



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 05:29 PM UTC

PDB ID : 7TNS / pdb_00007tns
EMDB ID : EMD-26019
Title : Subpellicular microtubule from detergent-extract *Toxoplasma gondii* cells
Authors : Sun, S.Y.; Pintilie, G.D.; Chen, M.; Chiu, W.
Deposited on : 2022-01-21
Resolution : 6.70 Å(reported)
Based on initial model : 7MIZ

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:

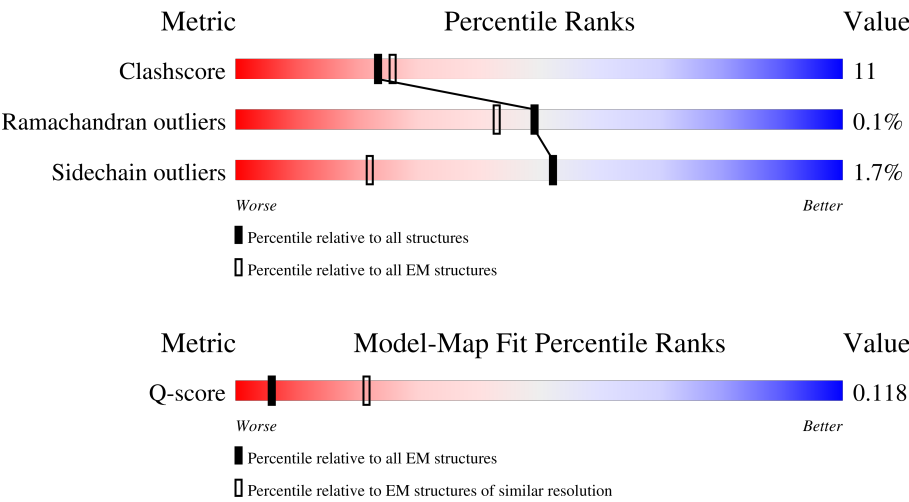
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 6.70 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.



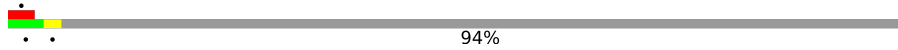
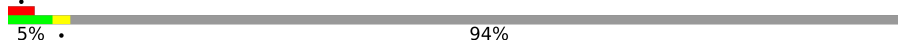
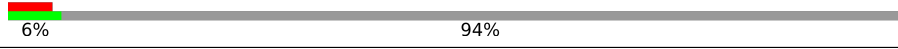
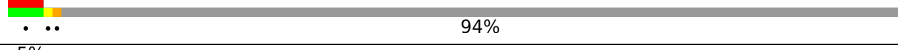
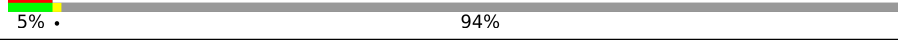
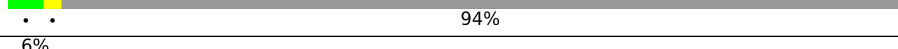
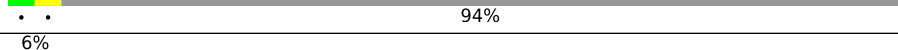
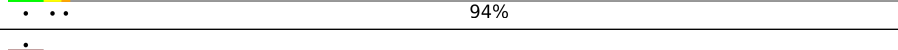
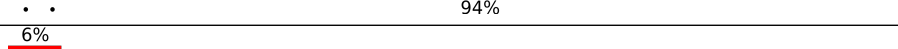
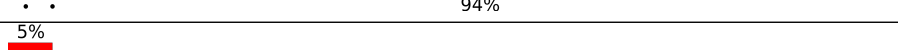
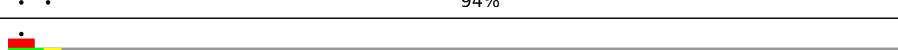
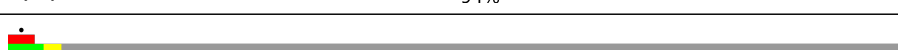
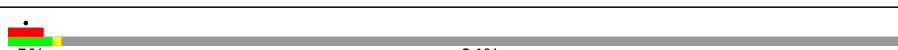
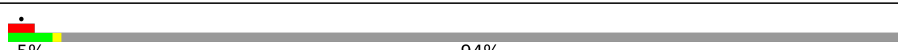
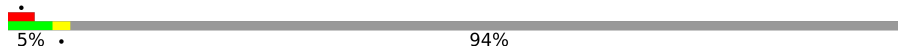
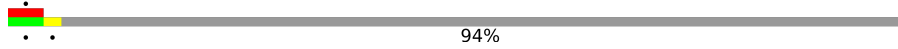
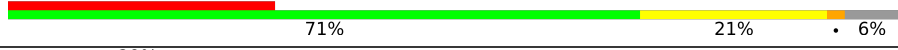
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	523 (6.20 - 7.20)

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	0	351	 94%
1	1	351	 5% 94%
1	10	351	 94%
1	11	351	 94%

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Mol	Chain	Length	Quality of chain
1	12	351	 94%
1	13	351	 94%
1	14	351	 94%
1	15	351	 94%
1	16	351	 94%
1	17	351	 94%
1	18	351	 94%
1	19	351	 94%
1	2	351	 94%
1	20	351	 94%
1	21	351	 94%
1	22	351	 94%
1	23	351	 94%
1	3	351	 94%
1	4	351	 94%
1	5	351	 94%
1	6	351	 94%
1	7	351	 94%
1	8	351	 94%
1	9	351	 94%
2	A0	453	 31% 69% 23% 6%
2	A2	453	 30% 71% 21% 6%
2	A4	453	 29% 75% 18% 6%
2	A6	453	 29% 71% 22% 6%
2	A8	453	 28% 71% 22% 6%

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Mol	Chain	Length	Quality of chain
2	B0	453	
2	B2	453	
2	B4	453	
2	B6	453	
2	B8	453	
2	C0	453	
2	C2	453	
2	C4	453	
2	C6	453	
2	C8	453	
2	D0	453	
2	D2	453	
2	D4	453	
2	D6	453	
2	D8	453	
2	E0	453	
2	E2	453	
2	E4	453	
2	E6	453	
2	E8	453	
2	F0	453	
3	A1	449	
3	A3	449	
3	A5	449	
3	A7	449	

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Mol	Chain	Length	Quality of chain
3	A9	449	
3	B1	449	
3	B3	449	
3	B5	449	
3	B7	449	
3	B9	449	
3	C1	449	
3	C3	449	
3	C5	449	
3	C7	449	
3	C9	449	
3	D1	449	
3	D3	449	
3	D5	449	
3	D7	449	
3	D9	449	
3	E1	449	
3	E3	449	
3	E5	449	
3	E7	449	
3	E9	449	
3	F1	449	
4	a	220	
4	b	220	
4	c	220	

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Mol	Chain	Length	Quality of chain
4	d	220	
4	e	220	
4	f	220	
4	g	220	
4	h	220	
4	i	220	
4	j	220	
4	k	220	
4	l	220	
4	m	220	
4	n	220	
4	o	220	
4	p	220	
4	q	220	
4	r	220	
4	s	220	
4	t	220	
4	u	220	
4	v	220	
4	x	220	
4	y	220	
5	w	189	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 216148 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 Microtubule associated protein SPM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	1	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	10	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	11	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	12	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	13	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	14	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	15	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	16	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	17	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	18	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	19	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	2	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	20	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	21	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	22	20	Total	C	N	O	S	0	0
			160	105	26	28	1		
1	23	20	Total	C	N	O	S	0	0
			160	105	26	28	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	4	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	5	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	6	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	7	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	8	22	Total	C	N	O	S	0	0
			174	114	28	31	1		
1	9	22	Total	C	N	O	S	0	0
			174	114	28	31	1		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	263	ALA	VAL	conflict	UNP S8F1Y1
1	263	ALA	VAL	conflict	UNP S8F1Y1
10	263	ALA	VAL	conflict	UNP S8F1Y1
11	263	ALA	VAL	conflict	UNP S8F1Y1
12	263	ALA	VAL	conflict	UNP S8F1Y1
13	263	ALA	VAL	conflict	UNP S8F1Y1
14	263	ALA	VAL	conflict	UNP S8F1Y1
15	263	ALA	VAL	conflict	UNP S8F1Y1
16	263	ALA	VAL	conflict	UNP S8F1Y1
17	263	ALA	VAL	conflict	UNP S8F1Y1
18	263	ALA	VAL	conflict	UNP S8F1Y1
19	263	ALA	VAL	conflict	UNP S8F1Y1
2	263	ALA	VAL	conflict	UNP S8F1Y1
20	263	ALA	VAL	conflict	UNP S8F1Y1
21	263	ALA	VAL	conflict	UNP S8F1Y1
22	263	ALA	VAL	conflict	UNP S8F1Y1
23	263	ALA	VAL	conflict	UNP S8F1Y1
3	263	ALA	VAL	conflict	UNP S8F1Y1
4	263	ALA	VAL	conflict	UNP S8F1Y1
5	263	ALA	VAL	conflict	UNP S8F1Y1
6	263	ALA	VAL	conflict	UNP S8F1Y1
7	263	ALA	VAL	conflict	UNP S8F1Y1
8	263	ALA	VAL	conflict	UNP S8F1Y1
9	263	ALA	VAL	conflict	UNP S8F1Y1

- Molecule 2 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	A8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	B8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	C8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	D8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	E2	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E4	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E6	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	E8	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
2	F0	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

- Molecule 3 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A1	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A3	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A5	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A7	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	A9	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B1	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B3	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B5	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B7	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	B9	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C1	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C3	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C5	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
3	C7	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	C9	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D1	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D3	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D5	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D7	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	D9	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E1	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E3	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E5	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E7	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	E9	426	Total 3331	C 2094	N 569	O 641	S 27	0	0
3	F1	426	Total 3331	C 2094	N 569	O 641	S 27	0	0

- Molecule 4 is a protein called PDI family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	150	Total 1198	C 763	N 213	O 217	S 5	0	0
4	b	150	Total 1198	C 763	N 213	O 217	S 5	0	0
4	c	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	d	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	e	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	f	201	Total 1608	C 1021	N 283	O 297	S 7	0	0
4	g	201	Total 1608	C 1021	N 283	O 297	S 7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	h	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	i	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	j	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	k	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	l	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	m	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	n	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	o	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	p	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	q	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	r	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	s	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	t	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	u	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	v	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	x	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		
4	y	201	Total	C	N	O	S	0	0
			1608	1021	283	297	7		

- Molecule 5 is a protein called PDI family protein.

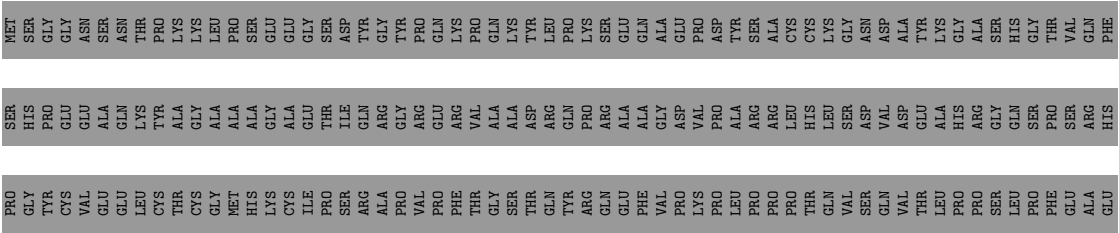
Mol	Chain	Residues	Atoms					AltConf	Trace
5	w	143	Total	C	N	O	S	0	0
			1172	755	207	205	5		

