:341:ARG:HH22	1.82	0.44
1:2:313:THR:OG1	1:2:314:ASN:N	2.44	0.44
2:e:289:ILE:HG13	2:e:293:LEU:HD13	1.99	0.44
4:F:651:VAL:HG23	4:F:748:ILE:HG12	1.99	0.44
3:G:356:LEU:HD12	3:G:440:PRO:HG3	1.98	0.44
2:e:218:TYR:HE2	2:e:220:ALA:HB2	1.82	0.44
3:A:737:CYS:SG	3:A:738:MET:N	2.87	0.44
3:A:752:MET:HE3	3:A:752:MET:HB3	1.93	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:251:VAL:HB	4:D:366:ARG:HH22	1.83	0.44
4:D:433:TRP:CD2	4:D:487:GLY:HA3	2.52	0.44
4:F:451:ASP:O	4:F:463:LYS:NZ	2.41	0.44
3:G:397:ARG:HA	3:G:457:LEU:HD13	1.99	0.44
3:G:484:TYR:O	3:G:488:ILE:HG12	2.17	0.44
1:R:246:PRO:HD2	1:R:362:ARG:HH21	1.83	0.44
1:V:156:ARG:HD3	1:V:156:ARG:HA	1.75	0.44
3:E:762:MET:HE1	3:E:818:PHE:HE1	1.82	0.44
4:H:320:VAL:HG12	4:H:396:LEU:HD23	1.99	0.44
7:J:212:ASP:OD1	7:J:212:ASP:N	2.50	0.44
6:K:2:ILE:HG13	6:K:3:HIS:H	1.83	0.44
6:K:3:HIS:HA	6:K:6:LEU:HD12	1.98	0.44
3:M:320:SER:H	3:M:323:LYS:HD2	1.83	0.44
4:N:866:THR:HG23	4:N:867:THR:HG22	2.00	0.44
1:R:377:MET:HB3	1:R:377:MET:HE2	1.78	0.44
1:T:246:PRO:HD2	1:T:362:ARG:HH21	1.83	0.44
1:X:156:ARG:HD3	1:X:156:ARG:HA	1.75	0.44
1:Y:156:ARG:HA	1:Y:156:ARG:HD3	1.75	0.44
2:e:100:GLU:N	2:e:100:GLU:OE2	2.51	0.44
2:e:297:THR:HG23	2:e:329:ILE:HG13	1.99	0.44
4:D:887:LYS:HD3	4:D:889:ARG:HH22	1.82	0.44
4:H:626:LEU:HD21	7:I:74:ILE:HG21	1.98	0.44
7:J:246:TRP:CD1	7:J:306:THR:HG21	2.53	0.44
7:J:358:PHE:CE1	7:J:429:ASN:HB2	2.53	0.44
8:L:1609:THR:HG23	8:L:1612:CYS:H	1.83	0.44
4:N:542:SER:O	4:N:546:LEU:HG	2.18	0.44
1:P:246:PRO:HD2	1:P:362:ARG:HH21	1.83	0.44
1:W:164:LYS:HD3	1:W:164:LYS:HA	1.71	0.44
1:X:246:PRO:HD2	1:X:362:ARG:HH21	1.83	0.44
3:E:444:GLN:HA	3:E:447:ALA:HB2	1.98	0.44
2:e:162:THR:HG21	2:e:278:THR:HA	1.99	0.44
3:C:446:MET:HB2	3:C:446:MET:HE3	1.80	0.44
4:D:613:ASP:HB3	4:D:617:ILE:HD11	1.99	0.44
4:D:657:MET:O	4:D:661:LEU:HG	2.17	0.44
4:F:681:ARG:O	4:F:685:MET:HG2	2.18	0.44
4:H:321:GLY:HA2	4:H:324:PHE:HB3	2.00	0.44
7:J:720:LEU:HB3	7:J:724:ARG:HH12	1.83	0.44
1:Q:246:PRO:HD2	1:Q:362:ARG:HH21	1.83	0.44
1:R:221:GLN:O	1:R:224:SER:OG	2.36	0.44
1:W:246:PRO:HD2	1:W:362:ARG:HH21	1.83	0.44
5:i:33:ARG:O	4:h:107:GLN:NE2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:769:MET:HE3	3:E:769:MET:HB3	1.91	0.44
1:1:246:PRO:HD2	1:1:362:ARG:HH21	1.83	0.44
1:1:342:GLU:OE1	8:L:1556:LYS:HB3	2.17	0.44
1:2:156:ARG:HD3	1:2:156:ARG:HA	1.75	0.44
2:e:8:LEU:HD13	2:e:21:PHE:HA	1.99	0.44
3:A:238:LEU:HD13	3:A:244:ARG:HD2	2.00	0.44
3:A:663:LYS:HG2	1:O:264:PRO:HB3	2.00	0.44
3:G:205:ILE:HG13	3:G:213:GLN:HG2	1.99	0.44
3:M:512:HIS:CE1	3:M:630:ILE:HD13	2.53	0.44
1:T:323:ILE:HB	1:T:376:LEU:HG	1.98	0.44
1:Y:172:PHE:N	1:Y:205:LEU:O	2.50	0.44
5:d:60:LEU:HA	5:d:63:VAL:HG12	2.00	0.44
3:E:270:TYR:HD1	3:E:335:MET:HE1	1.82	0.44
3:E:503:LEU:HD12	3:E:719:ILE:HG12	2.00	0.44
3:E:874:ALA:O	3:E:875:GLU:HG3	2.17	0.44
4:h:88:LYS:HD3	4:h:88:LYS:HA	1.84	0.44
1:2:221:GLN:O	1:2:224:SER:OG	2.36	0.44
4:D:726:VAL:HA	4:D:761:ARG:HD3	1.99	0.44
4:F:657:MET:HE3	4:F:657:MET:HB3	1.74	0.44
3:G:565:ASN:OD1	3:G:565:ASN:N	2.51	0.44
4:H:317:PHE:HA	4:H:392:LYS:HZ2	1.82	0.44
6:K:481:TYR:O	6:K:484:SER:OG	2.35	0.44
1:S:221:GLN:O	1:S:224:SER:OG	2.36	0.44
1:U:246:PRO:HD2	1:U:362:ARG:HH21	1.83	0.44
4:a:62:LEU:HD22	4:a:67:ARG:HB2	2.00	0.44
4:B:879:ARG:NE	1:P:337:LEU:HD22	2.32	0.43
4:D:433:TRP:CE2	4:D:487:GLY:HA3	2.53	0.43
4:D:718:MET:HE1	4:D:876:LEU:HD21	1.99	0.43
3:G:651:VAL:O	3:G:655:LEU:HG	2.17	0.43
3:G:746:LYS:O	3:G:749:SER:OG	2.30	0.43
3:M:311:GLU:O	3:M:315:ARG:HD3	2.18	0.43
4:N:862:LEU:HD23	4:N:865:LEU:HD23	1.99	0.43
1:Q:4:GLU:O	1:Q:133:GLU:N	2.51	0.43
1:U:377:MET:HE2	1:U:377:MET:HB3	1.78	0.43
1:Y:221:GLN:O	1:Y:224:SER:OG	2.36	0.43
5:d:68:ARG:HA	5:d:71:THR:HG22	1.99	0.43
1:2:246:PRO:HD2	1:2:362:ARG:HH21	1.83	0.43
2:e:104:LEU:HD13	2:e:133:TYR:HB3	2.00	0.43
2:e:357:ILE:HD12	2:e:358:SER:H	1.83	0.43
4:B:393:GLY:HA2	4:B:445:GLU:HB3	2.00	0.43
3:C:860:ASP:HB3	3:C:866:THR:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:391:ARG:HG2	4:D:395:GLU:HG3	2.00	0.43
6:K:630:LEU:HD22	6:K:645:LEU:HG	2.00	0.43
8:L:365:SER:H	8:L:368:PHE:HB2	1.82	0.43
4:N:666:PHE:HB2	4:N:764:LEU:HD11	1.99	0.43
1:O:246:PRO:HD2	1:O:362:ARG:HH21	1.83	0.43
1:S:246:PRO:HD2	1:S:362:ARG:HH21	1.83	0.43
1:Y:4:GLU:O	1:Y:133:GLU:N	2.51	0.43
1:Z:172:PHE:N	1:Z:205:LEU:O	2.50	0.43
1:Z:246:PRO:HD2	1:Z:362:ARG:HH21	1.83	0.43
3:A:696:TYR:CD2	3:A:858:ARG:HG3	2.52	0.43
4:B:409:PRO:O	4:B:413:SER:OG	2.31	0.43
4:N:320:VAL:HG21	4:N:393:GLY:HA2	1.98	0.43
1:O:221:GLN:O	1:O:224:SER:OG	2.36	0.43
1:O:377:MET:HE2	1:O:377:MET:HB3	1.78	0.43
1:P:221:GLN:O	1:P:224:SER:OG	2.36	0.43
1:R:401:ARG:HD3	1:R:404:PHE:HE2	1.84	0.43
1:V:33:PRO:HA	1:V:85:LEU:HD13	2.01	0.43
1:V:401:ARG:HD3	1:V:404:PHE:HE2	1.84	0.43
1:X:321:LEU:HD23	1:X:378:MET:HB2	2.01	0.43
1:Y:246:PRO:HD2	1:Y:362:ARG:HH21	1.83	0.43
3:E:448:ASP:OD1	3:E:448:ASP:N	2.50	0.43
1:1:164:LYS:HA	1:1:164:LYS:HD3	1.71	0.43
1:1:224:SER:O	1:1:228:ILE:HG12	2.19	0.43
1:1:321:LEU:HD23	1:1:378:MET:HB2	2.01	0.43
1:2:401:ARG:HD3	1:2:404:PHE:HE2	1.84	0.43
3:A:517:LYS:HD2	3:A:706:TRP:CE2	2.53	0.43
3:A:861:PHE:CE1	1:O:356:ILE:HD13	2.53	0.43
4:F:663:VAL:O	4:F:667:LEU:HG	2.18	0.43
3:G:283:PHE:HA	3:G:290:HIS:CE1	2.54	0.43
7:J:479:TRP:CD1	7:J:485:LEU:HG	2.54	0.43
1:O:415:LYS:HZ2	1:O:419:ASP:H	1.66	0.43
1:R:321:LEU:HD23	1:R:378:MET:HB2	2.01	0.43
1:T:221:GLN:O	1:T:224:SER:OG	2.36	0.43
1:V:246:PRO:HD2	1:V:362:ARG:HH21	1.83	0.43
1:Y:321:LEU:HD23	1:Y:378:MET:HB2	2.01	0.43
1:Z:224:SER:O	1:Z:228:ILE:HG12	2.19	0.43
5:k:69:LYS:HE2	5:k:69:LYS:HB3	1.80	0.43
4:a:23:ARG:HB3	4:a:27:ASP:HB3	2.00	0.43
4:B:827:GLU:O	4:B:831:LYS:NZ	2.50	0.43
7:J:930:HIS:O	7:J:934:LEU:HG	2.19	0.43
1:O:33:PRO:HA	1:O:85:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:33:PRO:HA	1:P:85:LEU:HD13	2.01	0.43
1:U:106:SER:HB3	1:U:410:LYS:HG3	2.01	0.43
1:U:221:GLN:O	1:U:224:SER:OG	2.36	0.43
5:m:30:GLU:OE1	7:l:130:PRO:HG2	2.18	0.43
1:1:401:ARG:HD3	1:1:404:PHE:HE2	1.84	0.43
4:F:430:LEU:HA	4:F:430:LEU:HD12	1.77	0.43
4:F:477:MET:HE2	4:F:477:MET:HB2	1.79	0.43
4:F:563:ARG:HA	4:F:567:LEU:HD13	1.99	0.43
4:H:335:TYR:O	4:H:338:LEU:HG	2.18	0.43
3:M:655:LEU:HA	3:M:658:VAL:HG12	2.01	0.43
1:O:401:ARG:HD3	1:O:404:PHE:HE2	1.84	0.43
1:S:224:SER:O	1:S:228:ILE:HG12	2.19	0.43
1:T:4:GLU:O	1:T:133:GLU:N	2.51	0.43
1:T:106:SER:HB3	1:T:410:LYS:HG3	2.01	0.43
1:T:156:ARG:HD3	1:T:156:ARG:HA	1.75	0.43
1:U:33:PRO:HA	1:U:85:LEU:HD13	2.01	0.43
1:W:401:ARG:HD3	1:W:404:PHE:HE2	1.84	0.43
1:X:224:SER:O	1:X:228:ILE:HG12	2.19	0.43
3:E:427:TYR:HA	3:E:431:ARG:HD3	2.01	0.43
1:1:33:PRO:HA	1:1:85:LEU:HD13	2.01	0.43
1:1:221:GLN:O	1:1:224:SER:OG	2.36	0.43
1:2:141:ILE:HB	1:2:173:PRO:HD3	2.01	0.43
4:B:697:PHE:HE2	4:B:799:GLU:HG2	1.83	0.43
4:D:300:LEU:O	4:D:304:ILE:HG12	2.19	0.43
4:F:608:THR:HG23	4:F:610:ALA:H	1.84	0.43
6:K:647:LEU:HD21	1:Y:337:LEU:HD22	2.00	0.43
1:P:332:GLN:H	1:P:332:GLN:HG3	1.53	0.43
1:P:401:ARG:HD3	1:P:404:PHE:HE2	1.84	0.43
1:Q:141:ILE:HB	1:Q:173:PRO:HD3	2.01	0.43
1:Q:321:LEU:HD23	1:Q:378:MET:HB2	2.01	0.43
1:V:106:SER:HB3	1:V:410:LYS:HG3	2.01	0.43
1:V:321:LEU:HD23	1:V:378:MET:HB2	2.01	0.43
1:Y:106:SER:HB3	1:Y:410:LYS:HG3	2.01	0.43
1:1:26:CYS:HA	1:1:31:ILE:HD11	2.01	0.43
2:e:158:GLY:H	2:e:181:ALA:HB2	1.83	0.43
2:e:286:ASP:HB3	2:e:289:ILE:HG22	2.01	0.43
3:A:662:ASN:HD21	3:A:675:TRP:N	2.16	0.43
7:J:758:LEU:HD22	7:J:801:LEU:HD11	2.00	0.43
6:K:649:LEU:HD22	1:Y:341:ARG:NH2	2.34	0.43
8:L:438:ARG:HG2	3:M:333:ARG:HH22	1.83	0.43
4:N:384:LEU:HD22	4:N:400:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:577:LEU:HD11	4:N:601:LEU:HD12	1.99	0.43
1:R:26:CYS:HA	1:R:31:ILE:HD11	2.01	0.43
1:T:332:GLN:H	1:T:332:GLN:HG3	1.53	0.43
1:X:26:CYS:HA	1:X:31:ILE:HD11	2.01	0.43
1:Y:141:ILE:HB	1:Y:173:PRO:HD3	2.01	0.43
1:Z:221:GLN:O	1:Z:224:SER:OG	2.36	0.43
1:Z:321:LEU:HD23	1:Z:378:MET:HB2	2.01	0.43
5:m:50:LEU:HD21	7:l:18:ASP:HB3	2.01	0.43
3:E:479:LEU:HG	3:E:480:LYS:HG2	2.00	0.43
1:l:4:GLU:O	1:l:133:GLU:N	2.51	0.43
1:2:321:LEU:HD23	1:2:378:MET:HB2	2.01	0.43
3:A:640:MET:HB2	3:A:640:MET:HE2	1.78	0.43
4:B:582:LYS:HG2	4:B:583:PRO:HD3	2.01	0.43
4:B:633:THR:HG22	4:B:636:ASP:HB2	2.00	0.43
4:F:713:HIS:CD2	1:T:353:PRO:HB2	2.53	0.43
7:J:334:VAL:HG13	7:J:362:GLN:HE22	1.82	0.43
3:M:453:THR:HG22	3:M:492:PHE:HA	2.00	0.43
4:N:400:VAL:HG21	4:N:422:VAL:HG11	2.01	0.43
1:O:321:LEU:HD23	1:O:378:MET:HB2	2.01	0.43
1:P:141:ILE:HB	1:P:173:PRO:HD3	2.01	0.43
1:P:383:SER:O	1:P:386:SER:OG	2.31	0.43
1:R:156:ARG:HD3	1:R:156:ARG:HA	1.75	0.43
1:U:224:SER:O	1:U:228:ILE:HG12	2.19	0.43
1:W:224:SER:O	1:W:228:ILE:HG12	2.19	0.43
1:X:106:SER:HB3	1:X:410:LYS:HG3	2.01	0.43
1:2:33:PRO:HA	1:2:85:LEU:HD13	2.01	0.43
1:2:106:SER:HB3	1:2:410:LYS:HG3	2.01	0.43
4:B:555:LEU:HG	4:B:559:MET:HE3	2.01	0.43
4:B:601:LEU:HD21	4:B:621:LEU:HD23	2.01	0.43
4:B:664:PHE:O	4:B:668:TRP:HB2	2.18	0.43
4:B:782:ILE:HG22	4:B:786:GLN:HE21	1.84	0.43
6:I:165:LEU:HA	6:I:166:PRO:HD3	1.89	0.43
7:J:805:VAL:HG12	7:J:809:VAL:HG13	2.00	0.43
3:M:285:TYR:N	3:M:290:HIS:HE1	2.16	0.43
1:R:4:GLU:O	1:R:133:GLU:N	2.51	0.43
1:R:369:SER:HB3	1:R:372:ARG:HD3	2.01	0.43
1:S:401:ARG:HD3	1:S:404:PHE:HE2	1.84	0.43
1:T:77:ILE:O	1:T:80:SER:OG	2.37	0.43
1:U:141:ILE:HB	1:U:173:PRO:HD3	2.01	0.43
1:X:141:ILE:HB	1:X:173:PRO:HD3	2.01	0.43
5:d:25:MET:HE3	5:d:25:MET:HB3	1.94	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:342:GLU:OE1	8:L:1556:LYS:HE3	2.18	0.42
4:D:688:ALA:HB3	4:D:689:LYS:NZ	2.34	0.42
4:H:662:ARG:HG3	7:I:74:ILE:HD12	2.01	0.42
7:J:291:ASP:N	7:J:291:ASP:OD1	2.52	0.42
3:M:509:LEU:O	3:M:513:LEU:HG	2.19	0.42
1:O:141:ILE:HB	1:O:173:PRO:HD3	2.01	0.42
1:P:106:SER:HB3	1:P:410:LYS:HG3	2.01	0.42
1:P:321:LEU:HD23	1:P:378:MET:HB2	2.01	0.42
1:R:224:SER:O	1:R:228:ILE:HG12	2.19	0.42
1:V:224:SER:O	1:V:228:ILE:HG12	2.19	0.42
1:X:401:ARG:HD3	1:X:404:PHE:HE2	1.84	0.42
1:Y:125:GLU:O	1:Y:129:SER:N	2.42	0.42
1:Y:377:MET:HB3	1:Y:377:MET:HE2	1.78	0.42
1:Y:401:ARG:HD3	1:Y:404:PHE:HE2	1.84	0.42
1:Z:106:SER:HB3	1:Z:410:LYS:HG3	2.01	0.42