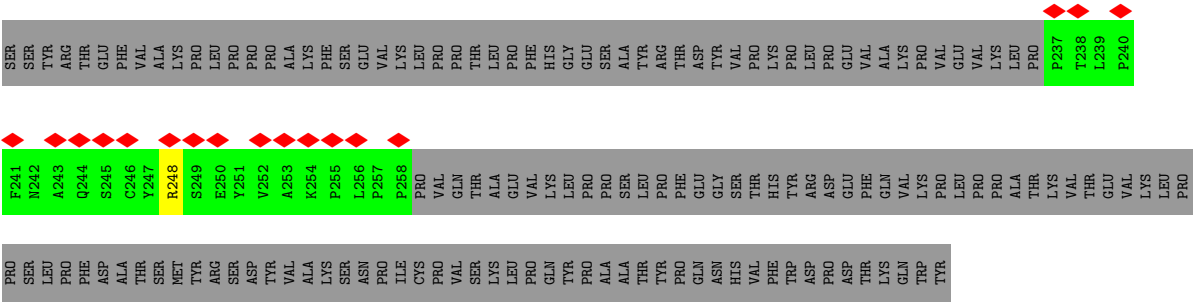


• Molecule 1: Microtubule associated protein SPM1

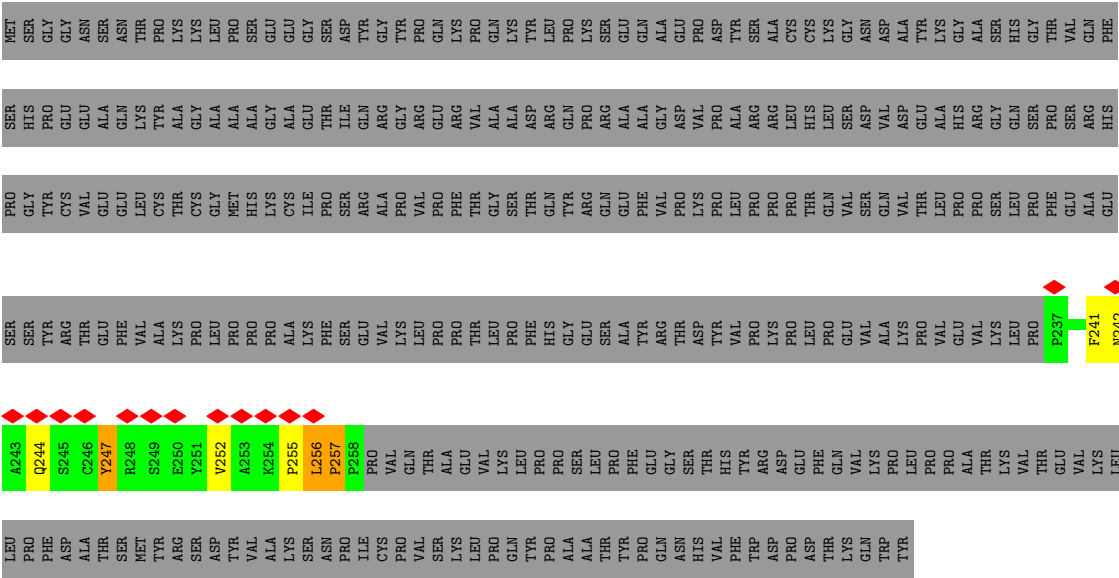


• Molecule 1: Microtubule associated protein SPM1

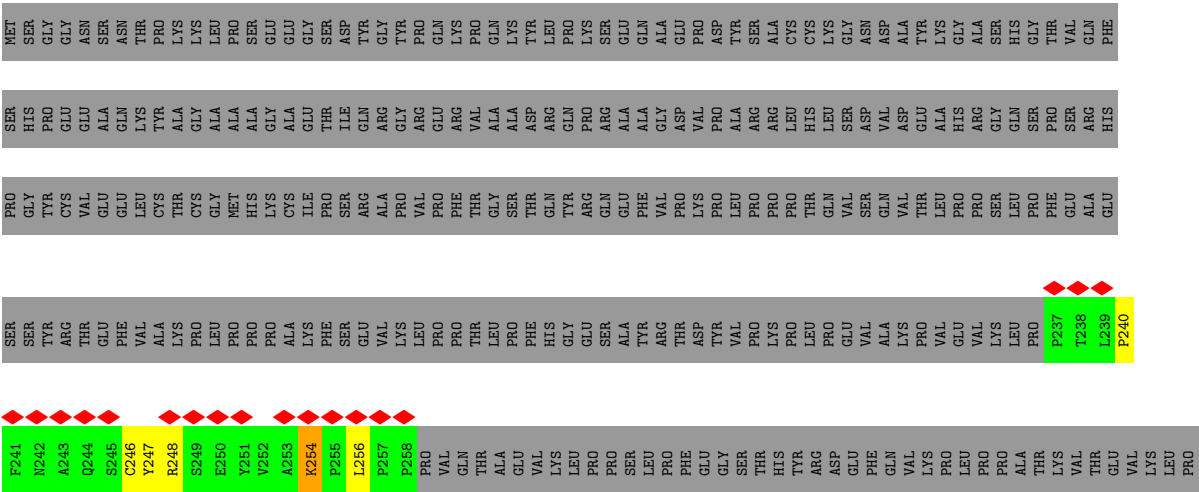


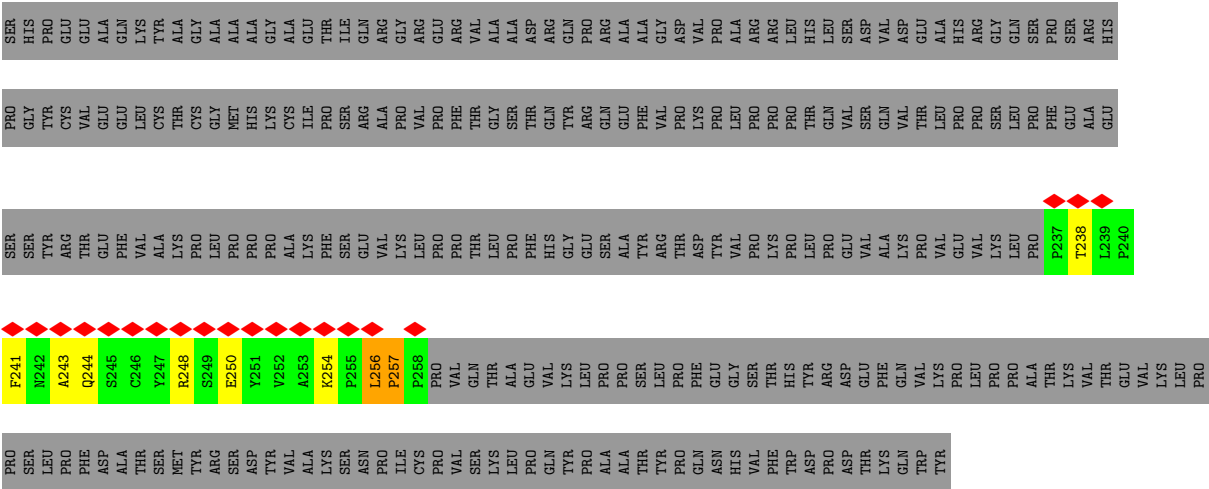


• Molecule 1: Microtubule associated protein SPM1

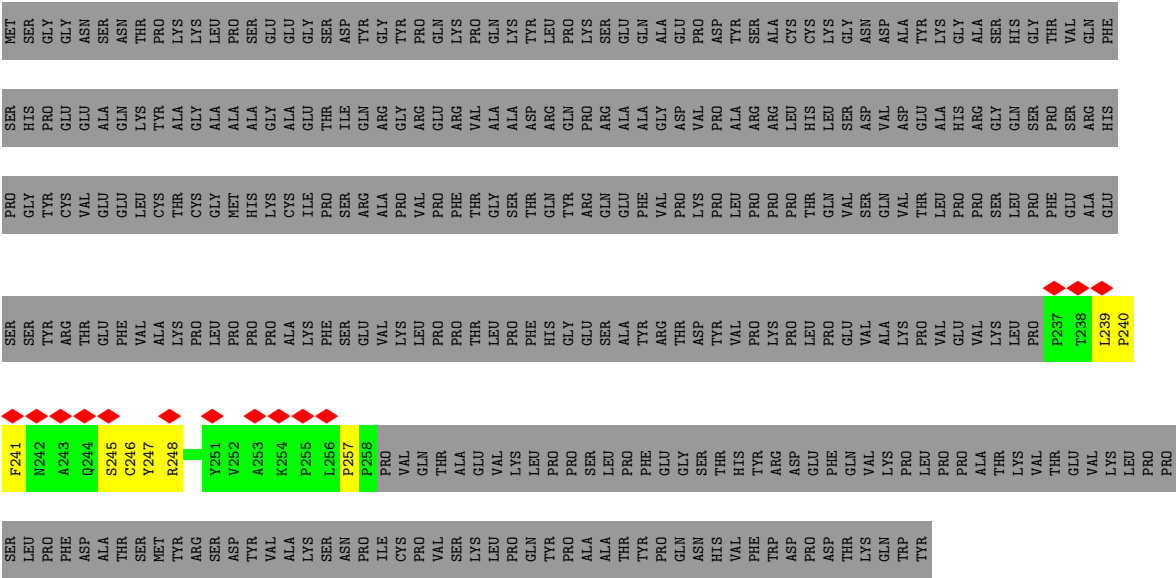


• Molecule 1: Microtubule associated protein SPM1

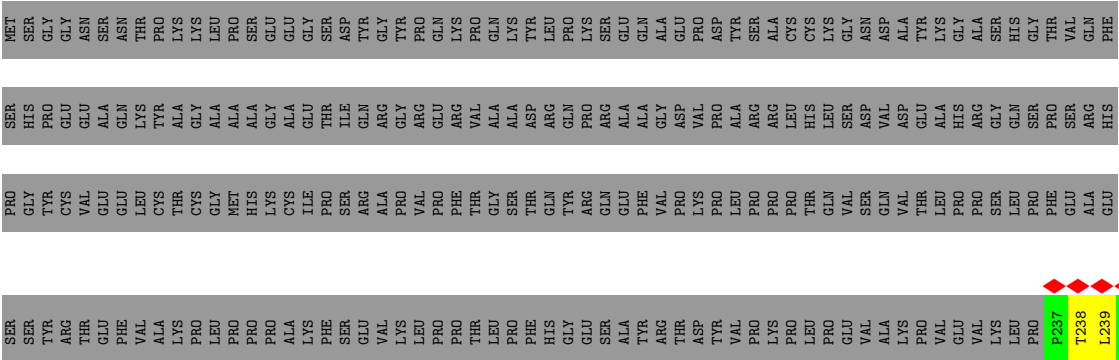


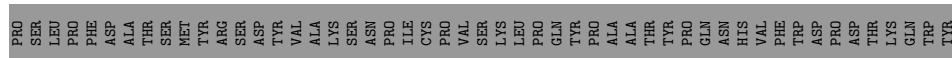


• Molecule 1: Microtubule associated protein SPM1

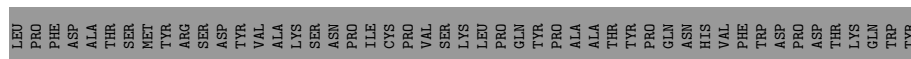
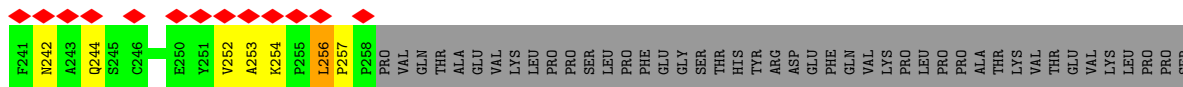
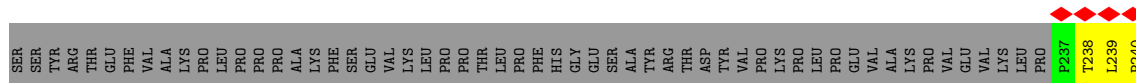
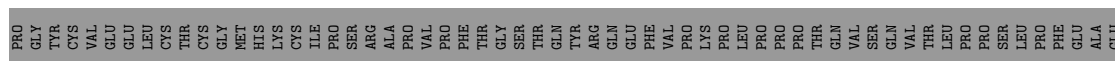
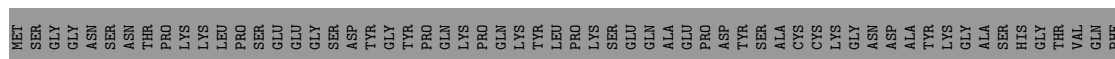


• Molecule 1: Microtubule associated protein SPM1

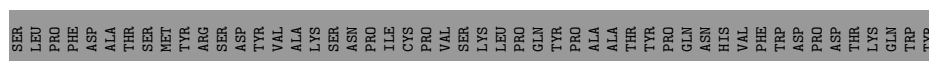
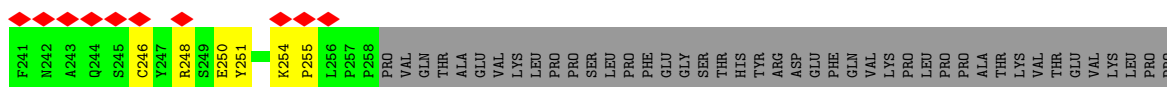
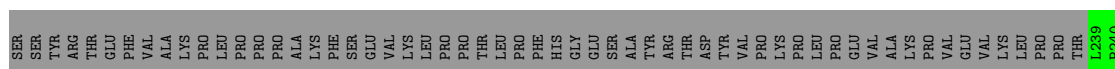
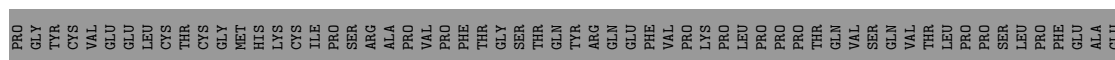
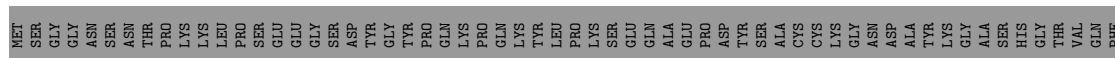




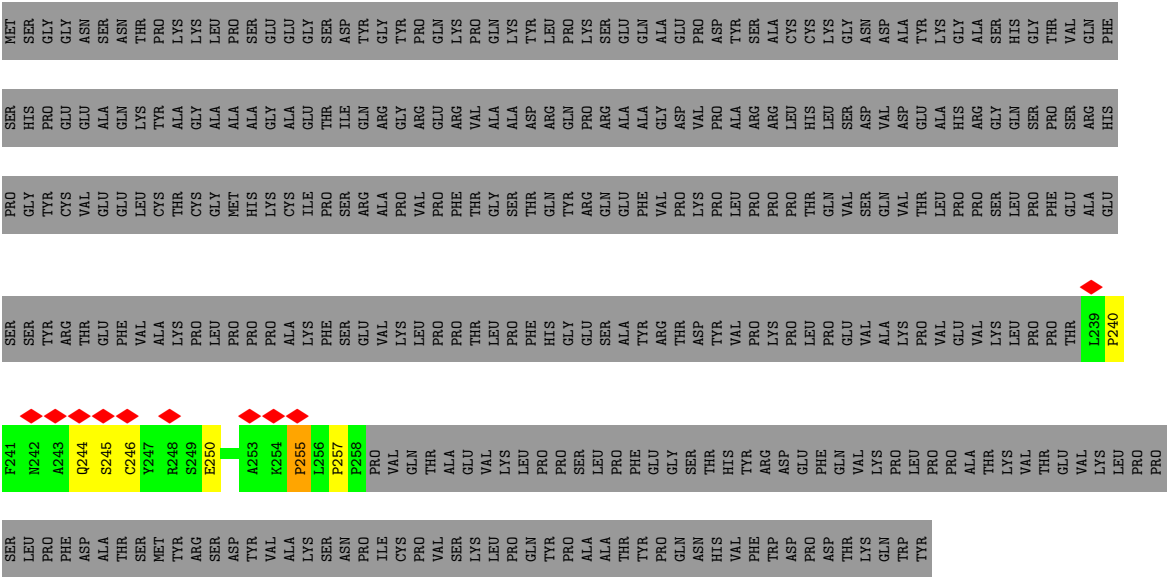
Chain 21:



Chain 22: 94%

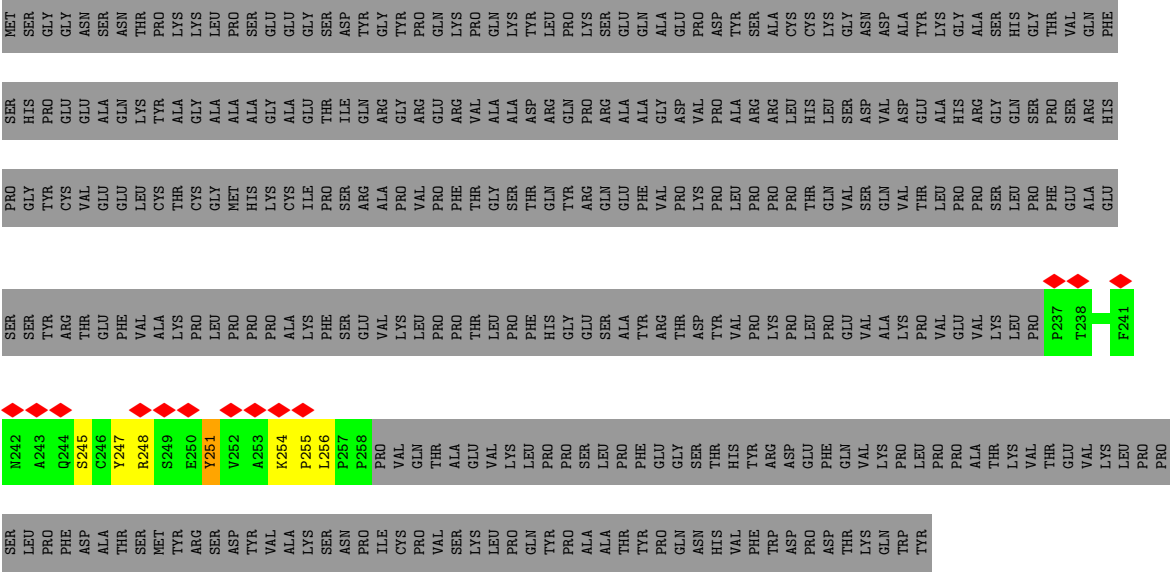


Chain 23: 94%



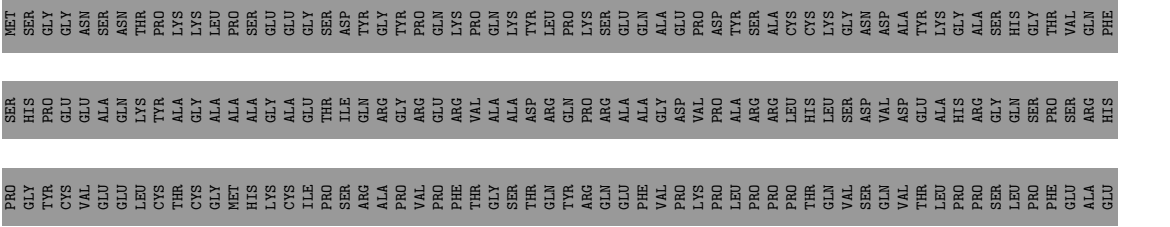
• Molecule 1: Microtubule associated protein SPM1