5:g:57:PRO:HG3	4:f:92:SER:HA	2.00	0.42
3:E:623:LYS:O	3:E:627:SER:OG	2.35	0.42
1:1:369:SER:HB3	1:1:372:ARG:HD3	2.01	0.42
4:B:879:ARG:CZ	1:P:337:LEU:HB3	2.49	0.42
4:D:680:ILE:HG23	4:D:789:GLN:HG2	2.01	0.42
1:O:224:SER:O	1:O:228:ILE:HG12	2.19	0.42
1:P:4:GLU:O	1:P:133:GLU:N	2.51	0.42
1:Q:221:GLN:O	1:Q:224:SER:OG	2.36	0.42
1:S:4:GLU:O	1:S:133:GLU:N	2.51	0.42
1:T:369:SER:HB3	1:T:372:ARG:HD3	2.01	0.42
1:V:141:ILE:HB	1:V:173:PRO:HD3	2.01	0.42
1:W:106:SER:HB3	1:W:410:LYS:HG3	2.01	0.42
1:X:4:GLU:O	1:X:133:GLU:N	2.51	0.42
4:a:113:SER:OG	4:a:114:TYR:N	2.43	0.42
3:E:712:ASN:HB3	3:E:725:HIS:CG	2.54	0.42
3:A:823:ASN:O	3:A:827:LYS:HE3	2.18	0.42
4:D:702:HIS:CD2	1:R:265:ARG:HH12	2.37	0.42
4:F:493:LEU:HD11	4:F:545:LEU:HB2	2.00	0.42
6:I:408:ASP:HB2	6:I:409:ASN:H	1.67	0.42
6:K:410:LEU:HA	6:K:413:LEU:HD22	2.00	0.42
1:Q:106:SER:HB3	1:Q:410:LYS:HG3	2.01	0.42
1:S:321:LEU:HD23	1:S:378:MET:HB2	2.01	0.42
1:U:401:ARG:HD3	1:U:404:PHE:HE2	1.84	0.42
1:W:141:ILE:HB	1:W:173:PRO:HD3	2.01	0.42
1:Y:369:SER:HB3	1:Y:372:ARG:HD3	2.01	0.42
7:l:74:ILE:HD12	7:l:74:ILE:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:327:ALA:HA	4:H:330:GLN:HE21	1.85	0.42
4:H:364:LEU:HG	4:a:52:PHE:CE2	2.55	0.42
4:H:620:ARG:HA	4:H:643:HIS:NE2	2.34	0.42
4:H:671:LYS:HA	4:H:674:GLU:HG3	2.01	0.42
7:J:274:THR:O	7:J:278:LEU:HG	2.20	0.42
7:J:307:HIS:HD1	7:J:310:LEU:HD22	1.85	0.42
8:L:1800:LEU:HD11	1:Z:337:LEU:HB3	2.00	0.42
1:O:156:ARG:HD3	1:O:156:ARG:HA	1.75	0.42
1:T:224:SER:O	1:T:228:ILE:HG12	2.19	0.42
1:T:321:LEU:HD23	1:T:378:MET:HB2	2.01	0.42
1:U:369:SER:HB3	1:U:372:ARG:HD3	2.01	0.42
1:V:369:SER:HB3	1:V:372:ARG:HD3	2.01	0.42
1:W:321:LEU:HD23	1:W:378:MET:HB2	2.01	0.42
1:Z:401:ARG:HD3	1:Z:404:PHE:HE2	1.84	0.42
5:k:25:MET:HE1	5:k:48:VAL:HG11	2.02	0.42
8:c:29:ASN:HD21	8:c:32:ARG:HG3	1.83	0.42
8:c:70:ILE:HG21	8:c:93:VAL:HG11	2.02	0.42
1:1:156:ARG:HA	1:1:156:ARG:HD3	1.75	0.42
1:2:224:SER:O	1:2:228:ILE:HG12	2.19	0.42
1:2:339:ARG:CZ	3:M:557:LEU:HB2	2.49	0.42
2:e:147:ARG:HH22	5:d:55:ILE:HG23	1.84	0.42
3:A:533:ASP:OD2	1:O:3:ARG:NH1	2.52	0.42
3:C:518:ARG:HG2	3:C:524:GLN:HG2	2.02	0.42
4:D:457:ASP:N	4:D:457:ASP:OD1	2.50	0.42
4:D:629:SER:OG	4:h:64:ARG:NH1	2.53	0.42
4:D:848:ARG:HD2	4:D:848:ARG:HA	1.92	0.42
4:F:283:LEU:HB2	4:F:287:LEU:H	1.85	0.42
4:F:419:LEU:HA	4:F:422:VAL:HG22	2.00	0.42
8:L:1512:LEU:HA	8:L:1568:HIS:NE2	2.33	0.42
3:M:240:GLY:O	3:M:275:ARG:NH1	2.52	0.42
1:O:4:GLU:O	1:O:133:GLU:N	2.51	0.42
1:P:377:MET:HE2	1:P:377:MET:HB3	1.78	0.42
1:Q:156:ARG:HA	1:Q:156:ARG:HD3	1.75	0.42
1:Q:224:SER:O	1:Q:228:ILE:HG12	2.19	0.42
1:X:221:GLN:O	1:X:224:SER:OG	2.36	0.42
5:i:36:ASN:CA	4:h:107:GLN:NE2	2.69	0.42
5:d:37:THR:HG23	5:d:39:LEU:H	1.85	0.42
8:c:78:ARG:NH2	8:c:90:GLU:OE2	2.45	0.42
1:2:4:GLU:O	1:2:133:GLU:N	2.51	0.42
2:e:188:TYR:CE1	2:e:267:LEU:HA	2.55	0.42
3:A:517:LYS:HD2	3:A:706:TRP:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:686:MET:H	3:A:686:MET:HG2	1.69	0.42
3:C:154:LEU:O	3:C:158:ARG:NH1	2.53	0.42
5:b:57:PRO:HB3	4:a:96:LEU:HG	2.02	0.42
5:b:61:SER:O	5:b:65:LYS:HE3	2.19	0.42
5:b:71:THR:HB	4:a:21:LEU:HD22	2.02	0.42
4:F:458:ARG:HH12	4:F:654:ARG:HE	1.68	0.42
4:F:752:GLU:O	4:F:755:LEU:HG	2.18	0.42
3:G:548:PRO:HA	3:G:551:LEU:HG	2.01	0.42
6:I:315:LYS:HA	6:I:315:LYS:HD2	1.87	0.42
7:J:360:THR:O	7:J:364:PHE:N	2.52	0.42
1:O:369:SER:HB3	1:O:372:ARG:HD3	2.01	0.42
1:S:106:SER:HB3	1:S:410:LYS:HG3	2.01	0.42
1:V:221:GLN:O	1:V:224:SER:OG	2.36	0.42
1:Z:26:CYS:HA	1:Z:31:ILE:HD11	2.01	0.42
4:f:69:ALA:CB	4:f:110:LYS:HG3	2.40	0.42
3:A:388:PHE:C	3:A:390:VAL:H	2.26	0.42
4:F:589:ALA:HA	4:F:592:LEU:HD13	2.01	0.42
4:H:672:ARG:HB3	4:H:673:MET:HE2	2.02	0.42
3:M:855:VAL:HG23	3:M:858:ARG:NH1	2.35	0.42
1:O:26:CYS:HA	1:O:31:ILE:HD11	2.01	0.42
1:Q:369:SER:HB3	1:Q:372:ARG:HD3	2.01	0.42
1:T:377:MET:HE2	1:T:377:MET:HB3	1.78	0.42
1:W:377:MET:HE2	1:W:377:MET:HB3	1.78	0.42
1:Y:348:PHE:HZ	1:Y:356:ILE:HD11	1.85	0.42
1:1:106:SER:HB3	1:1:410:LYS:HG3	2.01	0.42
1:2:26:CYS:HA	1:2:31:ILE:HD11	2.01	0.42
4:B:271:THR:OG1	4:B:272:GLU:OE2	2.35	0.42
4:B:697:PHE:CE2	4:B:799:GLU:HG2	2.54	0.42
5:b:62:SER:HA	5:b:65:LYS:HG2	2.01	0.42
4:N:768:SER:O	4:N:768:SER:OG	2.37	0.42
4:N:803:ARG:HH21	4:N:829:GLU:HG2	1.84	0.42
1:P:193:LYS:HD3	1:P:194:ARG:HD2	2.02	0.42
1:P:224:SER:O	1:P:228:ILE:HG12	2.19	0.42
1:R:141:ILE:HB	1:R:173:PRO:HD3	2.01	0.42
1:T:141:ILE:HB	1:T:173:PRO:HD3	2.01	0.42
1:U:4:GLU:O	1:U:133:GLU:N	2.51	0.42
1:W:172:PHE:N	1:W:205:LEU:O	2.50	0.42
1:W:327:GLU:HG2	1:W:372:ARG:HB2	2.02	0.42
1:X:33:PRO:HA	1:X:85:LEU:HD13	2.01	0.42
1:X:369:SER:HB3	1:X:372:ARG:HD3	2.01	0.42
1:Z:332:GLN:H	1:Z:332:GLN:HG3	1.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:327:GLU:HG2	1:2:372:ARG:HB2	2.02	0.42
2:e:117:GLU:OE2	2:e:368:SER:HA	2.20	0.42
4:B:499:ASP:HB3	4:B:501:THR:HG22	2.00	0.42
4:B:776:ARG:HH12	4:f:107:GLN:HA	1.85	0.42
3:C:214:GLU:O	3:C:218:VAL:HG23	2.20	0.42
4:D:887:LYS:HD3	4:D:887:LYS:HA	1.84	0.42
5:b:24:THR:O	5:b:28:LEU:HG	2.20	0.42
4:F:554:SER:O	4:F:558:HIS:ND1	2.53	0.42
4:F:583:PRO:HA	4:F:586:VAL:HG22	2.01	0.42
3:G:508:GLU:O	3:G:512:HIS:ND1	2.46	0.42
6:I:104:LEU:HD12	6:I:107:LEU:HD12	2.02	0.42
6:I:259:LEU:HD12	6:I:259:LEU:HA	1.89	0.42
7:J:912:GLU:O	7:J:916:GLN:HG2	2.19	0.42
6:K:478:VAL:HG21	6:K:568:LEU:HD13	2.01	0.42
3:M:550:ARG:O	3:M:554:LEU:HG	2.20	0.42
1:P:26:CYS:HA	1:P:31:ILE:HD11	2.01	0.42
1:R:86:TYR:HB2	1:R:87:ASN:H	1.68	0.42
1:T:427:ILE:HD13	1:T:427:ILE:HA	1.95	0.42
1:U:26:CYS:HA	1:U:31:ILE:HD11	2.01	0.42
1:U:193:LYS:HD3	1:U:194:ARG:HD2	2.02	0.42
1:V:26:CYS:HA	1:V:31:ILE:HD11	2.01	0.42
1:W:26:CYS:HA	1:W:31:ILE:HD11	2.01	0.42
1:Y:33:PRO:HA	1:Y:85:LEU:HD13	2.01	0.42
1:Z:33:PRO:HA	1:Z:85:LEU:HD13	2.01	0.42
1:Z:86:TYR:HB2	1:Z:87:ASN:H	1.68	0.42
1:Z:141:ILE:HB	1:Z:173:PRO:HD3	2.01	0.42
5:g:62:SER:HA	5:g:65:LYS:HE2	2.00	0.42
5:k:64:ILE:HG22	5:k:68:ARG:HE	1.84	0.42
8:c:137:LYS:HA	8:c:137:LYS:HD2	1.95	0.42
3:E:363:SER:HA	3:E:376:CYS:SG	2.60	0.42
2:e:153:MET:HE2	2:e:278:THR:HG1	1.85	0.42
4:B:251:VAL:HG21	4:B:363:THR:HG22	2.02	0.42
4:B:830:ASN:HB2	4:B:831:LYS:HZ2	1.85	0.42
3:C:517:LYS:HG2	3:C:521:LEU:HB2	2.02	0.42
4:F:325:CYS:HA	4:F:328:LEU:HG	2.02	0.42
3:G:408:MET:HG3	3:G:439:ILE:HG12	2.02	0.42
7:J:802:SER:OG	7:J:803:TYR:N	2.51	0.42
3:M:290:HIS:HD2	4:N:411:MET:HE2	1.85	0.42
4:N:304:ILE:O	4:N:308:THR:HG23	2.19	0.42
1:Q:26:CYS:HA	1:Q:31:ILE:HD11	2.01	0.42
1:R:106:SER:HB3	1:R:410:LYS:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:33:PRO:HA	1:S:85:LEU:HD13	2.01	0.42
1:S:193:LYS:HD3	1:S:194:ARG:HD2	2.02	0.42
1:V:4:GLU:O	1:V:133:GLU:N	2.51	0.42
1:V:327:GLU:HG2	1:V:372:ARG:HB2	2.02	0.42
1:W:33:PRO:HA	1:W:85:LEU:HD13	2.01	0.42
1:W:221:GLN:O	1:W:224:SER:OG	2.36	0.42
1:W:369:SER:HB3	1:W:372:ARG:HD3	2.01	0.42
1:Y:26:CYS:HA	1:Y:31:ILE:HD11	2.01	0.42
1:Y:77:ILE:O	1:Y:80:SER:OG	2.37	0.42
1:Y:224:SER:O	1:Y:228:ILE:HG12	2.19	0.42
1:Z:369:SER:HB3	1:Z:372:ARG:HD3	2.01	0.42
1:1:141:ILE:HB	1:1:173:PRO:HD3	2.01	0.41
1:2:369:SER:HB3	1:2:372:ARG:HD3	2.01	0.41
4:B:626:LEU:HD23	4:f:64:ARG:HD3	2.02	0.41
3:C:641:LEU:HD21	3:C:734:LEU:HA	2.01	0.41
3:M:295:ALA:O	3:M:298:THR:OG1	2.37	0.41
3:M:522:MET:HG2	3:M:528:PHE:CE2	2.54	0.41
3:M:547:THR:HA	3:M:548:PRO:HD3	1.92	0.41
1:U:321:LEU:HD23	1:U:378:MET:HB2	2.01	0.41
1:V:193:LYS:HD3	1:V:194:ARG:HD2	2.02	0.41
1:Y:206:ASP:HB2	1:Y:305:VAL:HG13	2.02	0.41
5:m:42:GLU:OE2	5:m:42:GLU:N	2.53	0.41
1:1:86:TYR:HB2	1:1:87:ASN:H	1.68	0.41
2:e:217:CYS:HA	2:e:254:ARG:HD2	2.01	0.41
3:A:320:SER:OG	3:A:321:LEU:N	2.53	0.41
4:B:466:LEU:HG	4:B:468:LYS:HG3	2.01	0.41
5:b:16:ALA:HB1	8:L:302:CYS:SG	2.60	0.41
4:F:494:HIS:CD2	4:F:500:GLN:HG3	2.55	0.41
4:F:671:LYS:HE3	4:F:671:LYS:HB3	1.83	0.41
4:F:689:LYS:NZ	1:T:196:THR:O	2.53	0.41
3:G:313:LEU:HD11	3:G:318:LEU:HD23	2.02	0.41
6:K:19:TRP:HH2	6:K:54:ARG:HE	1.66	0.41
8:L:503:SER:O	8:L:506:TYR:HB3	2.21	0.41
8:L:1773:LYS:HD2	8:L:1773:LYS:HA	1.76	0.41
3:M:461:ARG:HD3	3:M:467:VAL:HG22	2.02	0.41
4:N:341:VAL:O	4:N:345:GLN:HG2	2.20	0.41
1:Q:33:PRO:HA	1:Q:85:LEU:HD13	2.01	0.41
1:T:193:LYS:HD3	1:T:194:ARG:HD2	2.02	0.41
4:a:13:LEU:HD21	4:a:35:ALA:HB3	2.02	0.41
1:2:206:ASP:HB2	1:2:305:VAL:HG13	2.03	0.41
3:A:376:CYS:SG	3:A:377:LEU:N	2.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:474:PHE:HB2	4:B:524:THR:HG21	2.01	0.41
3:C:364:PHE:HA	3:C:367:THR:HB	2.02	0.41
5:b:67:LEU:HD23	4:a:31:GLN:HE21	1.86	0.41
3:G:398:GLY:N	3:G:457:LEU:HD22	2.35	0.41
6:I:3:HIS:HB2	8:L:297:TRP:CZ2	2.55	0.41
6:I:582:CYS:O	6:I:586:ILE:HG12	2.20	0.41
6:K:646:LEU:HD12	1:Y:338:GLN:OE1	2.20	0.41
4:N:737:LYS:HA	4:N:740:GLN:HE21	1.85	0.41
1:O:106:SER:HB3	1:O:410:LYS:HG3	2.01	0.41
1:P:156:ARG:HA	1:P:156:ARG:HD3	1.75	0.41
1:P:369:SER:HB3	1:P:372:ARG:HD3	2.01	0.41
1:Q:401:ARG:HD3	1:Q:404:PHE:HE2	1.84	0.41
1:S:427:ILE:HD13	1:S:427:ILE:HA	1.95	0.41
1:X:164:LYS:HD3	1:X:164:LYS:HA	1.71	0.41
1:X:193:LYS:HD3	1:X:194:ARG:HD2	2.02	0.41
1:Z:4:GLU:O	1:Z:133:GLU:N	2.51	0.41
4:a:73:LEU:O	4:a:77:LEU:HG	2.20	0.41
4:f:77:LEU:HD23	4:f:80:LYS:HE2	2.02	0.41
3:A:476:ILE:H	3:A:483:ALA:HB2	1.86	0.41
3:C:613:LEU:HD22	3:C:650:HIS:CE1	2.55	0.41
3:C:661:SER:O	3:C:770:LYS:HD3	2.19	0.41
3:C:674:GLN:O	1:Q:265:ARG:NH2	2.53	0.41
4:D:879:ARG:HA	4:D:879:ARG:NH2	2.35	0.41
3:G:689:PHE:O	3:G:693:ILE:HG12	2.21	0.41
7:J:473:LEU:HA	7:J:476:VAL:HG22	2.01	0.41
7:J:485:LEU:HD23	7:J:485:LEU:HA	1.88	0.41
4:N:377:ARG:HE	4:N:377:ARG:HB3	1.77	0.41
4:N:444:HIS:HD2	4:N:467:ARG:NH2	2.18	0.41
1:O:206:ASP:HB2	1:O:305:VAL:HG13	2.03	0.41
1:P:327:GLU:HG2	1:P:372:ARG:HB2	2.02	0.41
1:R:164:LYS:HD3	1:R:164:LYS:HA	1.71	0.41
1:R:327:GLU:HG2	1:R:372:ARG:HB2	2.02	0.41
1:S:26:CYS:HA	1:S:31:ILE:HD11	2.01	0.41
1:S:206:ASP:HB2	1:S:305:VAL:HG13	2.03	0.41
1:T:401:ARG:HD3	1:T:404:PHE:HE2	1.84	0.41
1:X:172:PHE:N	1:X:205:LEU:O	2.50	0.41
5:k:42:GLU:O	5:k:45:SER:OG	2.32	0.41
3:E:762:MET:HE1	3:E:818:PHE:CE1	2.55	0.41
4:B:889:ARG:HB2	4:B:893:LEU:HG	2.03	0.41
6:K:48:LEU:H	6:K:48:LEU:HG	1.72	0.41
3:M:565:ASN:HA	3:M:570:LYS:HE3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:651:VAL:O	3:M:654:GLN:HG2	2.20	0.41
3:M:691:GLN:HA	3:M:694:GLN:HE21	1.86	0.41
1:O:172:PHE:N	1:O:205:LEU:O	2.50	0.41
1:S:327:GLU:HG2	1:S:372:ARG:HB2	2.02	0.41
1:S:383:SER:O	1:S:386:SER:OG	2.32	0.41
1:T:33:PRO:HA	1:T:85:LEU:HD13	2.01	0.41
1:T:383:SER:O	1:T:386:SER:OG	2.32	0.41
1:U:327:GLU:HG2	1:U:372:ARG:HB2	2.02	0.41
5:i:36:ASN:HB2	4:h:107:GLN:HE22	1.75	0.41
8:c:152:ASP:HA	8:c:155:VAL:HG22	2.02	0.41
4:f:66:ARG:HD3	4:f:106:ARG:HG3	1.97	0.41
1:1:77:ILE:O	1:1:80:SER:OG	2.37	0.41
1:1:327:GLU:HG2	1:1:372:ARG:HB2	2.02	0.41
2:e:360:GLN:O	2:e:364:GLU:HG2	2.20	0.41
4:B:874:ARG:O	4:B:877:SER:OG	2.38	0.41
3:C:178:PRO:HG2	4:D:383:ALA:HB1	2.02	0.41
3:C:574:LYS:HD3	3:C:574:LYS:HA	1.89	0.41
3:G:298:THR:HA	3:G:301:LYS:HD2	2.03	0.41
3:G:624:TRP:O	3:G:627:SER:OG	2.32	0.41
3:G:766:THR:O	3:G:770:LYS:HG2	2.21	0.41
4:H:846:GLN:O	4:H:850:LEU:HG	2.21	0.41
6:K:341:TRP:CE2	6:K:552:ARG:HA	2.56	0.41
1:Q:327:GLU:HG2	1:Q:372:ARG:HB2	2.02	0.41
5:m:26:ASP:HA	5:m:29:LEU:HG	2.02	0.41
3:E:645:MET:H	3:E:645:MET:HG2	1.67	0.41
1:1:353:PRO:HD3	3:M:864:PHE:CD2	2.56	0.41
1:2:193:LYS:HD3	1:2:194:ARG:HD2	2.02	0.41
4:B:800:LEU:O	4:B:804:LEU:HG	2.20	0.41
7:J:942:LEU:HD12	7:J:942:LEU:HA	1.84	0.41
6:K:540:GLN:HG3	6:K:564:PHE:CD1	2.56	0.41
4:N:247:GLU:CD	4:N:366:ARG:HE	2.29	0.41
4:N:697:PHE:HB2	4:N:701:LEU:HD23	2.01	0.41
1:O:77:ILE:O	1:O:80:SER:OG	2.37	0.41
1:R:33:PRO:HA	1:R:85:LEU:HD13	2.01	0.41
1:T:26:CYS:HA	1:T:31:ILE:HD11	2.01	0.41
1:U:206:ASP:HB2	1:U:305:VAL:HG13	2.03	0.41
1:X:327:GLU:HG2	1:X:372:ARG:HB2	2.02	0.41
5:m:35:LEU:HD21	7:l:119:ASP:OD2	2.21	0.41
1:1:427:ILE:HD13	1:1:427:ILE:HA	1.95	0.41
3:G:319:LEU:HD21	3:G:327:TYR:HE2	1.84	0.41
4:H:669:ARG:O	4:H:673:MET:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:93:LEU:HA	6:I:96:VAL:HG22	2.03	0.41
7:J:826:LEU:O	7:J:829:LEU:HG	2.21	0.41
6:K:356:ILE:HG13	6:K:360:PHE:CD1	2.56	0.41
1:P:313:THR:OG1	1:P:314:ASN:N	2.44	0.41
1:Q:193:LYS:HD3	1:Q:194:ARG:HD2	2.02	0.41
1:Z:327:GLU:HG2	1:Z:372:ARG:HB2	2.02	0.41
1:2:77:ILE:O	1:2:80:SER:OG	2.37	0.41
1:2:233:SER:HA	1:2:236:MET:HG3	2.03	0.41
1:2:339:ARG:HG2	3:M:554:LEU:HD23	2.03	0.41
1:2:408:PHE:HD1	1:2:408:PHE:HA	1.80	0.41
2:e:235:SER:O	2:e:235:SER:OG	2.39	0.41
3:A:861:PHE:CD1	1:O:356:ILE:HD13	2.55	0.41
4:D:535:ASP:OD1	4:D:535:ASP:N	2.54	0.41
5:b:61:SER:HA	5:b:64:ILE:HG22	2.03	0.41
4:F:559:MET:HB3	4:F:559:MET:HE2	1.78	0.41
3:G:319:LEU:HD23	3:G:319:LEU:HA	1.86	0.41
3:G:333:ARG:O	3:G:337:ILE:HG12	2.21	0.41
3:G:436:GLN:H	3:G:436:GLN:CD	2.29	0.41
4:H:703:GLN:HG2	4:H:847:LEU:HD22	2.02	0.41
4:H:715:ILE:HD12	4:H:715:ILE:HG23	1.90	0.41
4:H:887:LYS:HD3	4:H:887:LYS:HA	1.99	0.41
7:J:702:CYS:SG	7:J:703:CYS:N	2.94	0.41
8:L:1545:LEU:HA	8:L:1579:LEU:HD12	2.03	0.41
3:M:509:LEU:HD12	3:M:509:LEU:H	1.86	0.41
1:P:233:SER:HA	1:P:236:MET:HG3	2.03	0.41
1:R:408:PHE:HD1	1:R:408:PHE:HA	1.80	0.41
1:T:292:ASP:HB3	1:T:296:ARG:CZ	2.51	0.41
1:V:206:ASP:HB2	1:V:305:VAL:HG13	2.03	0.41
1:W:206:ASP:HB2	1:W:305:VAL:HG13	2.03	0.41
1:X:292:ASP:HB3	1:X:296:ARG:CZ	2.51	0.41
1:Y:292:ASP:HB3	1:Y:296:ARG:CZ	2.51	0.41
1:Z:193:LYS:HD3	1:Z:194:ARG:HD2	2.02	0.41
1:Z:206:ASP:HB2	1:Z:305:VAL:HG13	2.03	0.41
5:i:33:ARG:NH2	4:h:109:SER:OG	2.54	0.41
4:a:88:LYS:HA	4:a:88:LYS:HD3	1.84	0.41
4:a:90:LYS:O	4:a:94:LEU:HG	2.20	0.41
3:E:635:LEU:O	3:E:639:GLN:HG2	2.20	0.41
2:e:68:LYS:HA	2:e:68:LYS:HD2	1.75	0.41
4:F:305:ARG:NE	4:F:306:ARG:HH12	2.19	0.41
4:F:416:GLN:HA	4:F:419:LEU:HD22	2.01	0.41
4:H:681:ARG:CZ	4:H:712:VAL:HG21	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:681:ARG:O	4:H:685:MET:HG2	2.21	0.41
7:J:707:MET:HE3	7:J:707:MET:HB3	1.94	0.41
4:N:494:HIS:NE2	4:N:500:GLN:HG3	2.36	0.41
4:N:680:ILE:HG21	4:N:785:LEU:HD21	2.03	0.41
4:N:880:LEU:HD23	4:N:880:LEU:HA	1.95	0.41
1:O:292:ASP:HB3	1:O:296:ARG:CZ	2.51	0.41
1:O:327:GLU:HG2	1:O:372:ARG:HB2	2.02	0.41
1:P:117:ASP:OD1	1:P:117:ASP:N	2.36	0.41
3:E:306:LEU:O	3:E:310:LEU:HG	2.21	0.41
1:2:249:MET:HA	4:N:575:ARG:HH12	1.86	0.40
4:D:862:LEU:HD23	4:D:862:LEU:HA	1.91	0.40
4:F:543:LYS:HD2	4:F:543:LYS:HA	1.80	0.40
3:G:876:ARG:NH2	4:j:39:ILE:HD13	2.35	0.40
6:I:535:ASP:HA	6:I:538:GLU:HG2	2.02	0.40
6:K:6:LEU:HD21	6:K:111:PHE:HE1	1.86	0.40
4:N:455:LYS:H	4:N:455:LYS:HG2	1.51	0.40
1:O:233:SER:HA	1:O:236:MET:HG3	2.03	0.40
1:P:164:LYS:HD3	1:P:164:LYS:HA	1.71	0.40
1:S:141:ILE:HB	1:S:173:PRO:HD3	2.01	0.40
1:S:292:ASP:HB3	1:S:296:ARG:CZ	2.51	0.40
1:W:4:GLU:O	1:W:133:GLU:N	2.51	0.40
1:Y:415:LYS:HZ2	1:Y:419:ASP:H	1.68	0.40
1:Z:77:ILE:O	1:Z:80:SER:OG	2.37	0.40
1:2:86:TYR:HB2	1:2:87:ASN:H	1.68	0.40
2:e:153:MET:SD	2:e:274:ILE:HG23	2.62	0.40
2:e:315:LYS:HE3	2:e:315:LYS:HB3	1.95	0.40
3:A:824:LYS:HZ2	3:A:828:ASN:HB2	1.85	0.40
4:D:251:VAL:HB	4:D:366:ARG:NH2	2.36	0.40
4:D:304:ILE:HG22	4:D:328:LEU:HD21	2.03	0.40
4:F:667:LEU:O	4:F:671:LYS:HG3	2.21	0.40
3:G:521:LEU:HD12	3:G:521:LEU:HA	1.88	0.40
4:H:736:ASN:HA	4:H:739:GLN:HE21	1.85	0.40
7:J:556:LEU:HA	7:J:559:ILE:HD12	2.03	0.40
6:K:653:LYS:HG2	1:Y:351:TRP:O	2.21	0.40
4:N:564:ARG:HE	4:N:569:GLY:C	2.29	0.40
1:O:193:LYS:HD3	1:O:194:ARG:HD2	2.02	0.40
1:R:206:ASP:HB2	1:R:305:VAL:HG13	2.02	0.40
1:S:369:SER:HB3	1:S:372:ARG:HD3	2.01	0.40
1:U:172:PHE:N	1:U:205:LEU:O	2.50	0.40
1:Y:193:LYS:HD3	1:Y:194:ARG:HD2	2.02	0.40
1:Y:332:GLN:H	1:Y:332:GLN:HG3	1.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:i:67:LEU:HD13	4:h:20:ILE:HG21	2.04	0.40
5:k:51:CYS:SG	4:j:92:SER:HB2	2.61	0.40
8:c:3:SER:OG	8:c:4:ILE:N	2.53	0.40
3:E:645:MET:O	3:E:649:LYS:HE3	2.21	0.40
3:E:707:HIS:O	3:E:711:LYS:NZ	2.50	0.40
2:e:314:GLN:HE22	5:d:53:GLN:HE22	1.69	0.40
3:C:552:GLU:O	3:C:556:GLU:HG2	2.22	0.40
4:H:603:THR:HG21	1:W:342:GLU:HB2	2.03	0.40
6:I:549:ASN:OD1	6:I:549:ASN:N	2.53	0.40
7:J:938:HIS:NE2	7:J:943:LEU:HB2	2.36	0.40
3:M:504:MET:SD	3:M:510:VAL:HG23	2.61	0.40
1:S:136:VAL:HG22	1:S:167:GLN:HB3	2.04	0.40
1:U:348:PHE:HZ	1:U:356:ILE:HD12	1.85	0.40
1:V:160:ARG:HD2	1:V:160:ARG:HA	1.98	0.40
1:X:206:ASP:HB2	1:X:305:VAL:HG13	2.03	0.40
1:Z:136:VAL:HG22	1:Z:167:GLN:HB3	2.04	0.40
4:f:108:PRO:C	4:f:109:SER:HG	2.26	0.40
1:l:193:LYS:HD3	1:l:194:ARG:HD2	2.02	0.40
4:B:735:TRP:HA	4:B:738:VAL:HG22	2.02	0.40
3:C:169:ASN:HD22	3:C:413:GLU:HB3	1.87	0.40
4:D:679:ASP:HA	4:D:682:LYS:HG3	2.04	0.40
4:F:490:ILE:HD12	4:F:490:ILE:HA	1.90	0.40
3:G:190:ASP:OD1	3:G:271:SER:HA	2.21	0.40
3:G:266:VAL:HA	3:G:269:SER:HB3	2.03	0.40
3:G:449:LYS:O	3:G:453:THR:OG1	2.33	0.40
6:I:486:ARG:HH21	6:I:490:ALA:HA	1.86	0.40
6:K:52:TYR:OH	6:K:101:ARG:NH1	2.55	0.40
8:L:554:ILE:HD11	8:L:595:ILE:HG23	2.02	0.40
4:N:484:LEU:O	4:N:488:LYS:HG3	2.22	0.40
4:N:498:HIS:HB2	4:N:499:ASP:H	1.69	0.40
4:N:656:CYS:SG	4:N:751:HIS:HE1	2.45	0.40
1:P:172:PHE:N	1:P:205:LEU:O	2.50	0.40
1:R:136:VAL:HG22	1:R:167:GLN:HB3	2.04	0.40
1:S:233:SER:HA	1:S:236:MET:HG3	2.03	0.40
1:T:327:GLU:HG2	1:T:372:ARG:HB2	2.02	0.40
1:U:195:LEU:HD21	1:U:202:VAL:HG11	2.04	0.40
1:X:77:ILE:O	1:X:80:SER:OG	2.37	0.40
1:Z:117:ASP:OD1	1:Z:117:ASP:N	2.36	0.40
1:2:292:ASP:HB3	1:2:296:ARG:CZ	2.51	0.40
4:B:622:ASP:OD2	4:B:622:ASP:N	2.55	0.40
4:B:885:HIS:NE2	1:P:352:GLY:HA2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:548:VAL:HG23	4:D:549:LEU:HD22	2.03	0.40
4:D:588:PRO:HA	4:D:633:THR:HA	2.03	0.40
4:F:721:TYR:CG	4:F:876:LEU:HD13	2.56	0.40
3:G:753:SER:O	3:G:757:MET:HG2	2.22	0.40
4:H:287:LEU:H	4:H:287:LEU:HG	1.67	0.40
1:O:117:ASP:OD1	1:O:117:ASP:N	2.36	0.40
1:S:77:ILE:O	1:S:80:SER:OG	2.37	0.40
1:S:172:PHE:N	1:S:205:LEU:O	2.50	0.40
1:Y:136:VAL:HG22	1:Y:167:GLN:HB3	2.04	0.40
1:Y:327:GLU:HG2	1:Y:372:ARG:HB2	2.02	0.40
1:Z:156:ARG:HD3	1:Z:156:ARG:HA	1.75	0.40
1:Z:348:PHE:HZ	1:Z:356:ILE:HD12	1.87	0.40
3:E:415:ARG:HA	3:E:415:ARG:HD3	1.72	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	1	408/451 (90%)	382 (94%)	26 (6%)	0	100	100
1	2	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	O	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	P	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	Q	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	R	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	S	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	T	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	U	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	V	408/451 (90%)	383 (94%)	25 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	X	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	Y	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
1	Z	408/451 (90%)	383 (94%)	24 (6%)	1 (0%)	43	78
2	e	360/375 (96%)	340 (94%)	20 (6%)	0	100	100
3	A	599/902 (66%)	567 (95%)	32 (5%)	0	100	100
3	C	606/902 (67%)	563 (93%)	42 (7%)	1 (0%)	43	78
3	E	628/902 (70%)	594 (95%)	32 (5%)	2 (0%)	36	72
3	G	628/902 (70%)	591 (94%)	33 (5%)	4 (1%)	21	59
3	M	624/902 (69%)	590 (95%)	32 (5%)	2 (0%)	36	72
4	B	602/907 (66%)	581 (96%)	19 (3%)	2 (0%)	36	72
4	D	571/907 (63%)	554 (97%)	17 (3%)	0	100	100
4	F	591/907 (65%)	566 (96%)	25 (4%)	0	100	100
4	H	584/907 (64%)	563 (96%)	20 (3%)	1 (0%)	43	78
4	N	584/907 (64%)	553 (95%)	28 (5%)	3 (0%)	24	63
4	a	112/907 (12%)	107 (96%)	5 (4%)	0	100	100
4	f	105/907 (12%)	97 (92%)	5 (5%)	3 (3%)	3	23
4	h	105/907 (12%)	97 (92%)	6 (6%)	2 (2%)	6	32
4	j	105/907 (12%)	98 (93%)	6 (6%)	1 (1%)	12	49
5	b	63/82 (77%)	60 (95%)	3 (5%)	0	100	100
5	d	57/82 (70%)	56 (98%)	1 (2%)	0	100	100
5	g	63/82 (77%)	61 (97%)	2 (3%)	0	100	100
5	i	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
5	k	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
5	m	63/82 (77%)	63 (100%)	0	0	100	100
6	I	511/667 (77%)	487 (95%)	20 (4%)	4 (1%)	16	54
6	K	548/667 (82%)	534 (97%)	12 (2%)	2 (0%)	30	67
7	J	506/1024 (49%)	473 (94%)	30 (6%)	3 (1%)	21	59
7	l	104/1024 (10%)	100 (96%)	2 (2%)	2 (2%)	6	32
8	L	540/1819 (30%)	504 (93%)	33 (6%)	3 (1%)	21	59
8	c	148/1819 (8%)	140 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	15245/26874 (57%)	14424 (95%)	774 (5%)	47 (0%)	37	72