Chain 3: 94%

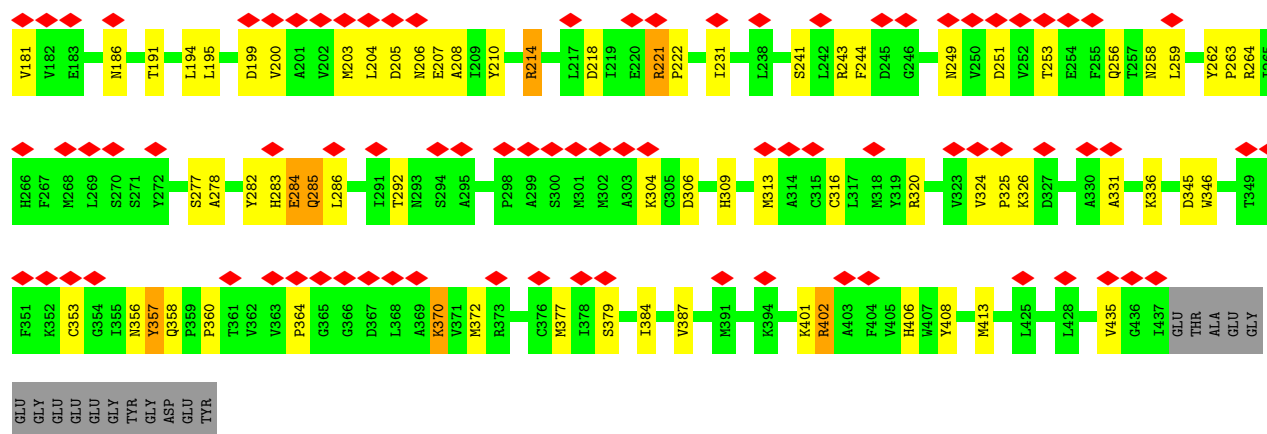


• Molecule 1: Microtubule associated protein SPM1

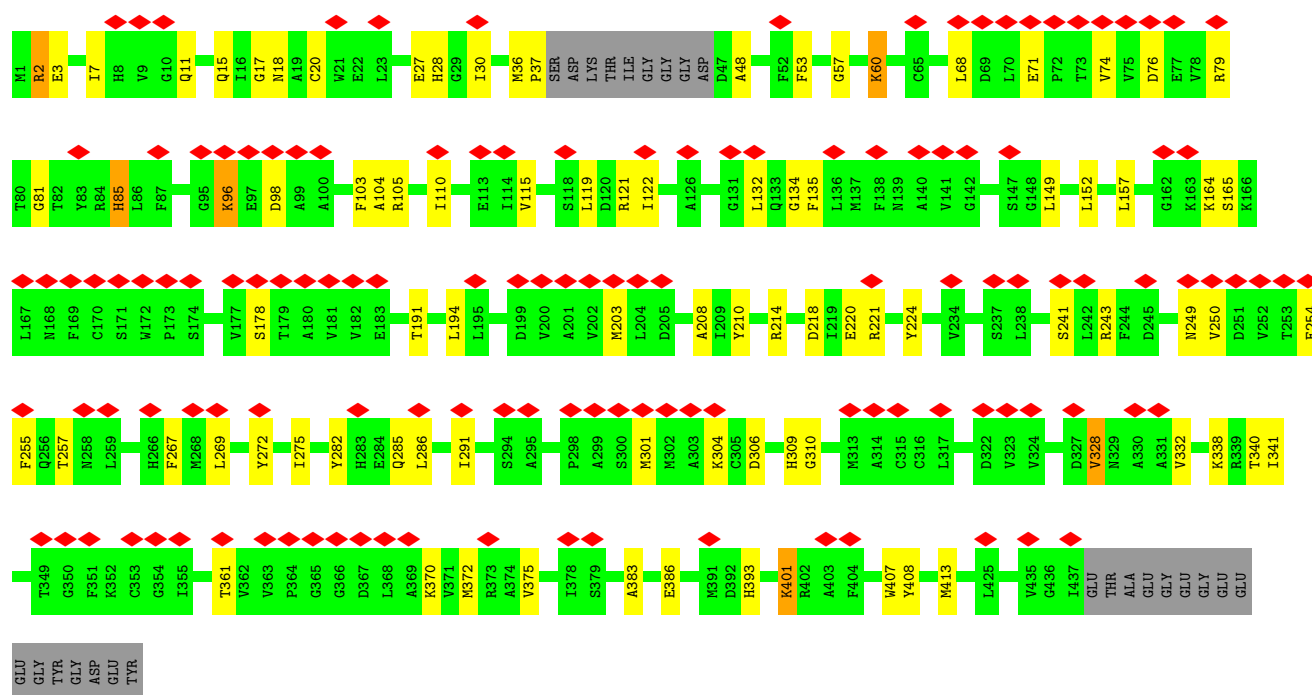
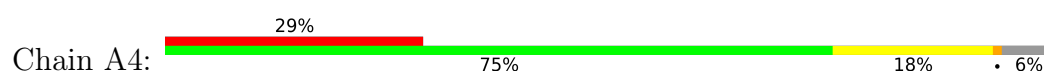
Chain 4: 5%



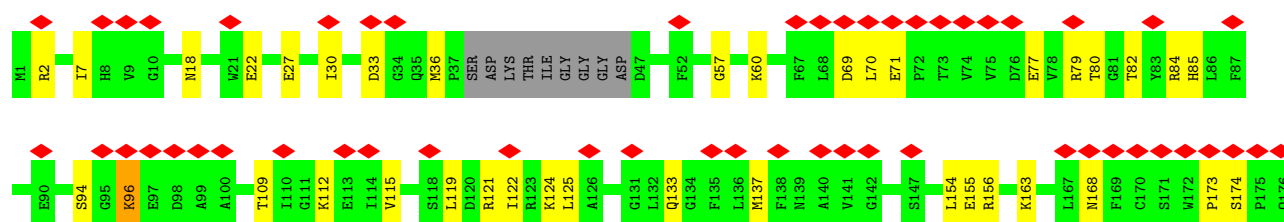
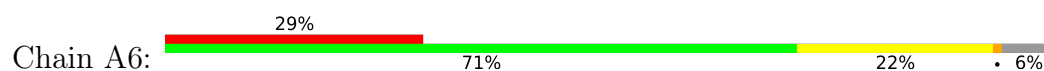


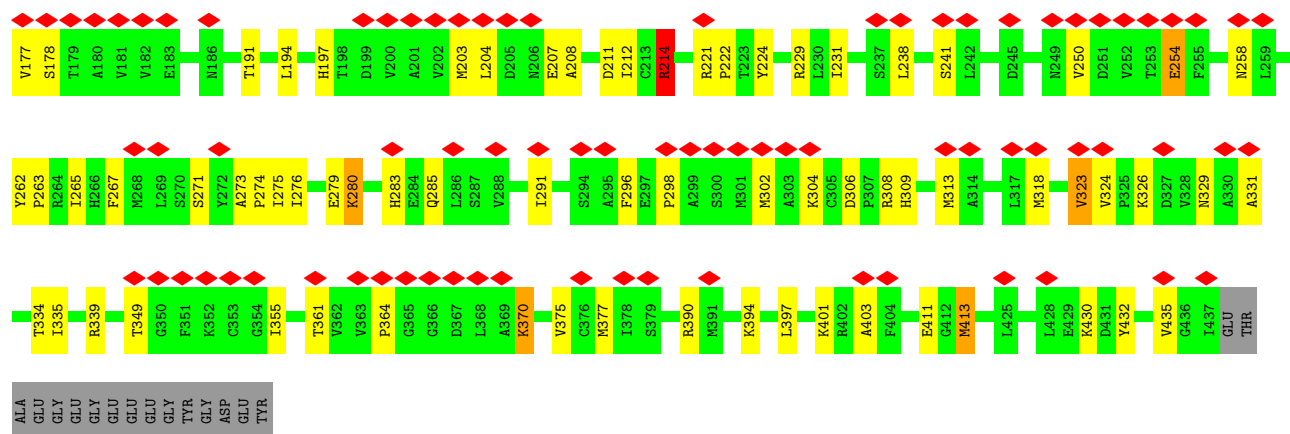


• Molecule 2: Tubulin alpha chain

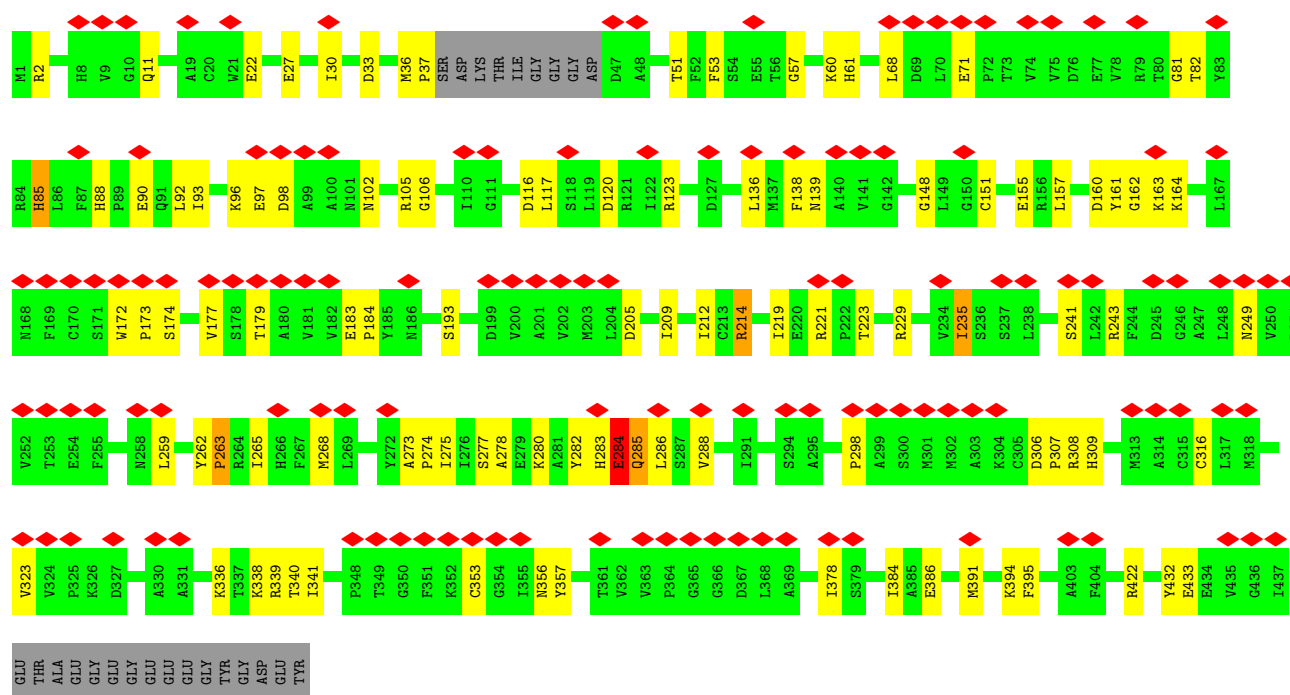
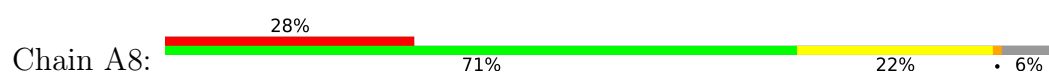


• Molecule 2: Tubulin alpha chain

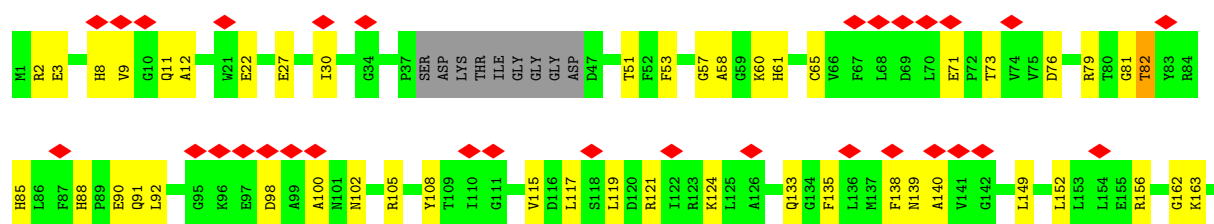
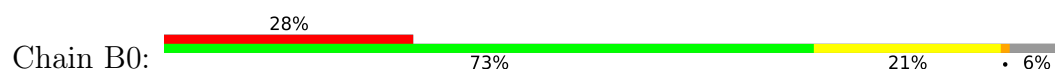