All (47) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	871	GLU
3	G	241	ARG
6	I	408	ASP
6	I	508	ASN
7	J	236	LEU
7	J	238	LEU
7	J	257	TYR
6	K	255	LYS
6	K	409	ASN
3	M	241	ARG
3	M	675	TRP
4	N	455	LYS
4	N	498	HIS
3	E	241	ARG
4	h	112	SER
4	f	105	ARG
4	f	108	PRO
3	G	581	ASP
6	I	405	LEU
8	L	307	ARG
8	L	451	PRO
1	2	348	PHE
1	P	348	PHE
1	Q	348	PHE
1	W	348	PHE
1	Y	348	PHE
3	C	466	ASP
3	G	676	PHE
4	N	499	ASP
1	R	348	PHE
1	T	348	PHE
1	X	348	PHE
1	Z	348	PHE
4	j	108	PRO
3	E	581	ASP
4	B	870	ASP
3	G	675	TRP

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Mol	Chain	Res	Type
4	H	455	LYS
1	O	348	PHE
1	S	348	PHE
1	U	348	PHE
7	l	129	THR
4	h	108	PRO
4	f	107	GLN
6	I	404	LEU
7	l	120	SER
8	L	452	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	1	376/400 (94%)	317 (84%)	59 (16%)	2	12
1	2	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	O	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	P	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	Q	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	R	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	S	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	T	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	U	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	V	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	W	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	X	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	Y	376/400 (94%)	319 (85%)	57 (15%)	3	12
1	Z	376/400 (94%)	319 (85%)	57 (15%)	3	12
2	e	310/318 (98%)	304 (98%)	6 (2%)	50	67
3	A	549/791 (69%)	543 (99%)	6 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	556/791 (70%)	555 (100%)	1 (0%)	87	87
3	E	575/791 (73%)	570 (99%)	5 (1%)	70	79
3	G	575/791 (73%)	575 (100%)	0	100	100
3	M	572/791 (72%)	566 (99%)	6 (1%)	68	78
4	B	551/798 (69%)	546 (99%)	5 (1%)	70	79
4	D	525/798 (66%)	522 (99%)	3 (1%)	78	83
4	F	542/798 (68%)	538 (99%)	4 (1%)	76	81
4	H	539/798 (68%)	531 (98%)	8 (2%)	57	72
4	N	539/798 (68%)	531 (98%)	8 (2%)	57	72
4	a	101/798 (13%)	100 (99%)	1 (1%)	68	78
4	f	96/798 (12%)	96 (100%)	0	100	100
4	h	96/798 (12%)	96 (100%)	0	100	100
4	j	96/798 (12%)	96 (100%)	0	100	100
5	b	53/62 (86%)	52 (98%)	1 (2%)	50	67
5	d	53/62 (86%)	53 (100%)	0	100	100
5	g	53/62 (86%)	53 (100%)	0	100	100
5	i	53/62 (86%)	53 (100%)	0	100	100
5	k	53/62 (86%)	52 (98%)	1 (2%)	50	67
5	m	53/62 (86%)	53 (100%)	0	100	100
6	I	472/594 (80%)	467 (99%)	5 (1%)	65	76
6	K	509/594 (86%)	504 (99%)	5 (1%)	68	78
7	J	498/933 (53%)	493 (99%)	5 (1%)	68	78
7	l	96/933 (10%)	96 (100%)	0	100	100
8	L	501/1546 (32%)	496 (99%)	5 (1%)	68	78
8	c	135/1546 (9%)	134 (99%)	1 (1%)	76	81
All	All	14015/23573 (60%)	13139 (94%)	876 (6%)	18	37

All (876) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	20	GLU
1	1	24	GLN
1	1	34	GLU

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Mol	Chain	Res	Type
1	1	38	GLU
1	1	39	GLU
1	1	49	ASP
1	1	50	VAL
1	1	66	LEU
1	1	78	LEU
1	1	91	ILE
1	1	106	SER
1	1	117	ASP
1	1	118	ILE
1	1	120	ASP
1	1	132	LEU
1	1	137	LEU
1	1	140	SER
1	1	153	LEU
1	1	157	LEU
1	1	165	LEU
1	1	166	VAL
1	1	168	THR
1	1	171	VAL
1	1	189	LEU
1	1	192	LEU
1	1	204	VAL
1	1	206	ASP
1	1	224	SER
1	1	233	SER
1	1	236	MET
1	1	254	ILE
1	1	256	LEU
1	1	265	ARG
1	1	269	LEU
1	1	270	MET
1	1	274	THR
1	1	277	THR
1	1	288	THR
1	1	295	ARG
1	1	297	LEU
1	1	298	LEU
1	1	304	MET
1	1	316	CYS
1	1	321	LEU
1	1	332	GLN

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Mol	Chain	Res	Type
1	1	337	LEU
1	1	338	GLN
1	1	343	ARG
1	1	345	LEU
1	1	348	PHE
1	1	356	ILE
1	1	358	VAL
1	1	361	SER
1	1	367	LEU
1	1	373	VAL
1	1	376	LEU
1	1	402	GLU
1	1	423	THR
1	1	431	LEU
1	2	20	GLU
1	2	24	GLN
1	2	34	GLU
1	2	38	GLU
1	2	39	GLU
1	2	49	ASP
1	2	50	VAL
1	2	66	LEU
1	2	78	LEU
1	2	91	ILE
1	2	106	SER
1	2	117	ASP
1	2	118	ILE
1	2	120	ASP
1	2	132	LEU
1	2	137	LEU
1	2	140	SER
1	2	153	LEU
1	2	157	LEU
1	2	165	LEU
1	2	166	VAL
1	2	168	THR
1	2	171	VAL
1	2	189	LEU
1	2	192	LEU
1	2	204	VAL
1	2	206	ASP
1	2	224	SER

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Mol	Chain	Res	Type
1	2	233	SER
1	2	236	MET
1	2	254	ILE
1	2	256	LEU
1	2	265	ARG
1	2	269	LEU
1	2	270	MET
1	2	274	THR
1	2	277	THR
1	2	288	THR
1	2	295	ARG
1	2	297	LEU
1	2	298	LEU
1	2	304	MET
1	2	316	CYS
1	2	321	LEU
1	2	332	GLN
1	2	337	LEU
1	2	338	GLN
1	2	343	ARG
1	2	356	ILE
1	2	358	VAL
1	2	361	SER
1	2	367	LEU
1	2	373	VAL
1	2	376	LEU
1	2	402	GLU
1	2	423	THR
1	2	431	LEU
2	e	33	SER
2	e	76	VAL
2	e	261	LEU
2	e	304	THR
2	e	334	GLU
2	e	357	ILE
3	A	176	ILE
3	A	388	PHE
3	A	389	GLU
3	A	651	VAL
3	A	660	ILE
3	A	698	MET
4	B	434	ILE

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Mol	Chain	Res	Type
4	B	586	VAL
4	B	629	SER
4	B	678	THR
4	B	689	LYS
3	C	866	THR
4	D	266	ILE
4	D	322	GLN
4	D	483	VAL
5	b	65	LYS
4	F	286	SER
4	F	406	THR
4	F	677	LEU
4	F	782	ILE
4	H	287	LEU
4	H	384	LEU
4	H	396	LEU
4	H	454	VAL
4	H	574	ILE
4	H	603	THR
4	H	694	MET
4	H	778	VAL
6	I	126	LEU
6	I	168	VAL
6	I	176	LEU
6	I	478	VAL
6	I	579	VAL
7	J	445	LEU
7	J	640	ASP
7	J	824	VAL
7	J	840	VAL
7	J	944	ARG
6	K	40	SER
6	K	140	VAL
6	K	500	MET
6	K	646	LEU
6	K	653	LYS
8	L	540	VAL
8	L	595	ILE
8	L	1491	VAL
8	L	1800	LEU
8	L	1805	ASN
3	M	313	LEU

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Mol	Chain	Res	Type
3	M	435	VAL
3	M	549	PRO
3	M	660	ILE
3	M	822	ILE
3	M	834	LEU
4	N	361	SER
4	N	404	THR
4	N	453	THR
4	N	454	VAL
4	N	592	LEU
4	N	621	LEU
4	N	667	LEU
4	N	712	VAL
1	O	20	GLU
1	O	24	GLN
1	O	34	GLU
1	O	38	GLU
1	O	39	GLU
1	O	49	ASP
1	O	50	VAL
1	O	66	LEU
1	O	78	LEU
1	O	91	ILE
1	O	106	SER
1	O	117	ASP
1	O	118	ILE
1	O	120	ASP
1	O	132	LEU
1	O	137	LEU
1	O	140	SER
1	O	153	LEU
1	O	157	LEU
1	O	165	LEU
1	O	166	VAL
1	O	168	THR
1	O	171	VAL
1	O	189	LEU
1	O	192	LEU
1	O	204	VAL
1	O	206	ASP
1	O	224	SER
1	O	233	SER

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Mol	Chain	Res	Type
1	O	236	MET
1	O	254	ILE
1	O	256	LEU
1	O	265	ARG
1	O	269	LEU
1	O	270	MET
1	O	274	THR
1	O	277	THR
1	O	288	THR
1	O	295	ARG
1	O	297	LEU
1	O	298	LEU
1	O	304	MET
1	O	316	CYS
1	O	321	LEU
1	O	332	GLN
1	O	337	LEU
1	O	338	GLN
1	O	343	ARG
1	O	356	ILE
1	O	358	VAL
1	O	361	SER
1	O	367	LEU
1	O	373	VAL
1	O	376	LEU
1	O	402	GLU
1	O	423	THR
1	O	431	LEU
1	P	20	GLU
1	P	24	GLN
1	P	34	GLU
1	P	38	GLU
1	P	39	GLU
1	P	49	ASP
1	P	50	VAL
1	P	66	LEU
1	P	78	LEU
1	P	91	ILE
1	P	106	SER
1	P	117	ASP
1	P	118	ILE
1	P	120	ASP

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Mol	Chain	Res	Type
1	P	132	LEU
1	P	137	LEU
1	P	140	SER
1	P	153	LEU
1	P	157	LEU
1	P	165	LEU
1	P	166	VAL
1	P	168	THR
1	P	171	VAL
1	P	189	LEU
1	P	192	LEU
1	P	204	VAL
1	P	206	ASP
1	P	224	SER
1	P	233	SER
1	P	236	MET
1	P	254	ILE
1	P	256	LEU
1	P	265	ARG
1	P	269	LEU
1	P	270	MET
1	P	274	THR
1	P	277	THR
1	P	288	THR
1	P	295	ARG
1	P	297	LEU
1	P	298	LEU
1	P	304	MET
1	P	316	CYS
1	P	321	LEU
1	P	332	GLN
1	P	337	LEU
1	P	338	GLN
1	P	343	ARG
1	P	356	ILE
1	P	358	VAL
1	P	361	SER
1	P	367	LEU
1	P	373	VAL
1	P	376	LEU
1	P	402	GLU
1	P	423	THR

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Mol	Chain	Res	Type
1	P	431	LEU
1	Q	20	GLU
1	Q	24	GLN
1	Q	34	GLU
1	Q	38	GLU
1	Q	39	GLU
1	Q	49	ASP
1	Q	50	VAL
1	Q	66	LEU
1	Q	78	LEU
1	Q	91	ILE
1	Q	106	SER
1	Q	117	ASP
1	Q	118	ILE
1	Q	120	ASP
1	Q	132	LEU
1	Q	137	LEU
1	Q	140	SER
1	Q	153	LEU
1	Q	157	LEU
1	Q	165	LEU
1	Q	166	VAL
1	Q	168	THR
1	Q	171	VAL
1	Q	189	LEU
1	Q	192	LEU
1	Q	204	VAL
1	Q	206	ASP
1	Q	224	SER
1	Q	233	SER
1	Q	236	MET
1	Q	254	ILE
1	Q	256	LEU
1	Q	265	ARG
1	Q	269	LEU
1	Q	270	MET
1	Q	274	THR
1	Q	277	THR
1	Q	288	THR
1	Q	295	ARG
1	Q	297	LEU
1	Q	298	LEU

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Mol	Chain	Res	Type
1	Q	304	MET
1	Q	316	CYS
1	Q	321	LEU
1	Q	332	GLN
1	Q	337	LEU
1	Q	338	GLN
1	Q	343	ARG
1	Q	356	ILE
1	Q	358	VAL
1	Q	361	SER
1	Q	367	LEU
1	Q	373	VAL
1	Q	376	LEU
1	Q	402	GLU
1	Q	423	THR
1	Q	431	LEU
1	R	20	GLU
1	R	24	GLN
1	R	34	GLU
1	R	38	GLU
1	R	39	GLU
1	R	49	ASP
1	R	50	VAL
1	R	66	LEU
1	R	78	LEU
1	R	91	ILE
1	R	106	SER
1	R	117	ASP
1	R	118	ILE
1	R	120	ASP
1	R	132	LEU
1	R	137	LEU
1	R	140	SER
1	R	153	LEU
1	R	157	LEU
1	R	165	LEU
1	R	166	VAL
1	R	168	THR
1	R	171	VAL
1	R	189	LEU
1	R	192	LEU
1	R	204	VAL

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Mol	Chain	Res	Type
1	R	206	ASP
1	R	224	SER
1	R	233	SER
1	R	236	MET
1	R	254	ILE
1	R	256	LEU
1	R	265	ARG
1	R	269	LEU
1	R	270	MET
1	R	274	THR
1	R	277	THR
1	R	288	THR
1	R	295	ARG
1	R	297	LEU
1	R	298	LEU
1	R	304	MET
1	R	316	CYS
1	R	321	LEU
1	R	332	GLN
1	R	337	LEU
1	R	338	GLN
1	R	343	ARG
1	R	356	ILE
1	R	358	VAL
1	R	361	SER
1	R	367	LEU
1	R	373	VAL
1	R	376	LEU
1	R	402	GLU
1	R	423	THR
1	R	431	LEU
1	S	20	GLU
1	S	24	GLN
1	S	34	GLU
1	S	38	GLU
1	S	39	GLU
1	S	49	ASP
1	S	50	VAL
1	S	66	LEU
1	S	78	LEU
1	S	91	ILE
1	S	106	SER

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Mol	Chain	Res	Type
1	S	117	ASP
1	S	118	ILE
1	S	120	ASP
1	S	132	LEU
1	S	137	LEU
1	S	140	SER
1	S	153	LEU
1	S	157	LEU
1	S	165	LEU
1	S	166	VAL
1	S	168	THR
1	S	171	VAL
1	S	189	LEU
1	S	192	LEU
1	S	204	VAL
1	S	206	ASP
1	S	224	SER
1	S	233	SER
1	S	236	MET
1	S	254	ILE
1	S	256	LEU
1	S	265	ARG
1	S	269	LEU
1	S	270	MET
1	S	274	THR
1	S	277	THR
1	S	288	THR
1	S	295	ARG
1	S	297	LEU
1	S	298	LEU
1	S	304	MET
1	S	316	CYS
1	S	321	LEU
1	S	332	GLN
1	S	337	LEU
1	S	338	GLN
1	S	343	ARG
1	S	356	ILE
1	S	358	VAL
1	S	361	SER
1	S	367	LEU
1	S	373	VAL

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Mol	Chain	Res	Type
1	S	376	LEU
1	S	402	GLU
1	S	423	THR
1	S	431	LEU
1	T	20	GLU
1	T	24	GLN
1	T	34	GLU
1	T	38	GLU
1	T	39	GLU
1	T	49	ASP
1	T	50	VAL
1	T	66	LEU
1	T	78	LEU
1	T	91	ILE
1	T	106	SER
1	T	117	ASP
1	T	118	ILE
1	T	120	ASP
1	T	132	LEU
1	T	137	LEU
1	T	140	SER
1	T	153	LEU
1	T	157	LEU
1	T	165	LEU
1	T	166	VAL
1	T	168	THR
1	T	171	VAL
1	T	189	LEU
1	T	192	LEU
1	T	204	VAL
1	T	206	ASP
1	T	224	SER
1	T	233	SER
1	T	236	MET
1	T	254	ILE
1	T	256	LEU
1	T	265	ARG
1	T	269	LEU
1	T	270	MET
1	T	274	THR
1	T	277	THR
1	T	288	THR

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Mol	Chain	Res	Type
1	T	295	ARG
1	T	297	LEU
1	T	298	LEU
1	T	304	MET
1	T	316	CYS
1	T	321	LEU
1	T	332	GLN
1	T	337	LEU
1	T	338	GLN
1	T	343	ARG
1	T	356	ILE
1	T	358	VAL
1	T	361	SER
1	T	367	LEU
1	T	373	VAL
1	T	376	LEU
1	T	402	GLU
1	T	423	THR
1	T	431	LEU
1	U	20	GLU
1	U	24	GLN
1	U	34	GLU
1	U	38	GLU
1	U	39	GLU
1	U	49	ASP
1	U	50	VAL
1	U	66	LEU
1	U	78	LEU
1	U	91	ILE
1	U	106	SER
1	U	117	ASP
1	U	118	ILE
1	U	120	ASP
1	U	132	LEU
1	U	137	LEU
1	U	140	SER
1	U	153	LEU
1	U	157	LEU
1	U	165	LEU
1	U	166	VAL
1	U	168	THR
1	U	171	VAL

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Mol	Chain	Res	Type
1	U	189	LEU
1	U	192	LEU
1	U	204	VAL
1	U	206	ASP
1	U	224	SER
1	U	233	SER
1	U	236	MET
1	U	254	ILE
1	U	256	LEU
1	U	265	ARG
1	U	269	LEU
1	U	270	MET
1	U	274	THR
1	U	277	THR
1	U	288	THR
1	U	295	ARG
1	U	297	LEU
1	U	298	LEU
1	U	304	MET
1	U	316	CYS
1	U	321	LEU
1	U	332	GLN
1	U	337	LEU
1	U	338	GLN
1	U	343	ARG
1	U	356	ILE
1	U	358	VAL
1	U	361	SER
1	U	367	LEU
1	U	373	VAL
1	U	376	LEU
1	U	402	GLU
1	U	423	THR
1	U	431	LEU
1	V	20	GLU
1	V	24	GLN
1	V	34	GLU
1	V	38	GLU
1	V	39	GLU
1	V	49	ASP
1	V	50	VAL
1	V	66	LEU

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Mol	Chain	Res	Type
1	V	78	LEU
1	V	91	ILE
1	V	106	SER
1	V	117	ASP
1	V	118	ILE
1	V	120	ASP
1	V	132	LEU
1	V	137	LEU
1	V	140	SER
1	V	153	LEU
1	V	157	LEU
1	V	165	LEU
1	V	166	VAL
1	V	168	THR
1	V	171	VAL
1	V	189	LEU
1	V	192	LEU
1	V	204	VAL
1	V	206	ASP
1	V	224	SER
1	V	233	SER
1	V	236	MET
1	V	254	ILE
1	V	256	LEU
1	V	265	ARG
1	V	269	LEU
1	V	270	MET
1	V	274	THR
1	V	277	THR
1	V	288	THR
1	V	295	ARG
1	V	297	LEU
1	V	298	LEU
1	V	304	MET
1	V	316	CYS
1	V	321	LEU
1	V	332	GLN
1	V	337	LEU
1	V	338	GLN
1	V	343	ARG
1	V	356	ILE
1	V	358	VAL