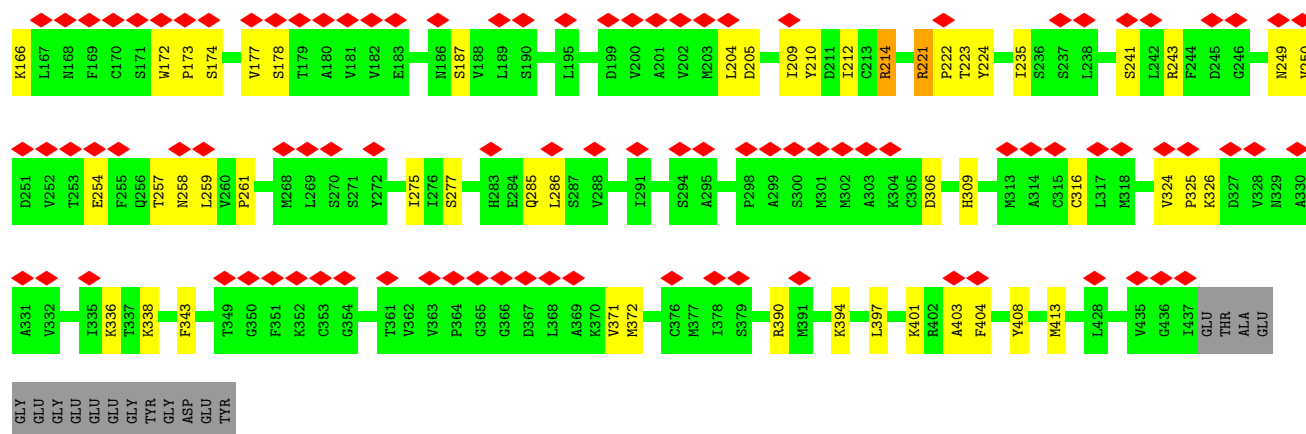


• Molecule 2: Tubulin alpha chain

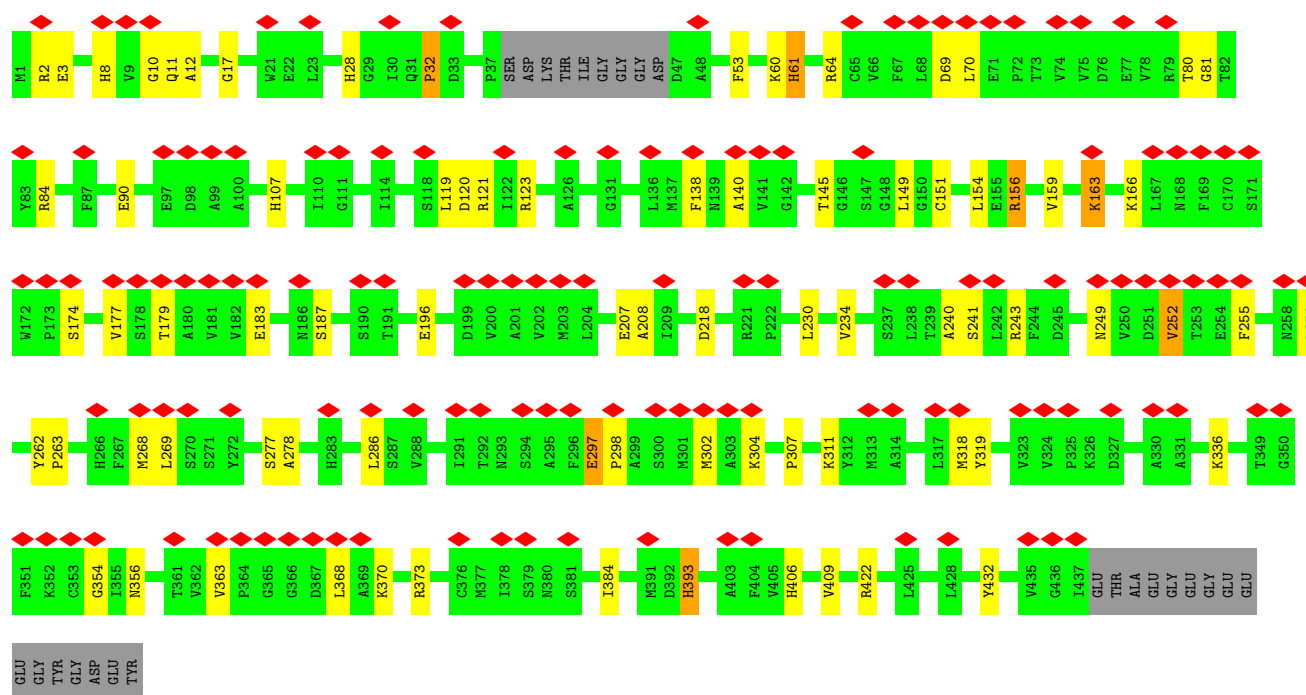
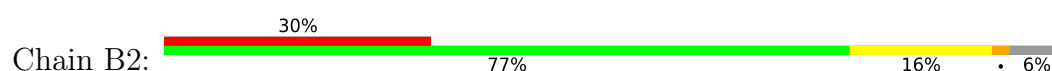


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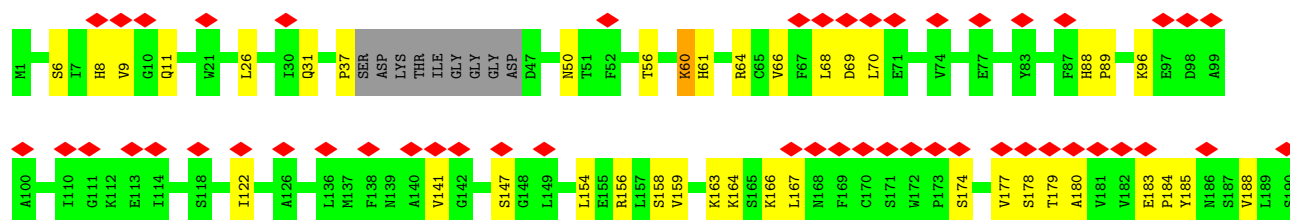
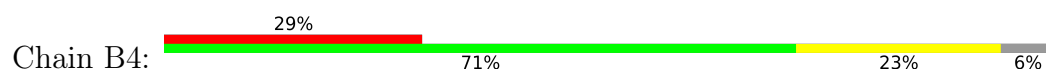


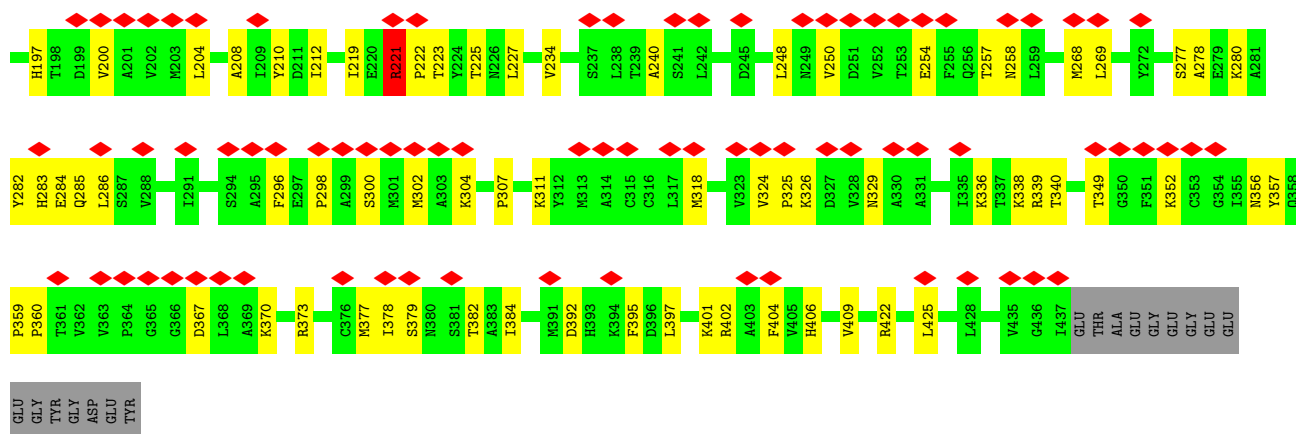


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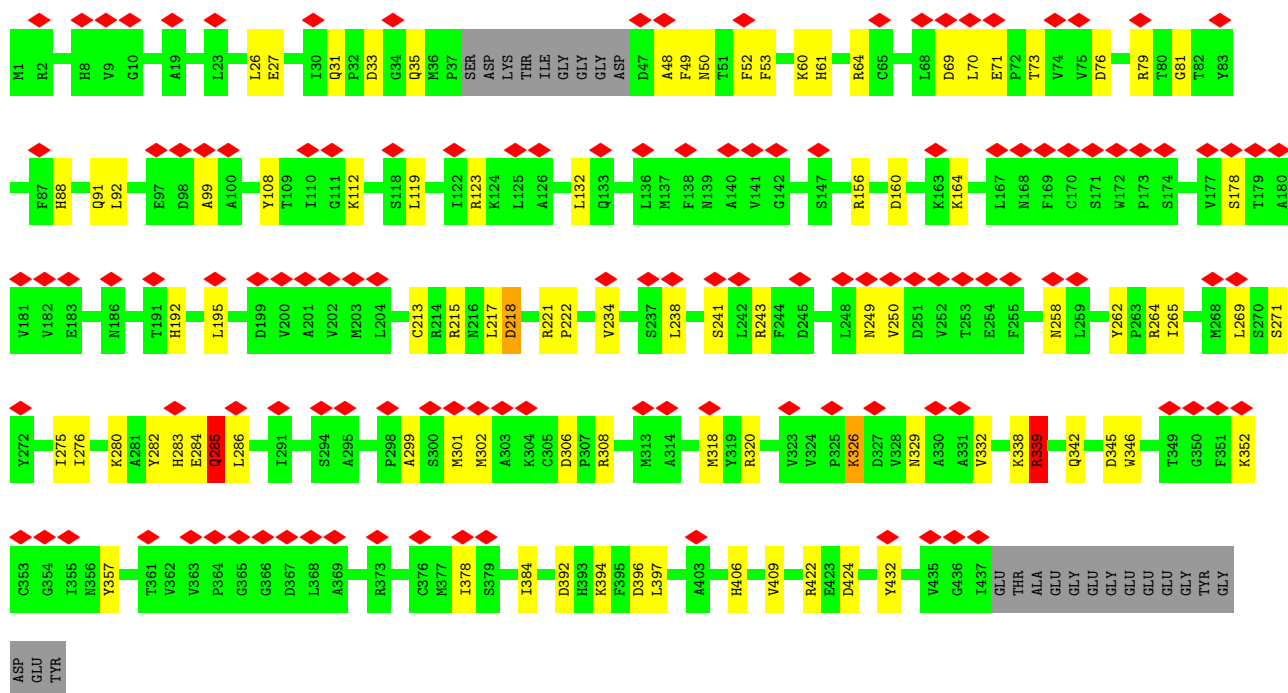
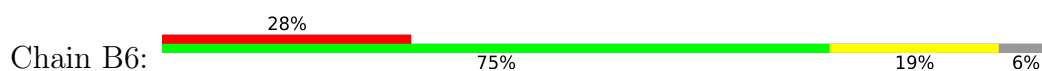


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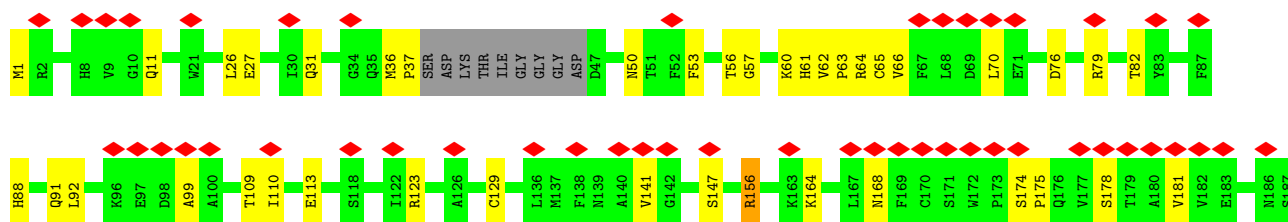
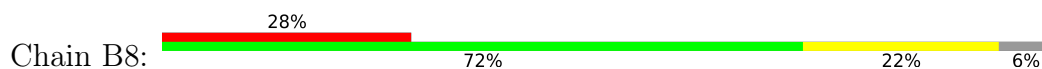


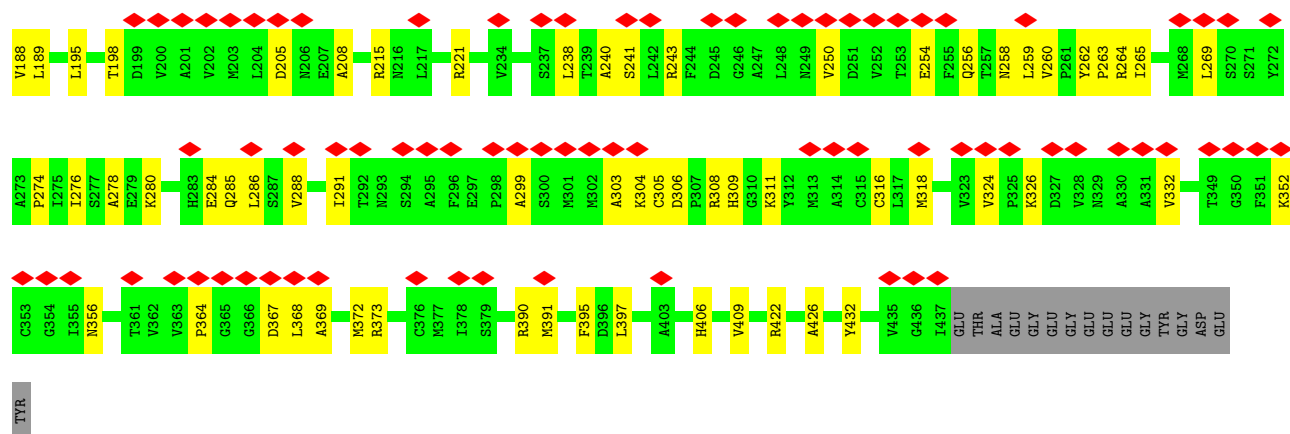


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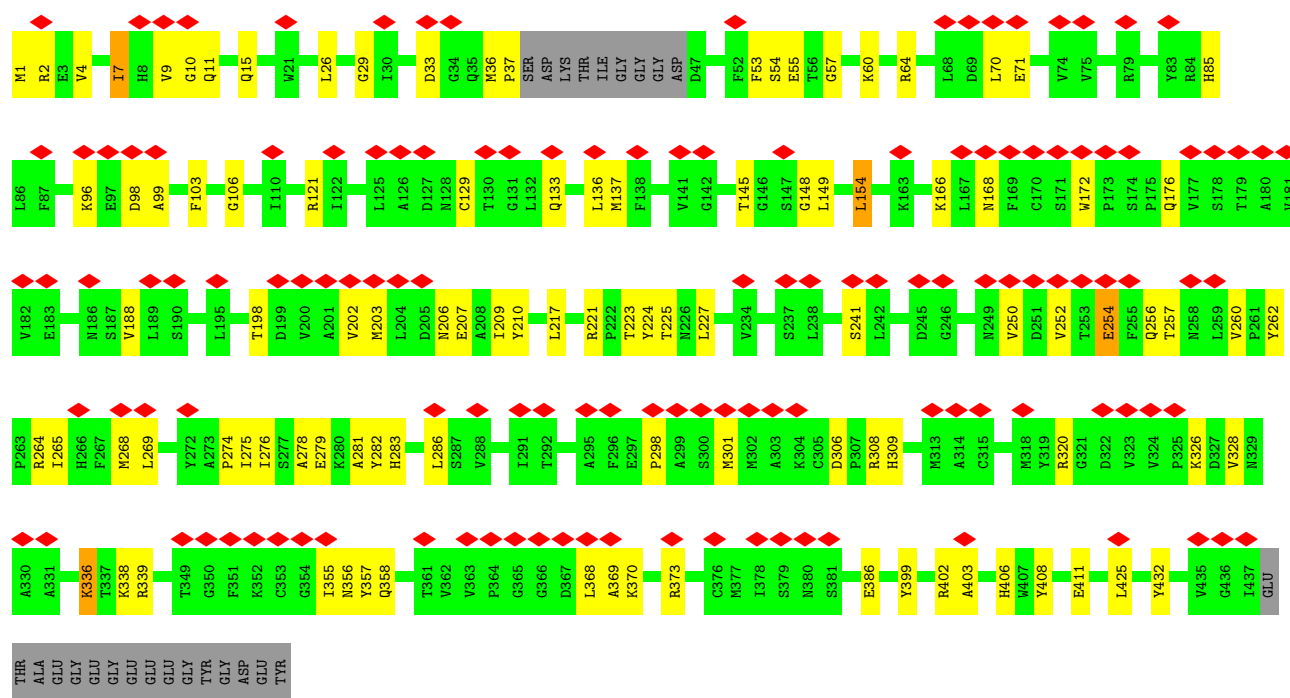
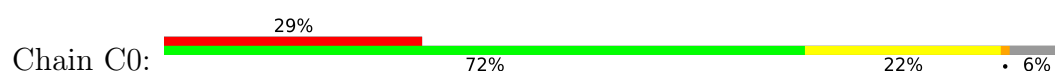