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Mol	Chain	Res	Type
1	V	361	SER
1	V	367	LEU
1	V	373	VAL
1	V	376	LEU
1	V	402	GLU
1	V	423	THR
1	V	431	LEU
1	W	20	GLU
1	W	24	GLN
1	W	34	GLU
1	W	38	GLU
1	W	39	GLU
1	W	49	ASP
1	W	50	VAL
1	W	66	LEU
1	W	78	LEU
1	W	91	ILE
1	W	106	SER
1	W	117	ASP
1	W	118	ILE
1	W	120	ASP
1	W	132	LEU
1	W	137	LEU
1	W	140	SER
1	W	153	LEU
1	W	157	LEU
1	W	165	LEU
1	W	166	VAL
1	W	168	THR
1	W	171	VAL
1	W	189	LEU
1	W	192	LEU
1	W	204	VAL
1	W	206	ASP
1	W	224	SER
1	W	233	SER
1	W	236	MET
1	W	254	ILE
1	W	256	LEU
1	W	265	ARG
1	W	269	LEU
1	W	270	MET

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Mol	Chain	Res	Type
1	W	274	THR
1	W	277	THR
1	W	288	THR
1	W	295	ARG
1	W	297	LEU
1	W	298	LEU
1	W	304	MET
1	W	316	CYS
1	W	321	LEU
1	W	332	GLN
1	W	337	LEU
1	W	338	GLN
1	W	343	ARG
1	W	356	ILE
1	W	358	VAL
1	W	361	SER
1	W	367	LEU
1	W	373	VAL
1	W	376	LEU
1	W	402	GLU
1	W	423	THR
1	W	431	LEU
1	X	20	GLU
1	X	24	GLN
1	X	34	GLU
1	X	38	GLU
1	X	39	GLU
1	X	49	ASP
1	X	50	VAL
1	X	66	LEU
1	X	78	LEU
1	X	91	ILE
1	X	106	SER
1	X	117	ASP
1	X	118	ILE
1	X	120	ASP
1	X	132	LEU
1	X	137	LEU
1	X	140	SER
1	X	153	LEU
1	X	157	LEU
1	X	165	LEU

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Mol	Chain	Res	Type
1	X	166	VAL
1	X	168	THR
1	X	171	VAL
1	X	189	LEU
1	X	192	LEU
1	X	204	VAL
1	X	206	ASP
1	X	224	SER
1	X	233	SER
1	X	236	MET
1	X	254	ILE
1	X	256	LEU
1	X	265	ARG
1	X	269	LEU
1	X	270	MET
1	X	274	THR
1	X	277	THR
1	X	288	THR
1	X	295	ARG
1	X	297	LEU
1	X	298	LEU
1	X	304	MET
1	X	316	CYS
1	X	321	LEU
1	X	332	GLN
1	X	337	LEU
1	X	338	GLN
1	X	343	ARG
1	X	356	ILE
1	X	358	VAL
1	X	361	SER
1	X	367	LEU
1	X	373	VAL
1	X	376	LEU
1	X	402	GLU
1	X	423	THR
1	X	431	LEU
1	Y	20	GLU
1	Y	24	GLN
1	Y	34	GLU
1	Y	38	GLU
1	Y	39	GLU

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Mol	Chain	Res	Type
1	Y	49	ASP
1	Y	50	VAL
1	Y	66	LEU
1	Y	78	LEU
1	Y	91	ILE
1	Y	106	SER
1	Y	117	ASP
1	Y	118	ILE
1	Y	120	ASP
1	Y	132	LEU
1	Y	137	LEU
1	Y	140	SER
1	Y	153	LEU
1	Y	157	LEU
1	Y	165	LEU
1	Y	166	VAL
1	Y	168	THR
1	Y	171	VAL
1	Y	189	LEU
1	Y	192	LEU
1	Y	204	VAL
1	Y	206	ASP
1	Y	224	SER
1	Y	233	SER
1	Y	236	MET
1	Y	254	ILE
1	Y	256	LEU
1	Y	265	ARG
1	Y	269	LEU
1	Y	270	MET
1	Y	274	THR
1	Y	277	THR
1	Y	288	THR
1	Y	295	ARG
1	Y	297	LEU
1	Y	298	LEU
1	Y	304	MET
1	Y	316	CYS
1	Y	321	LEU
1	Y	332	GLN
1	Y	337	LEU
1	Y	338	GLN

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Mol	Chain	Res	Type
1	Y	343	ARG
1	Y	356	ILE
1	Y	358	VAL
1	Y	361	SER
1	Y	367	LEU
1	Y	373	VAL
1	Y	376	LEU
1	Y	402	GLU
1	Y	423	THR
1	Y	431	LEU
1	Z	20	GLU
1	Z	24	GLN
1	Z	34	GLU
1	Z	38	GLU
1	Z	39	GLU
1	Z	49	ASP
1	Z	50	VAL
1	Z	66	LEU
1	Z	78	LEU
1	Z	91	ILE
1	Z	106	SER
1	Z	117	ASP
1	Z	118	ILE
1	Z	120	ASP
1	Z	132	LEU
1	Z	137	LEU
1	Z	140	SER
1	Z	153	LEU
1	Z	157	LEU
1	Z	165	LEU
1	Z	166	VAL
1	Z	168	THR
1	Z	171	VAL
1	Z	189	LEU
1	Z	192	LEU
1	Z	204	VAL
1	Z	206	ASP
1	Z	224	SER
1	Z	233	SER
1	Z	236	MET
1	Z	254	ILE
1	Z	256	LEU

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Mol	Chain	Res	Type
1	Z	265	ARG
1	Z	269	LEU
1	Z	270	MET
1	Z	274	THR
1	Z	277	THR
1	Z	288	THR
1	Z	295	ARG
1	Z	297	LEU
1	Z	298	LEU
1	Z	304	MET
1	Z	316	CYS
1	Z	321	LEU
1	Z	332	GLN
1	Z	337	LEU
1	Z	338	GLN
1	Z	343	ARG
1	Z	356	ILE
1	Z	358	VAL
1	Z	361	SER
1	Z	367	LEU
1	Z	373	VAL
1	Z	376	LEU
1	Z	402	GLU
1	Z	423	THR
1	Z	431	LEU
5	k	29	LEU
4	a	36	VAL
8	c	3	SER
3	E	233	VAL
3	E	547	THR
3	E	557	LEU
3	E	698	MET
3	E	722	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (379) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	16	GLN
1	1	167	GLN
1	1	174	ASN
1	1	207	ASN
1	1	227	GLN

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Mol	Chain	Res	Type
1	1	250	ASN
1	1	314	ASN
1	1	334	HIS
1	1	347	ASN
1	1	394	GLN
1	2	16	GLN
1	2	59	HIS
1	2	167	GLN
1	2	174	ASN
1	2	198	ASN
1	2	207	ASN
1	2	227	GLN
1	2	314	ASN
1	2	347	ASN
1	2	394	GLN
2	e	246	GLN
2	e	360	GLN
3	A	165	GLN
3	A	213	GLN
3	A	242	GLN
3	A	312	GLN
3	A	412	HIS
3	A	430	GLN
3	A	458	ASN
3	A	512	HIS
3	A	631	ASN
3	A	684	GLN
3	A	688	ASN
3	A	760	ASN
3	A	763	GLN
4	B	301	HIS
4	B	329	HIS
4	B	343	HIS
4	B	389	GLN
4	B	491	ASN
4	B	500	GLN
4	B	643	HIS
4	B	717	GLN
4	B	774	GLN
4	B	786	GLN
4	B	830	ASN
4	B	860	GLN

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Mol	Chain	Res	Type
4	B	885	HIS
3	C	166	ASN
3	C	242	GLN
3	C	322	GLN
3	C	371	GLN
3	C	373	GLN
3	C	412	HIS
3	C	465	HIS
3	C	639	GLN
3	C	650	HIS
3	C	707	HIS
4	D	330	GLN
4	D	424	HIS
4	D	491	ASN
4	D	495	GLN
4	D	717	GLN
4	D	751	HIS
4	D	773	ASN
4	D	774	GLN
4	D	859	GLN
4	D	860	GLN
4	D	883	ASN
4	D	885	HIS
5	b	19	ASN
4	F	259	GLN
4	F	322	GLN
4	F	329	HIS
4	F	330	GLN
4	F	417	HIS
4	F	424	HIS
4	F	491	ASN
4	F	528	ASN
4	F	531	GLN
4	F	560	GLN
4	F	570	GLN
4	F	576	HIS
4	F	659	HIS
4	F	693	ASN
4	F	705	HIS
4	F	713	HIS
4	F	717	GLN
4	F	740	GLN

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Mol	Chain	Res	Type
4	F	742	GLN
4	F	746	HIS
4	F	751	HIS
4	F	773	ASN
4	F	801	GLN
3	G	166	ASN
3	G	169	ASN
3	G	236	GLN
3	G	242	GLN
3	G	312	GLN
3	G	412	HIS
3	G	424	ASN
3	G	430	GLN
3	G	438	GLN
3	G	444	GLN
3	G	585	GLN
3	G	650	HIS
3	G	684	GLN
3	G	694	GLN
3	G	726	HIS
4	H	269	ASN
4	H	273	ASN
4	H	330	GLN
4	H	343	HIS
4	H	387	HIS
4	H	479	GLN
4	H	570	GLN
4	H	687	ASN
4	H	703	GLN
4	H	716	HIS
4	H	717	GLN
4	H	739	GLN
4	H	773	ASN
4	H	846	GLN
4	H	859	GLN
6	I	29	GLN
6	I	35	HIS
6	I	180	HIS
6	I	186	GLN
6	I	199	GLN
6	I	302	ASN
6	I	370	GLN

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Mol	Chain	Res	Type
6	I	460	GLN
6	I	489	GLN
6	I	509	GLN
6	I	533	GLN
6	I	547	GLN
6	I	599	GLN
6	I	600	ASN
7	J	298	ASN
7	J	299	ASN
7	J	322	GLN
7	J	362	GLN
7	J	435	HIS
7	J	698	GLN
7	J	721	GLN
7	J	761	GLN
7	J	763	GLN
7	J	818	GLN
7	J	830	GLN
7	J	879	GLN
7	J	892	HIS
7	J	916	GLN
6	K	43	ASN
6	K	65	HIS
6	K	68	GLN
6	K	98	GLN
6	K	142	GLN
6	K	152	GLN
6	K	180	HIS
6	K	186	GLN
6	K	199	GLN
6	K	284	GLN
6	K	339	HIS
6	K	353	GLN
6	K	393	ASN
6	K	397	GLN
6	K	401	HIS
6	K	489	GLN
6	K	519	ASN
6	K	547	GLN
6	K	561	HIS
6	K	567	ASN
6	K	639	ASN

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Mol	Chain	Res	Type
8	L	430	GLN
8	L	1605	ASN
8	L	1625	GLN
8	L	1654	GLN
8	L	1659	GLN
8	L	1667	HIS
8	L	1710	HIS
8	L	1730	HIS
8	L	1770	ASN
8	L	1806	ASN
3	M	151	GLN
3	M	172	GLN
3	M	329	GLN
3	M	424	ASN
3	M	458	ASN
3	M	465	HIS
3	M	585	GLN
3	M	684	GLN
3	M	692	ASN
3	M	694	GLN
3	M	726	HIS
3	M	760	ASN
3	M	862	ASN
4	N	269	ASN
4	N	273	ASN
4	N	302	ASN
4	N	347	GLN
4	N	416	GLN
4	N	444	HIS
4	N	495	GLN
4	N	528	ASN
4	N	570	GLN
4	N	576	HIS
4	N	609	ASN
4	N	665	ASN
4	N	702	HIS
4	N	716	HIS
4	N	739	GLN
4	N	740	GLN
4	N	751	HIS
4	N	787	ASN
4	N	885	HIS

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Mol	Chain	Res	Type
1	O	16	GLN
1	O	59	HIS
1	O	167	GLN
1	O	174	ASN
1	O	207	ASN
1	O	227	GLN
1	O	230	GLN
1	O	314	ASN
1	O	334	HIS
1	O	347	ASN
1	O	394	GLN
1	P	16	GLN
1	P	59	HIS
1	P	167	GLN
1	P	174	ASN
1	P	198	ASN
1	P	207	ASN
1	P	227	GLN
1	P	250	ASN
1	P	314	ASN
1	P	334	HIS
1	P	347	ASN
1	P	394	GLN
1	Q	16	GLN
1	Q	59	HIS
1	Q	167	GLN
1	Q	174	ASN
1	Q	198	ASN
1	Q	207	ASN
1	Q	227	GLN
1	Q	314	ASN
1	Q	334	HIS
1	Q	347	ASN
1	Q	394	GLN
1	R	16	GLN
1	R	59	HIS
1	R	167	GLN
1	R	174	ASN
1	R	198	ASN
1	R	207	ASN
1	R	227	GLN
1	R	250	ASN

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Mol	Chain	Res	Type
1	R	314	ASN
1	R	334	HIS
1	R	347	ASN
1	R	394	GLN
1	S	16	GLN
1	S	59	HIS
1	S	167	GLN
1	S	174	ASN
1	S	198	ASN
1	S	207	ASN
1	S	227	GLN
1	S	314	ASN
1	S	334	HIS
1	S	338	GLN
1	S	347	ASN
1	S	394	GLN
1	T	16	GLN
1	T	59	HIS
1	T	167	GLN
1	T	174	ASN
1	T	207	ASN
1	T	227	GLN
1	T	314	ASN
1	T	347	ASN
1	T	394	GLN
1	U	16	GLN
1	U	59	HIS
1	U	167	GLN
1	U	174	ASN
1	U	198	ASN
1	U	207	ASN
1	U	227	GLN
1	U	230	GLN
1	U	314	ASN
1	U	334	HIS
1	U	347	ASN
1	U	394	GLN
1	V	16	GLN
1	V	59	HIS
1	V	167	GLN
1	V	174	ASN
1	V	198	ASN

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Mol	Chain	Res	Type
1	V	207	ASN
1	V	227	GLN
1	V	314	ASN
1	V	334	HIS
1	V	347	ASN
1	V	394	GLN
1	W	16	GLN
1	W	59	HIS
1	W	167	GLN
1	W	174	ASN
1	W	198	ASN
1	W	207	ASN
1	W	227	GLN
1	W	314	ASN
1	W	334	HIS
1	W	347	ASN
1	W	394	GLN
1	X	16	GLN
1	X	59	HIS
1	X	167	GLN
1	X	174	ASN
1	X	198	ASN
1	X	207	ASN
1	X	227	GLN
1	X	314	ASN
1	X	347	ASN
1	X	394	GLN
1	Y	16	GLN
1	Y	59	HIS
1	Y	167	GLN
1	Y	174	ASN
1	Y	198	ASN
1	Y	207	ASN
1	Y	227	GLN
1	Y	314	ASN
1	Y	347	ASN
1	Y	394	GLN
1	Z	16	GLN
1	Z	59	HIS
1	Z	167	GLN
1	Z	174	ASN
1	Z	198	ASN

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Mol	Chain	Res	Type
1	Z	207	ASN
1	Z	227	GLN
1	Z	230	GLN
1	Z	314	ASN
1	Z	334	HIS
1	Z	347	ASN
1	Z	394	GLN
5	g	36	ASN
5	i	53	GLN
5	m	53	GLN
5	m	56	ASN
7	l	93	ASN
4	a	15	ASN
4	a	31	GLN
4	a	127	HIS
5	d	19	ASN
5	d	53	GLN
8	c	29	ASN
8	c	43	ASN
8	c	135	ASN
8	c	161	GLN
4	j	84	GLN
4	j	89	ASN
3	E	169	ASN
3	E	261	HIS
3	E	314	HIS
3	E	412	HIS
3	E	420	GLN
3	E	424	ASN
3	E	437	GLN
3	E	639	GLN
3	E	763	GLN
4	h	10	ASN
4	h	14	GLN
4	h	84	GLN
4	h	107	GLN
4	f	42	ASN
4	f	84	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.

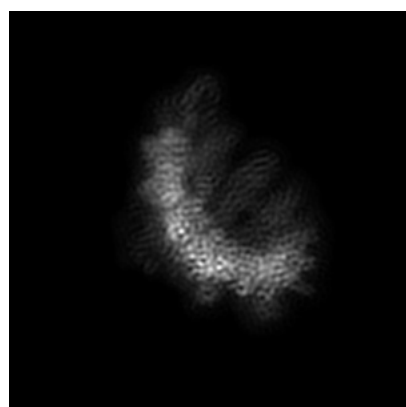
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14010. These allow visual inspection of the internal detail of the map and identification of artifacts.

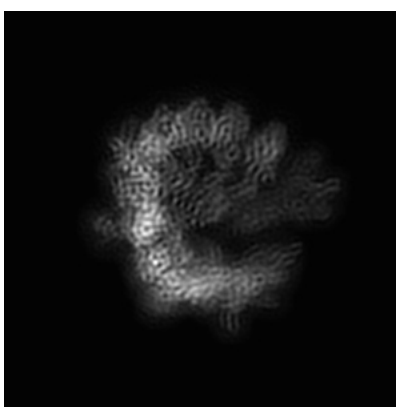
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

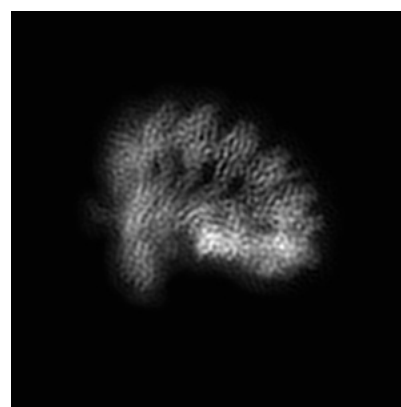
6.1.1 Primary map



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: 100



Y Index: 100



Z Index: 100

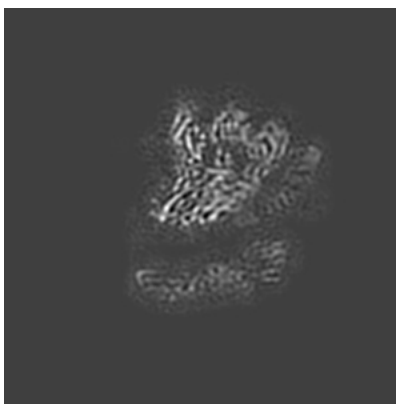
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

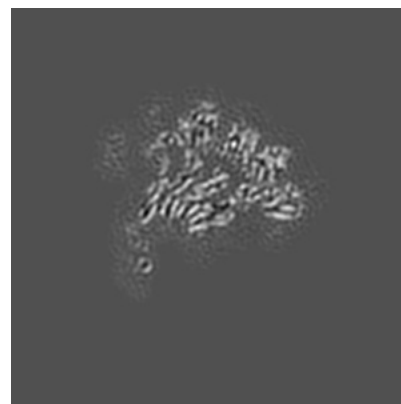
6.3.1 Primary map



X Index: 134



Y Index: 82

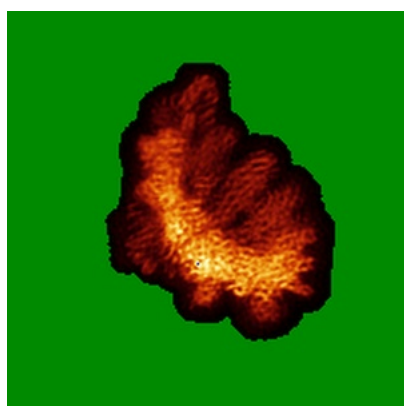


Z Index: 72

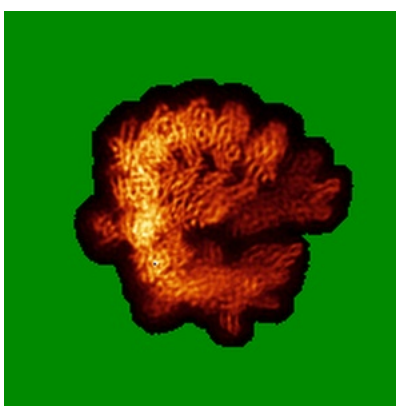
The images above show the largest variance slices of the map in three orthogonal directions.

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

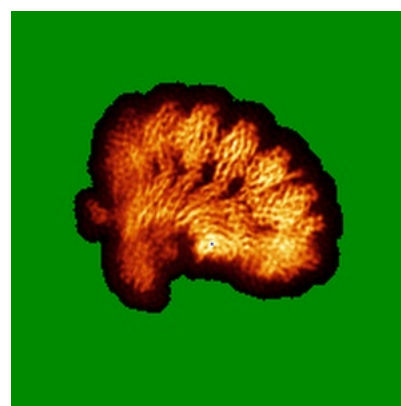
6.4.1 Primary map



X



Y

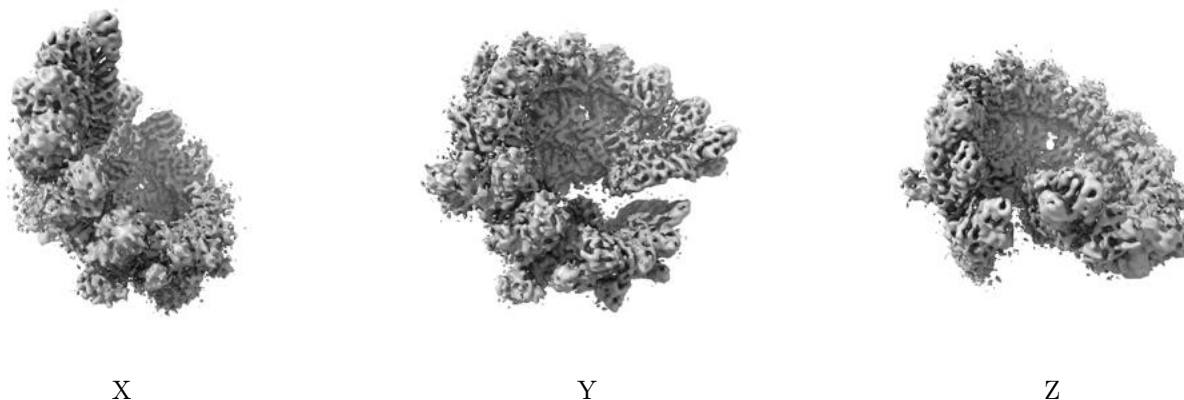


Z

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 0.0224. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

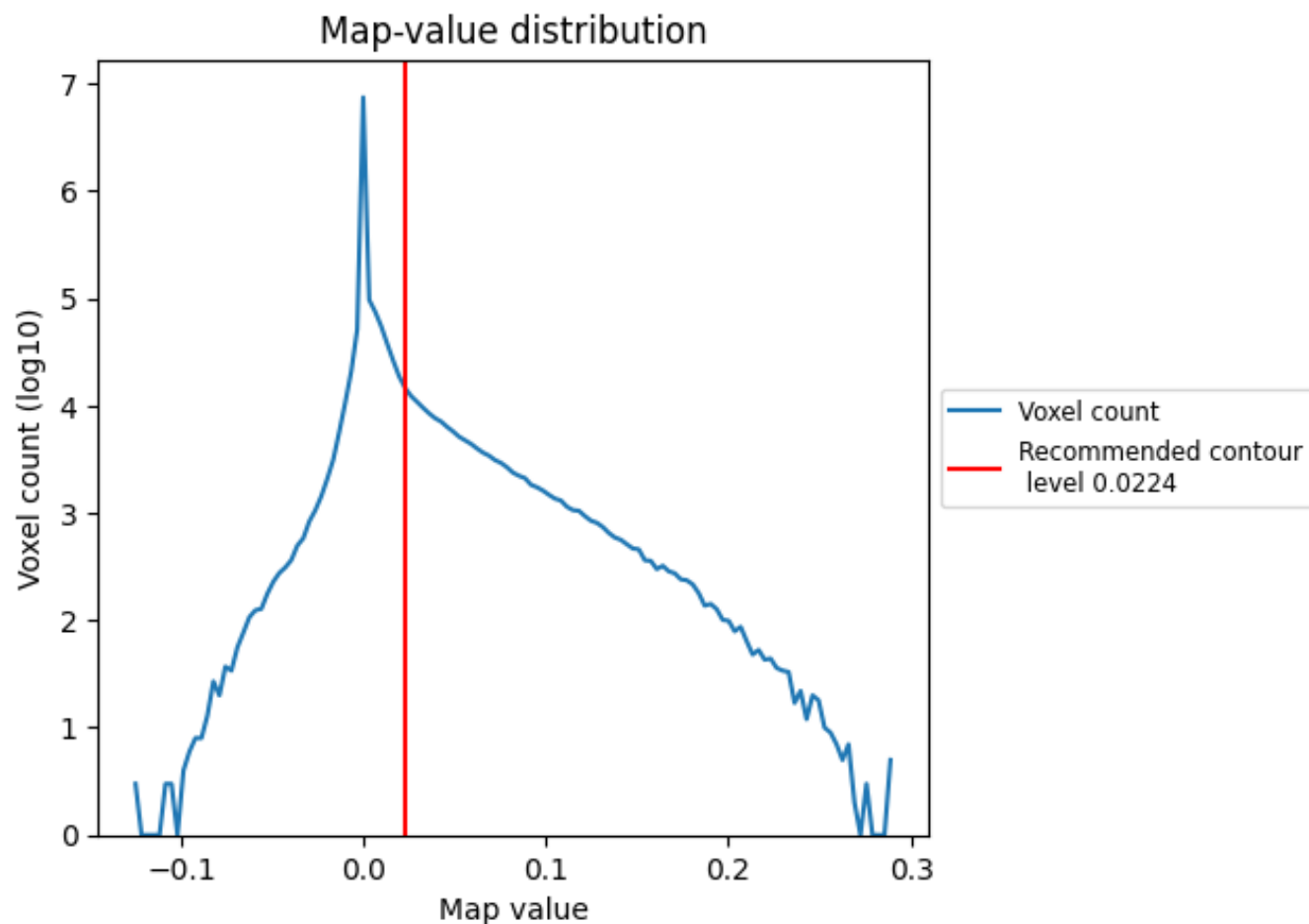
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

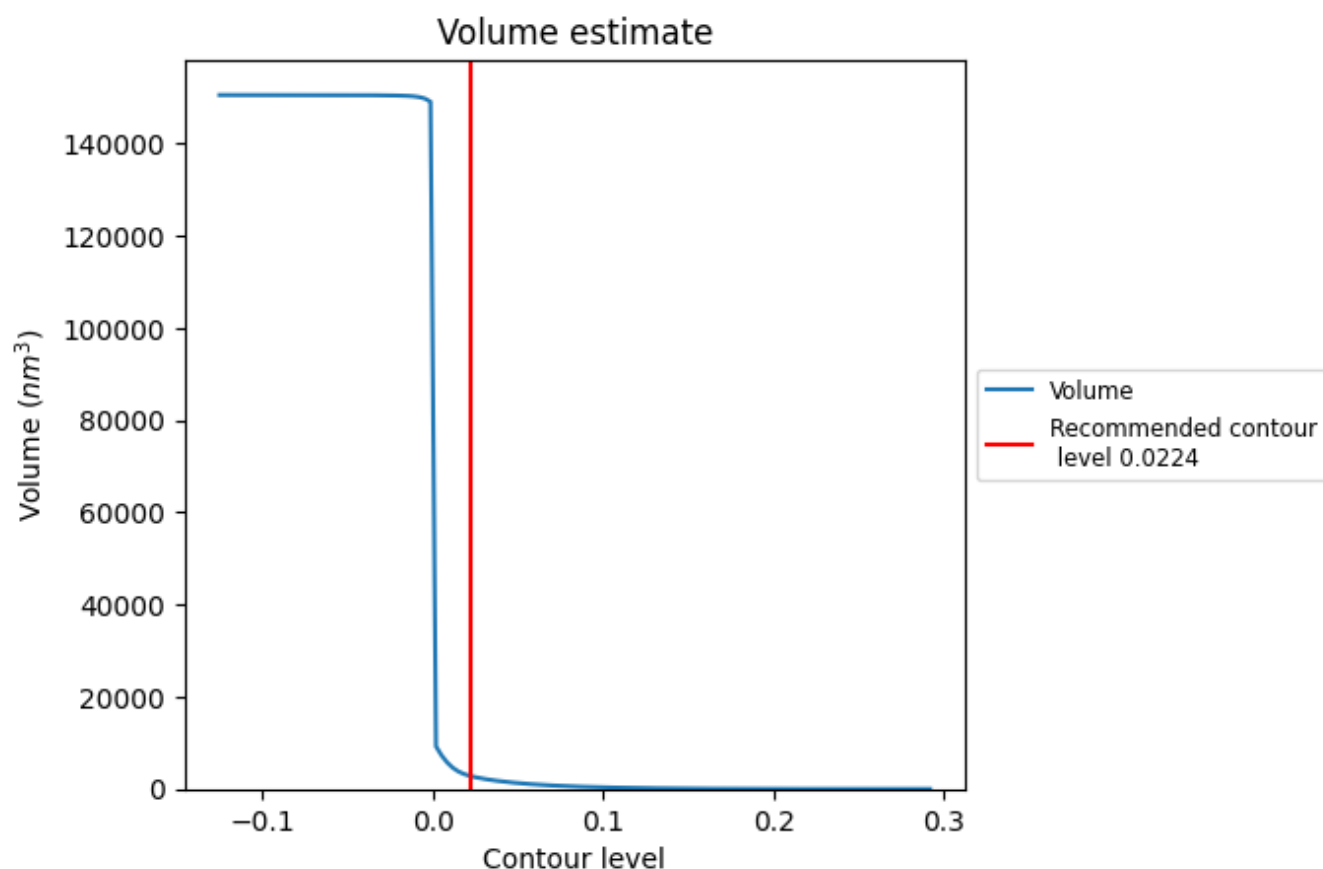
This section contains the results of statistical analysis of the map.