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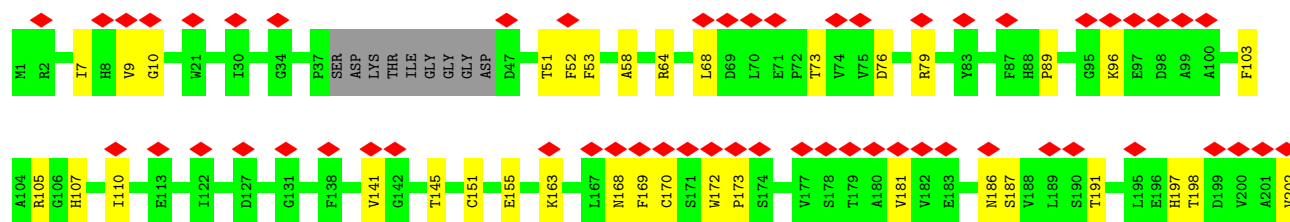
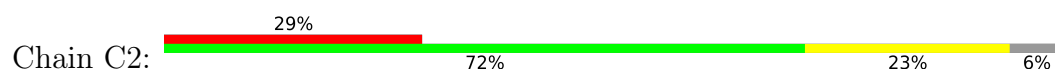


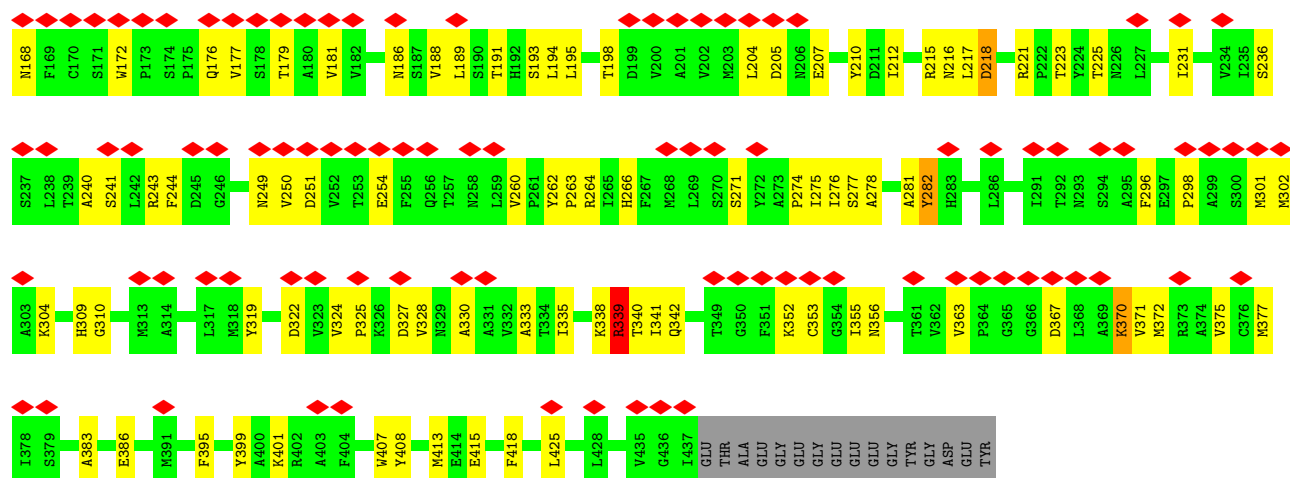


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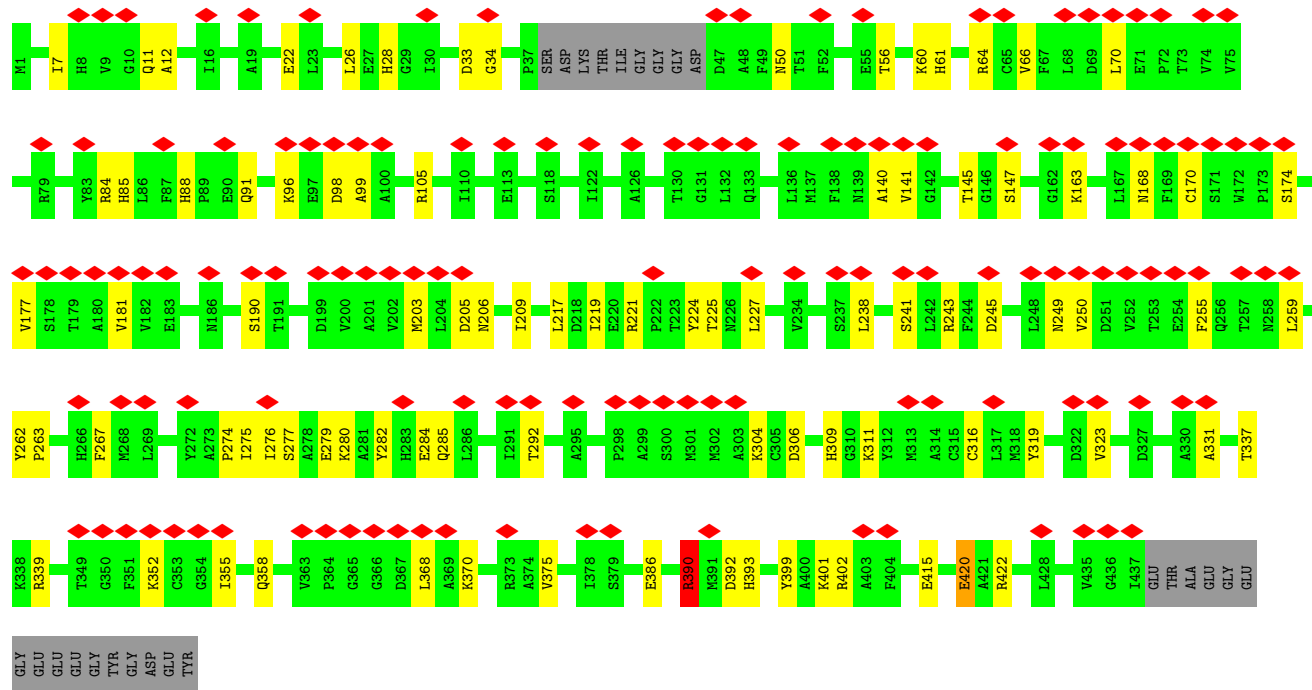
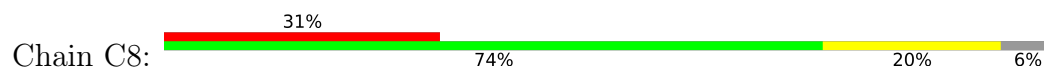


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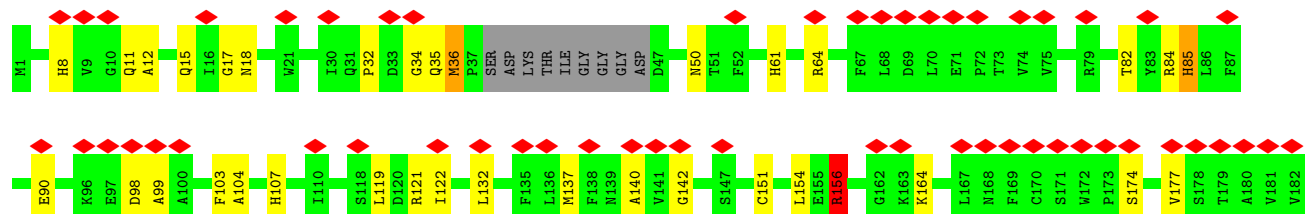
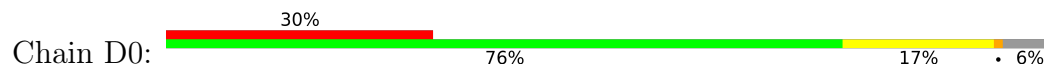


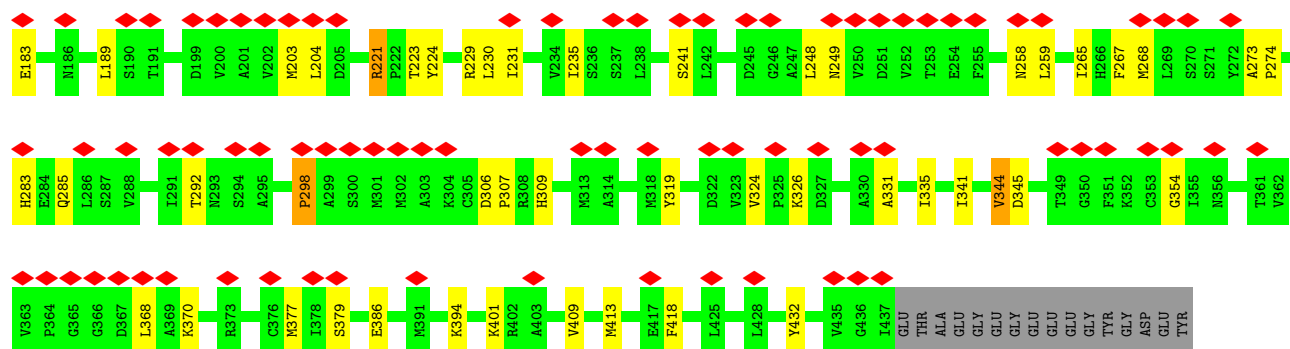


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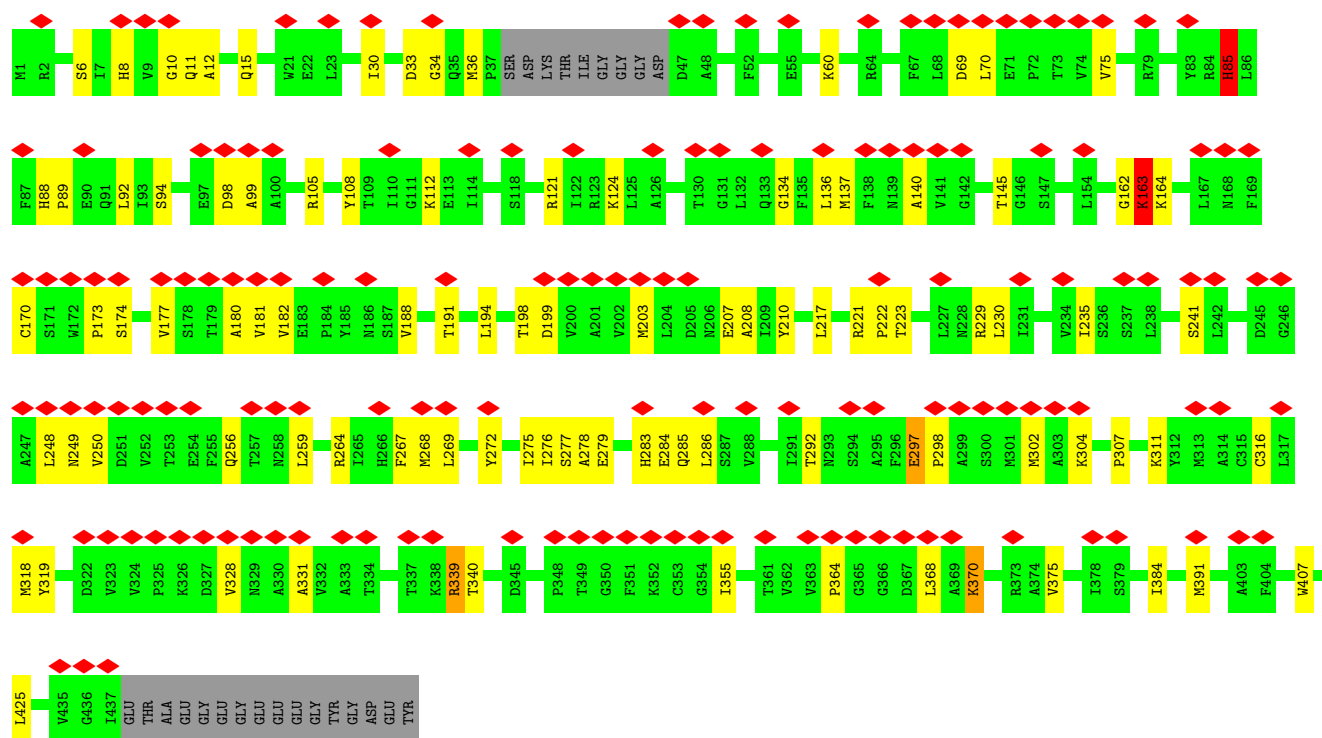
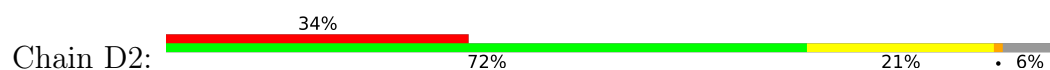