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.

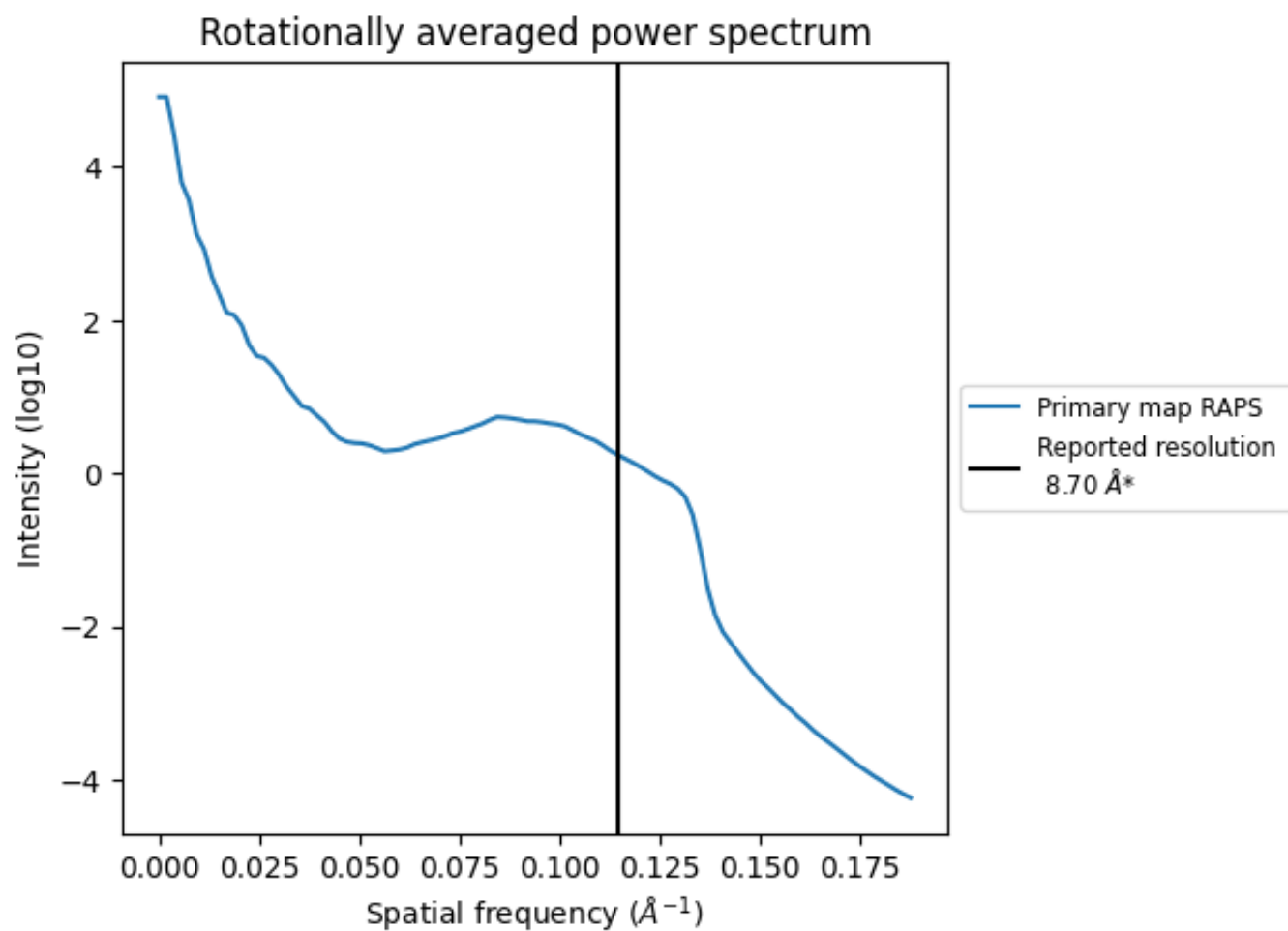
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2805 nm^3 ; this corresponds to an approximate mass of 2533 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 0.115 Å⁻¹

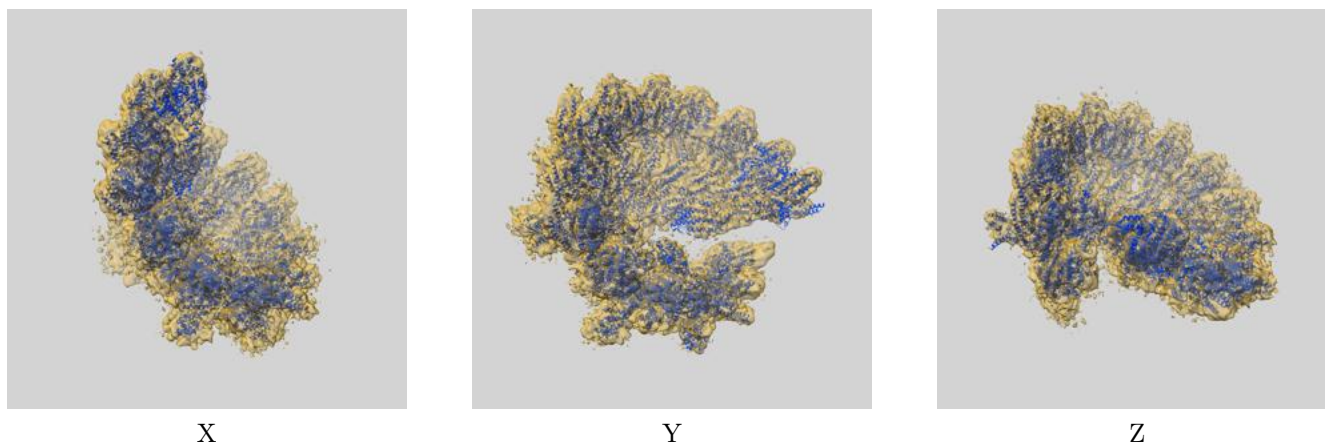
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

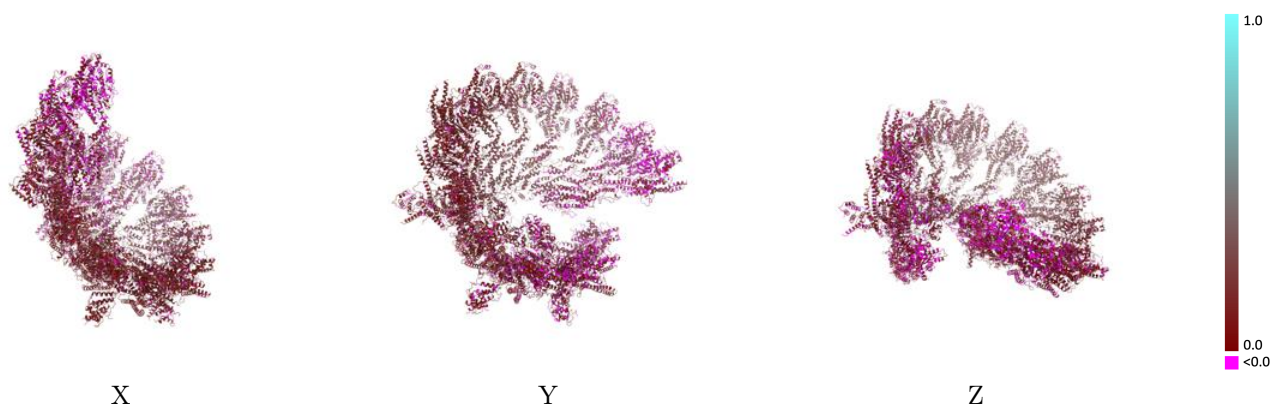
This section contains information regarding the fit between EMDB map EMD-14010 and PDB model 7QJ5. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



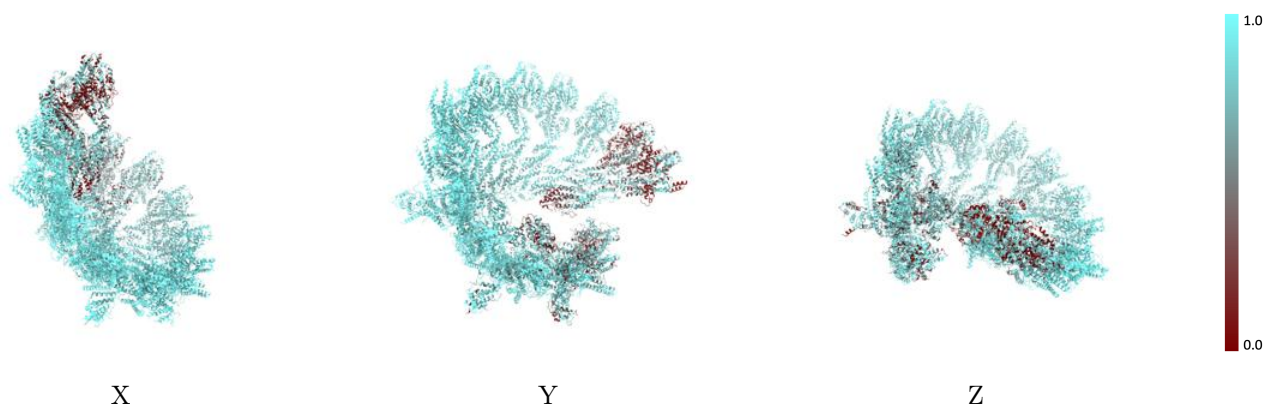
The images above show the 3D surface view of the map at the recommended contour level 0.0224 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



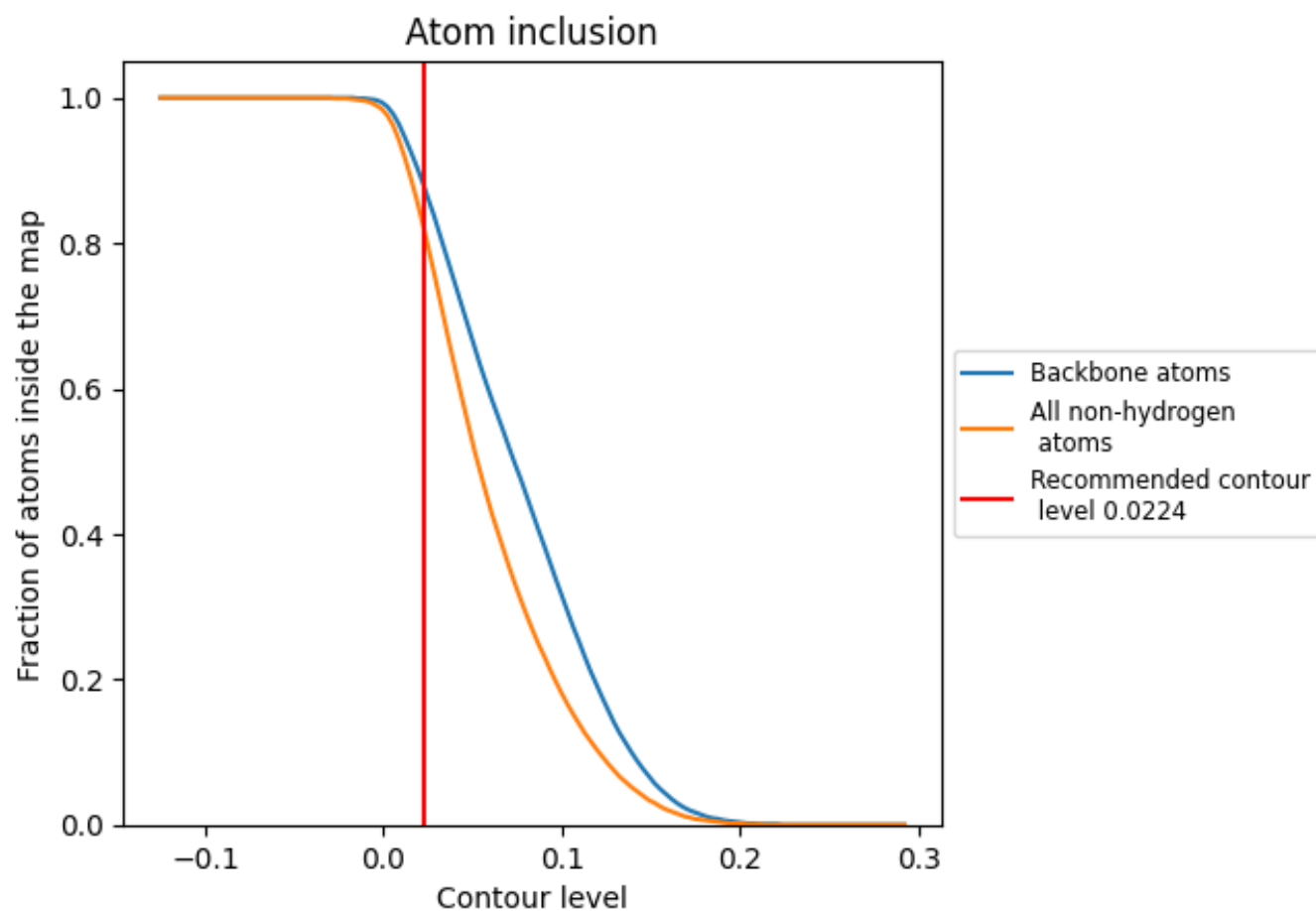
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0224).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 82% 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 (0.0224) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8230	 0.1190
1	 0.3540	 0.0160
2	 0.4000	 -0.0000
A	 0.7820	 0.0960
B	 0.7620	 0.1100
C	 0.9150	 0.1170
D	 0.9000	 0.1300
E	 0.9260	 0.1530
F	 0.9330	 0.1510
G	 0.9410	 0.1620
H	 0.9340	 0.1600
I	 0.9380	 0.1660
J	 0.9370	 0.1670
K	 0.9470	 0.1550
L	 0.9560	 0.1360
M	 0.5690	 0.0680
N	 0.5640	 0.0650
O	 0.5910	 0.0360
P	 0.6120	 0.0570
Q	 0.7610	 0.0590
R	 0.8860	 0.1090
S	 0.9230	 0.1450
T	 0.9310	 0.1460
U	 0.9270	 0.1470
V	 0.9360	 0.1650
W	 0.9420	 0.1550
X	 0.9420	 0.1510
Y	 0.9580	 0.1350
Z	 0.9220	 0.1080
a	 0.8720	 0.1550
b	 0.9080	 0.1770
c	 0.8290	 0.1480
d	 0.8050	 0.1460
e	 0.5710	 0.0840
f	 0.6160	 0.0880



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Chain	Atom inclusion	Q-score
g	 0.5860	 0.0680
h	 0.8390	 0.1160
i	 0.7980	 0.0960
j	 0.9310	 0.1400
k	 0.9540	 0.1570
l	 0.9240	 0.1630
m	 0.9410	 0.1620