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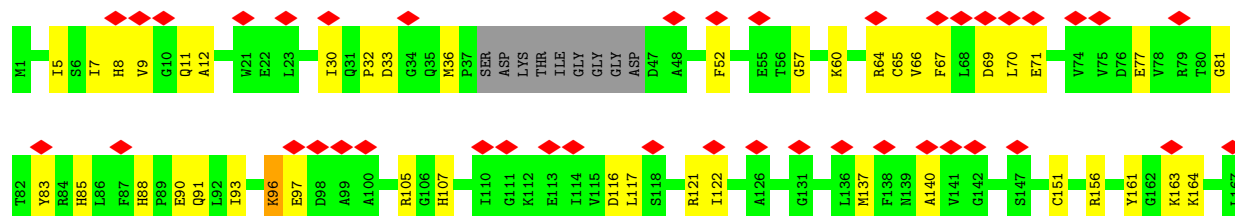
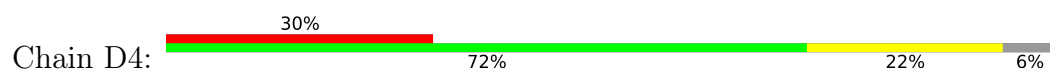


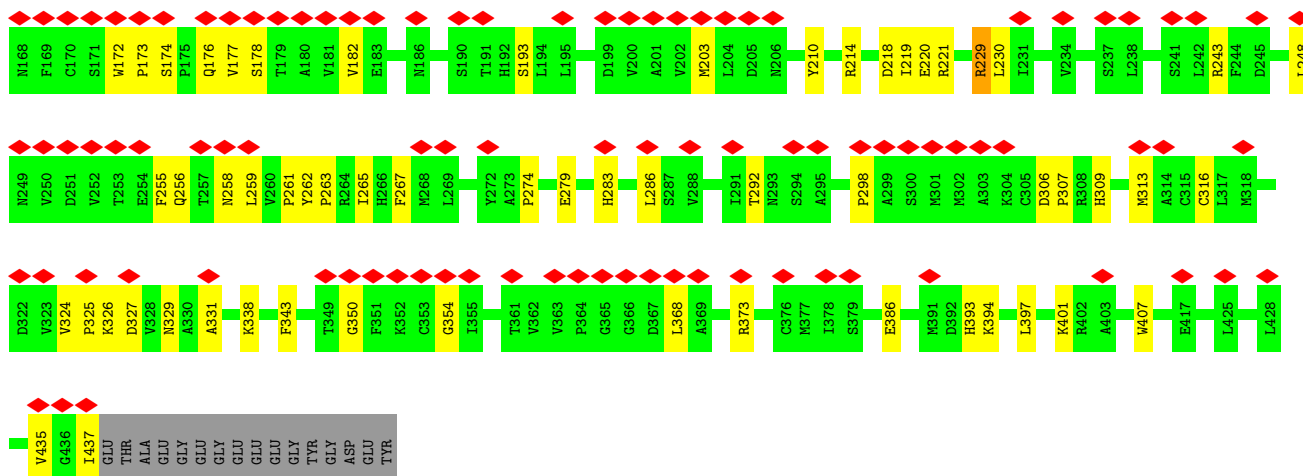


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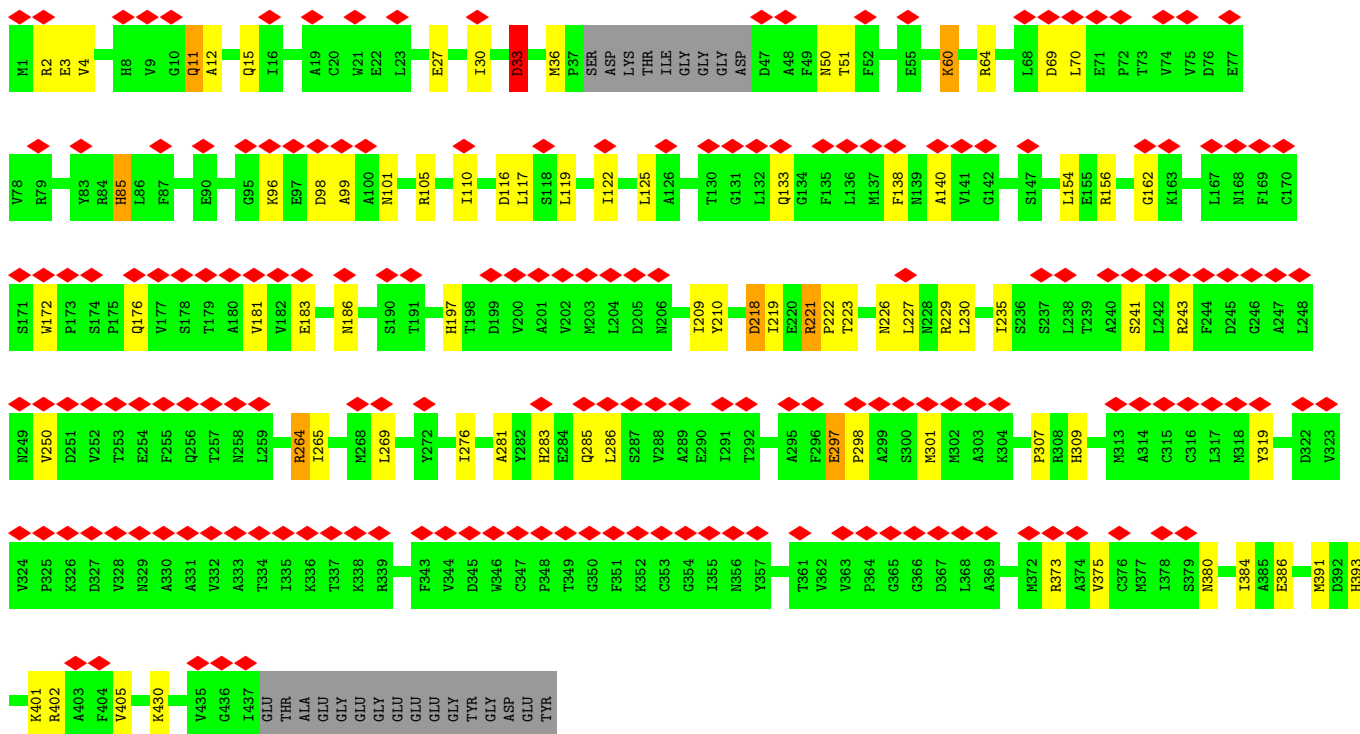
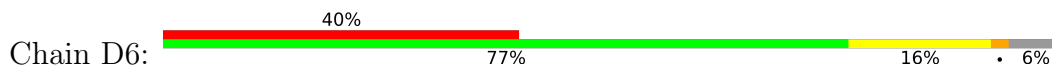


• Molecule 2: Tubulin alpha chain

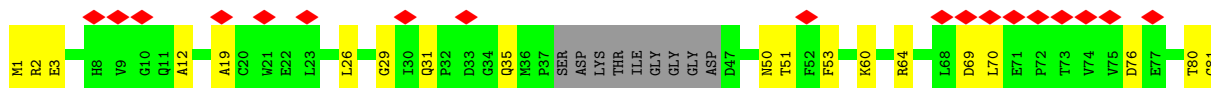
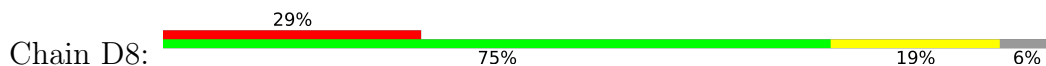


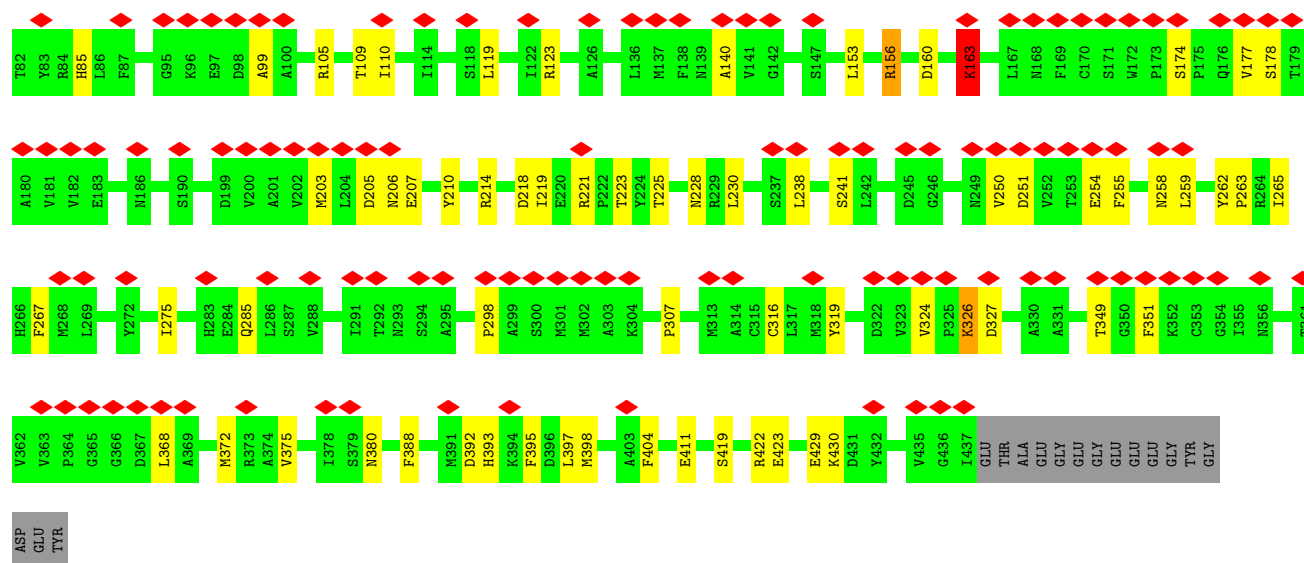


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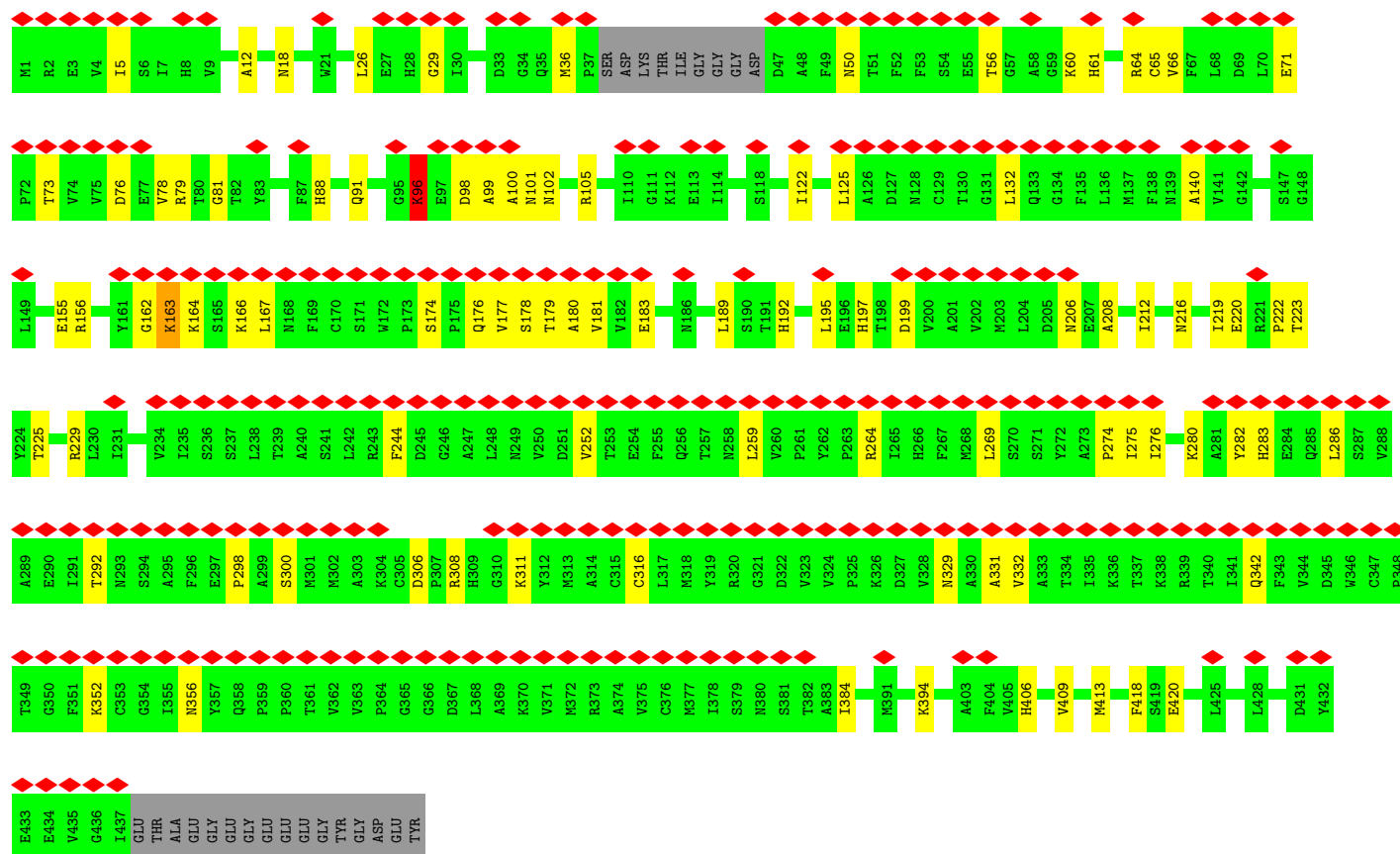
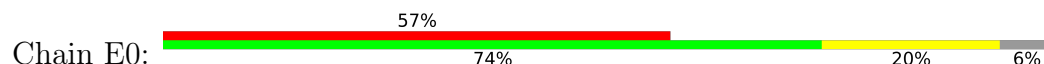


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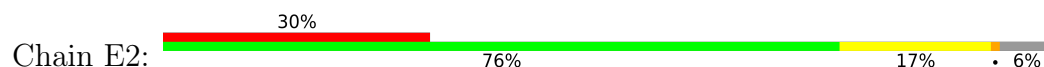




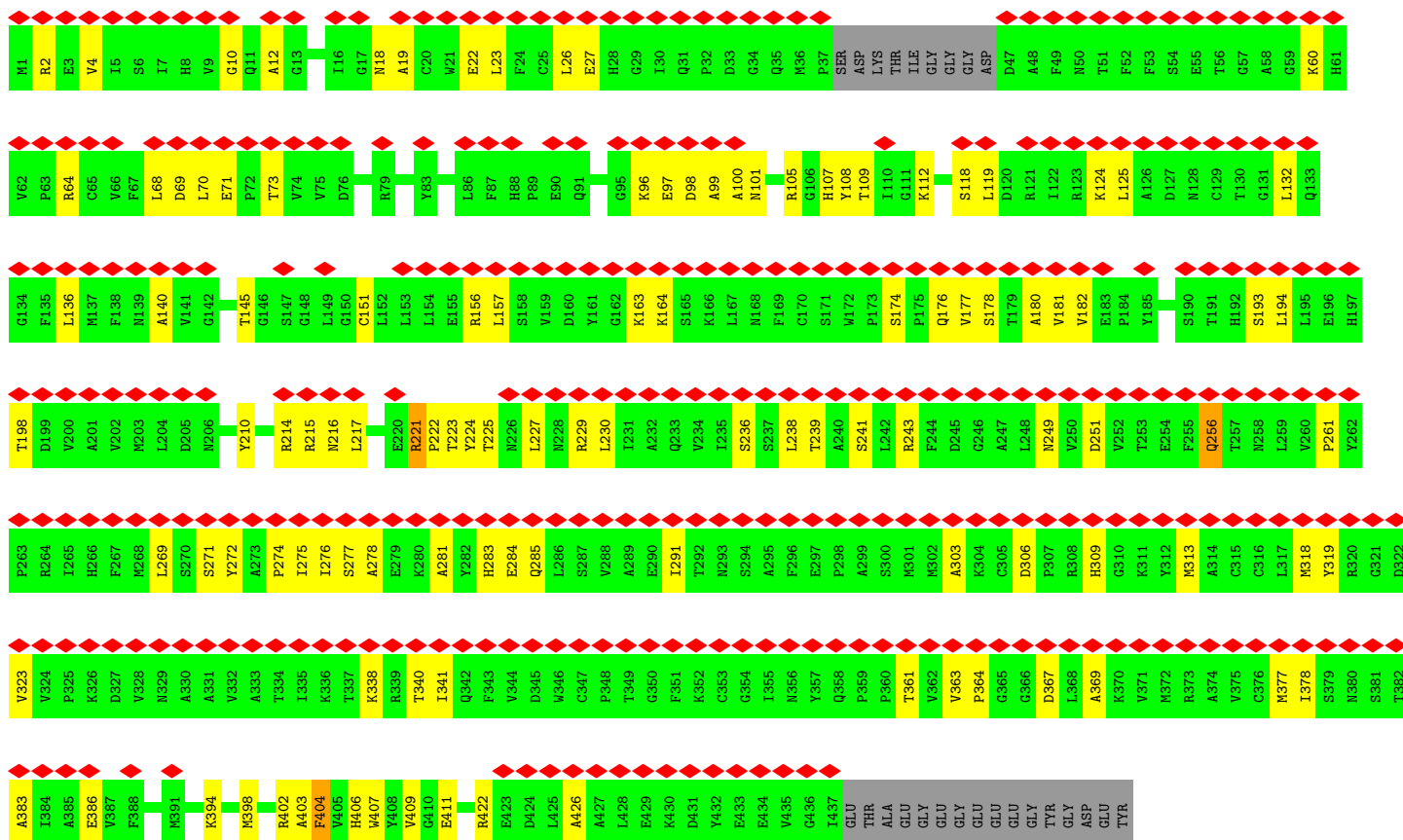
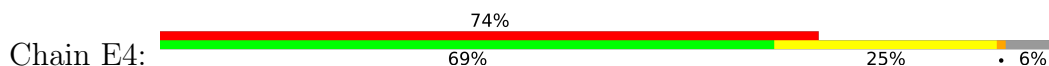
• Molecule 2: Tubulin alpha chain



• Molecule 2: Tubulin alpha chain

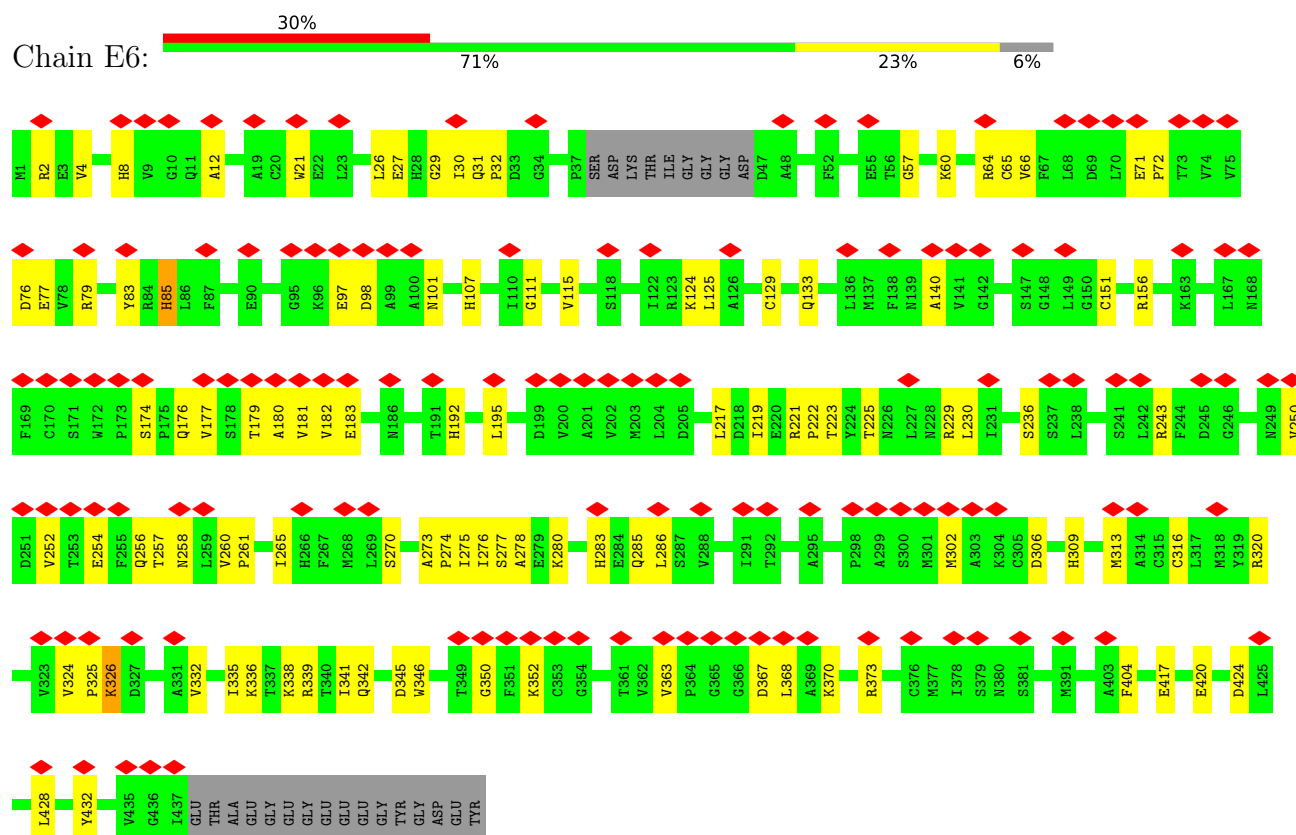


- Molecule 2: Tubulin alpha chain



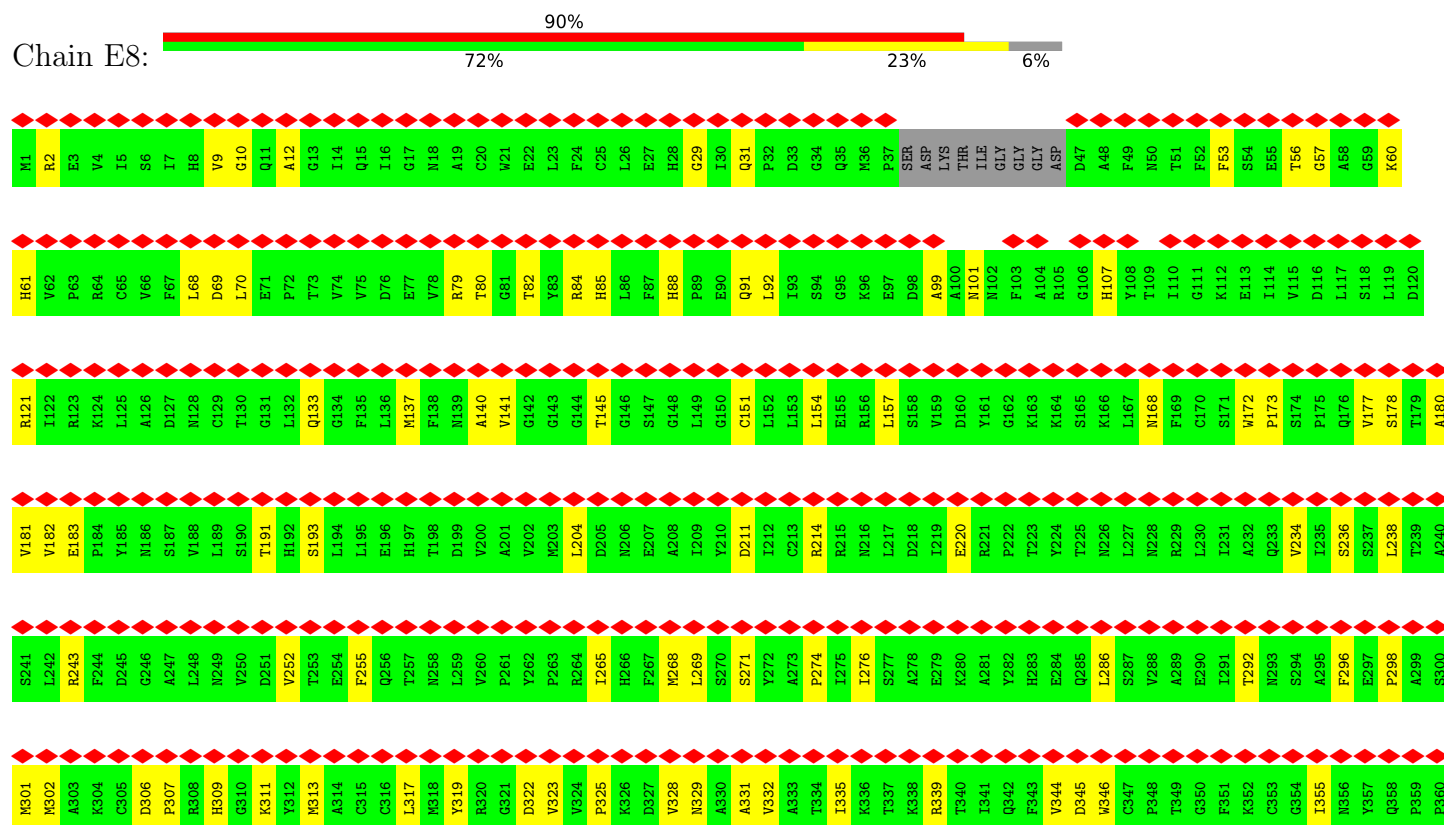
- Molecule 2: Tubulin alpha chain

Chain E6:



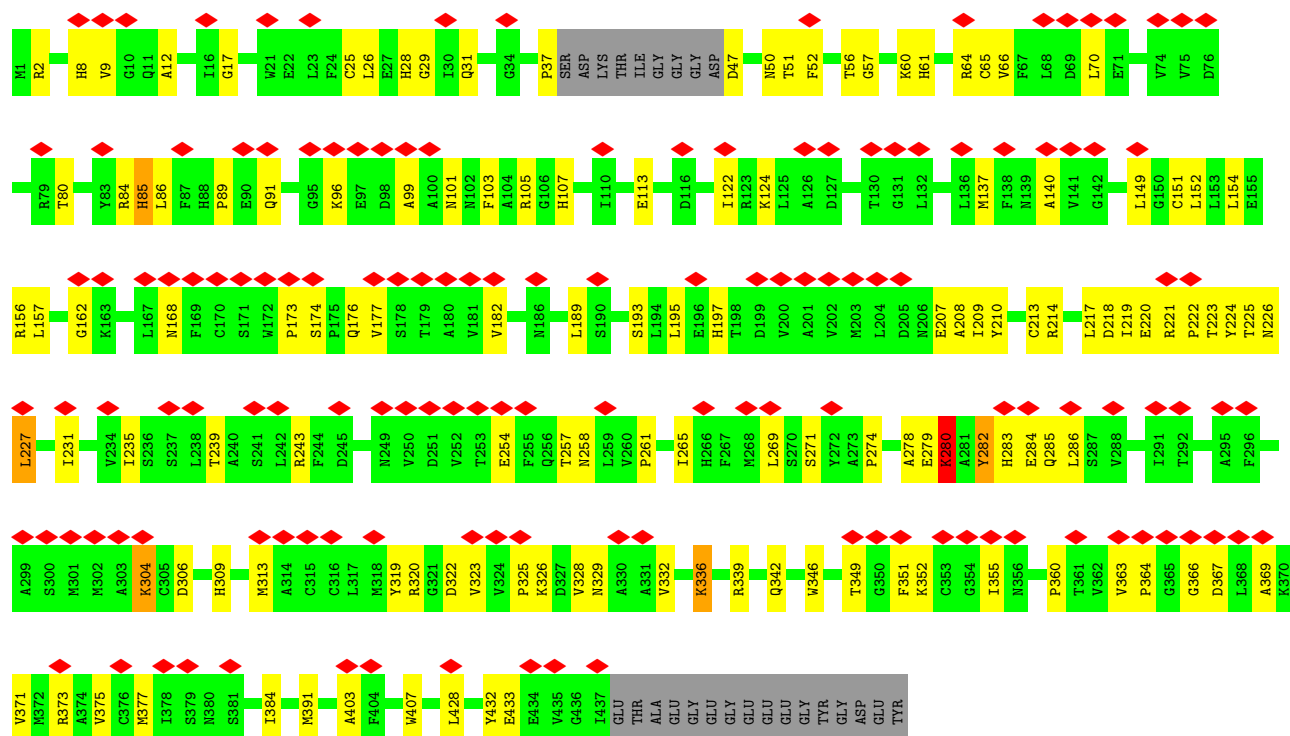
- Molecule 2: Tubulin alpha chain

Chain E8:

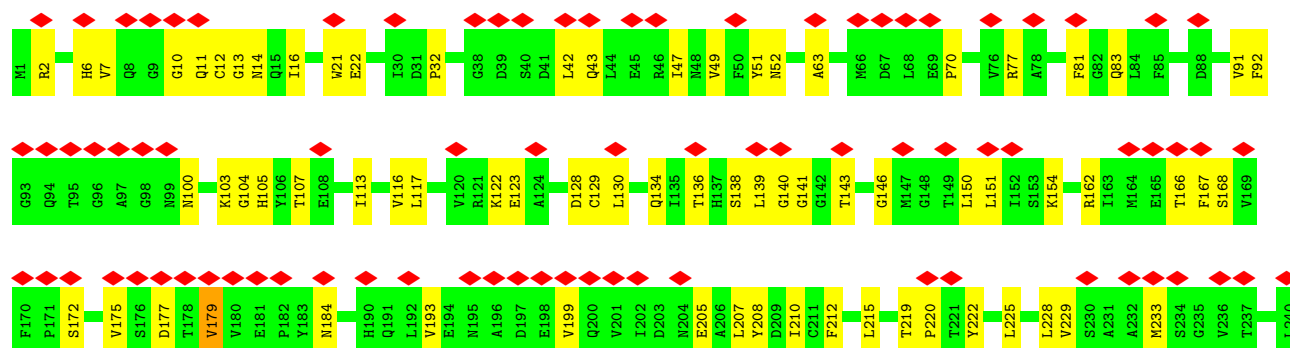


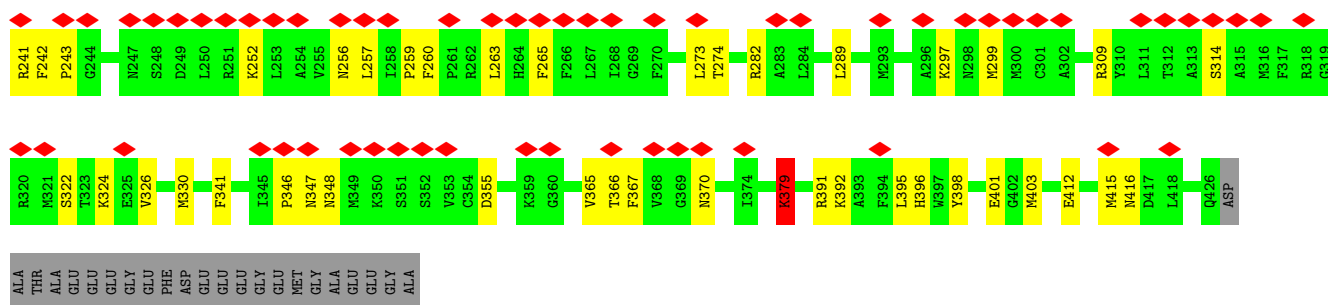


• Molecule 2: Tubulin alpha chain

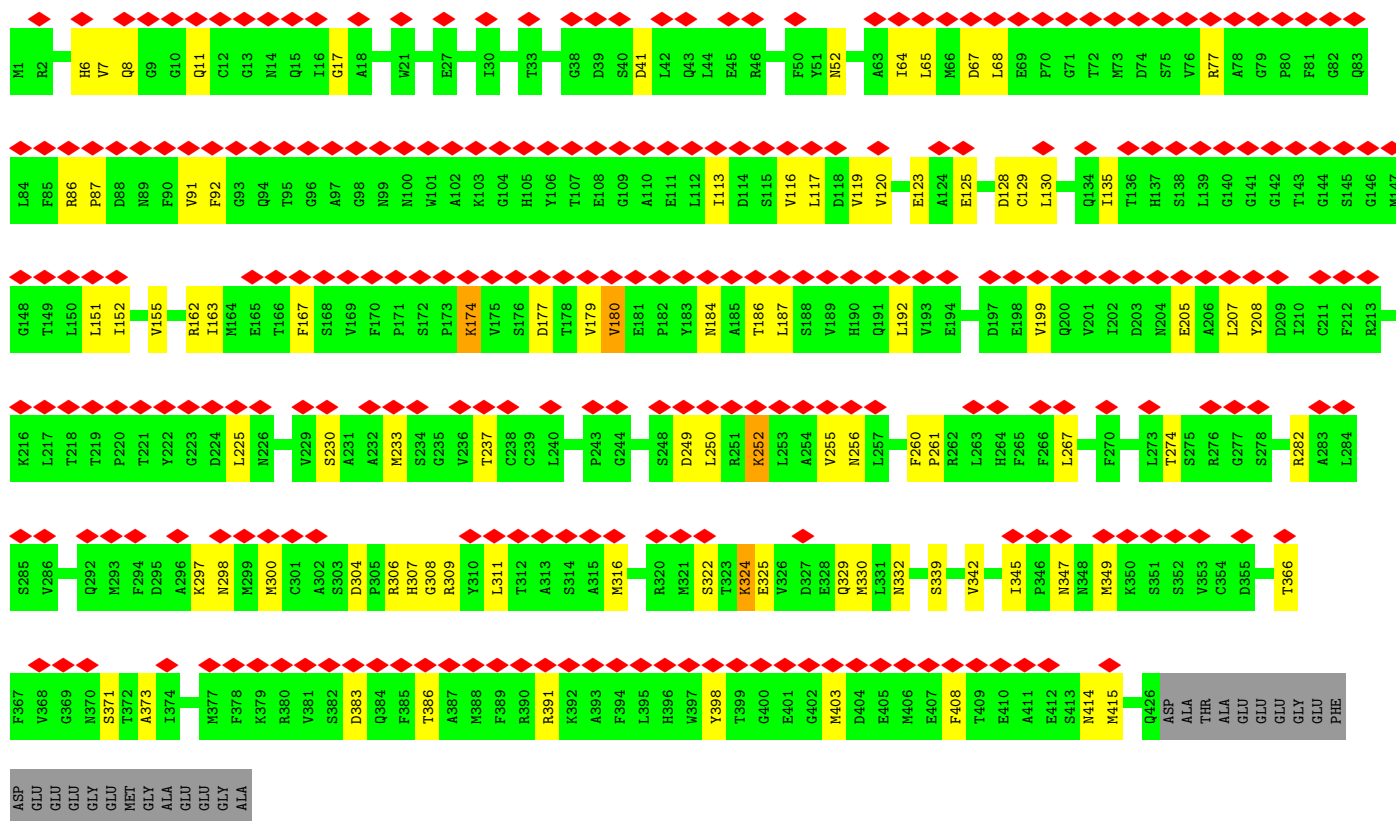
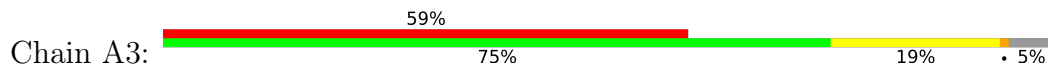


• Molecule 3: Tubulin beta chain

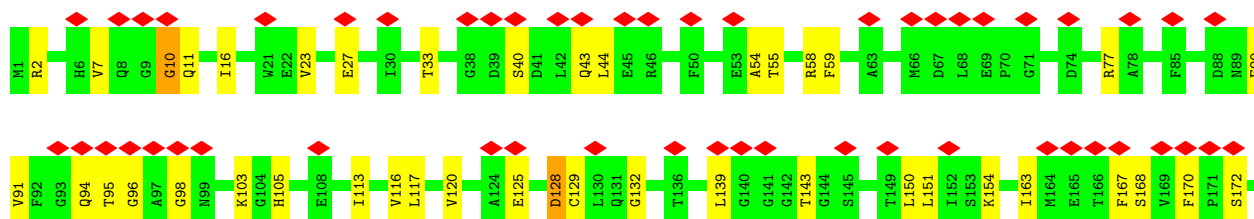
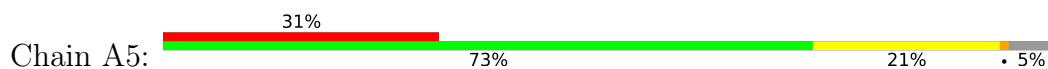


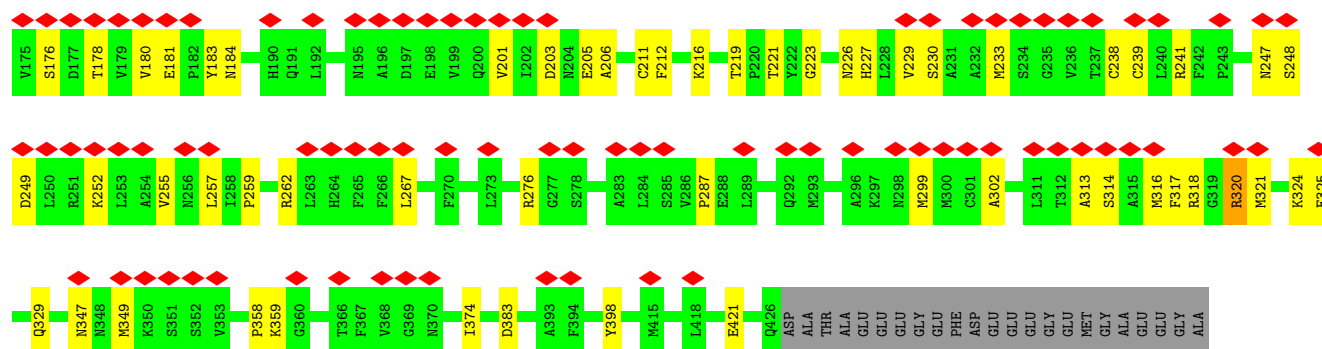


• Molecule 3: Tubulin beta chain

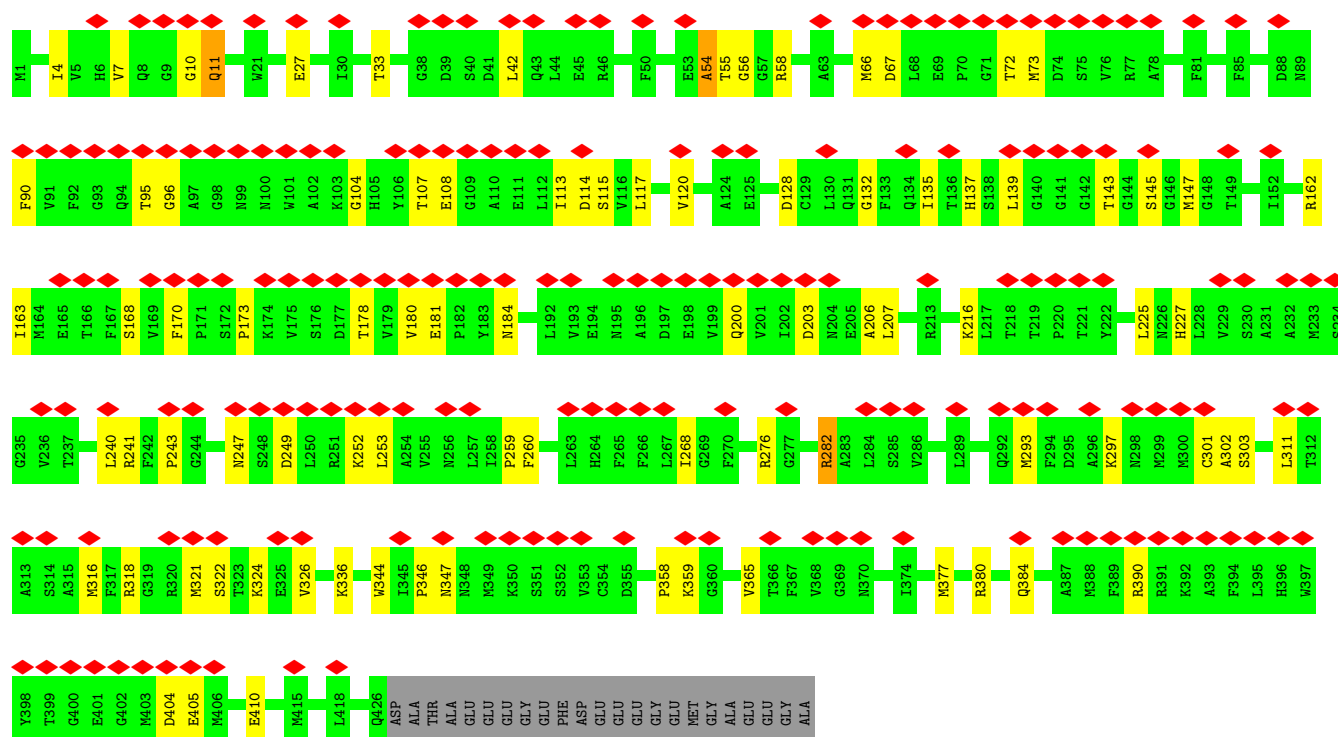
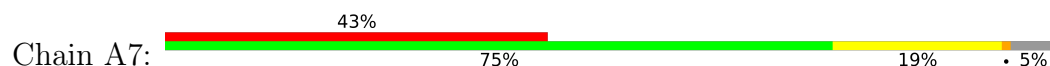


• Molecule 3: Tubulin beta chain

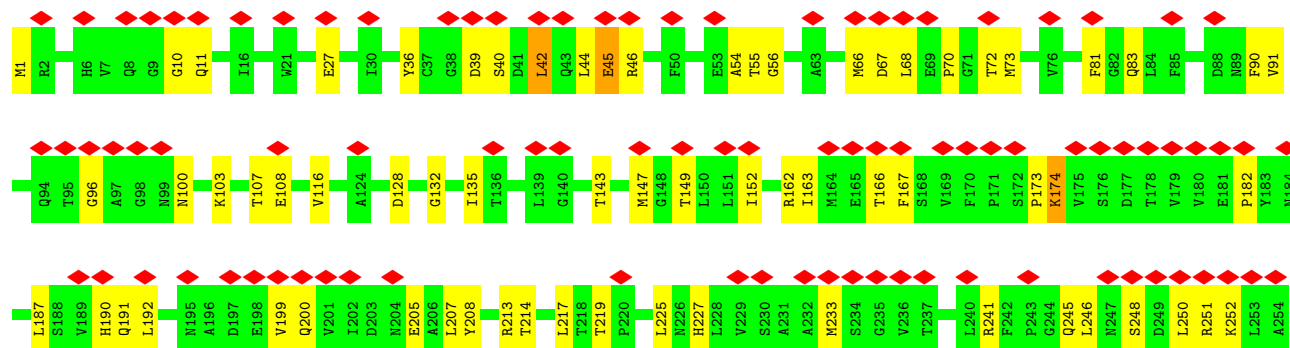


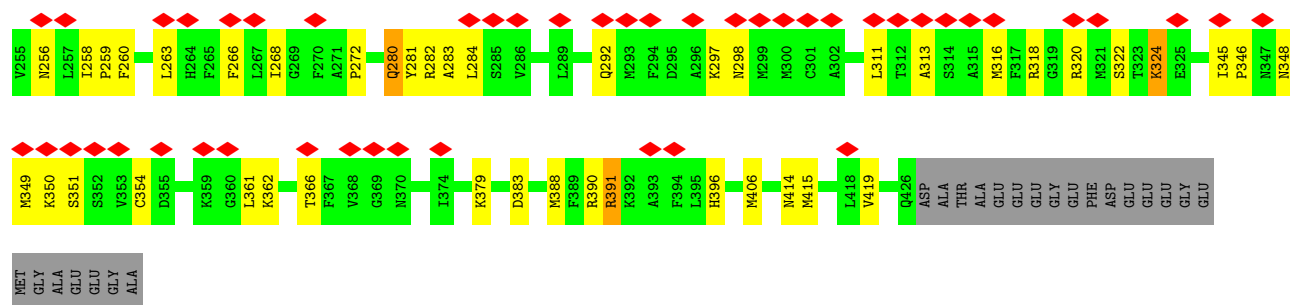


• Molecule 3: Tubulin beta chain

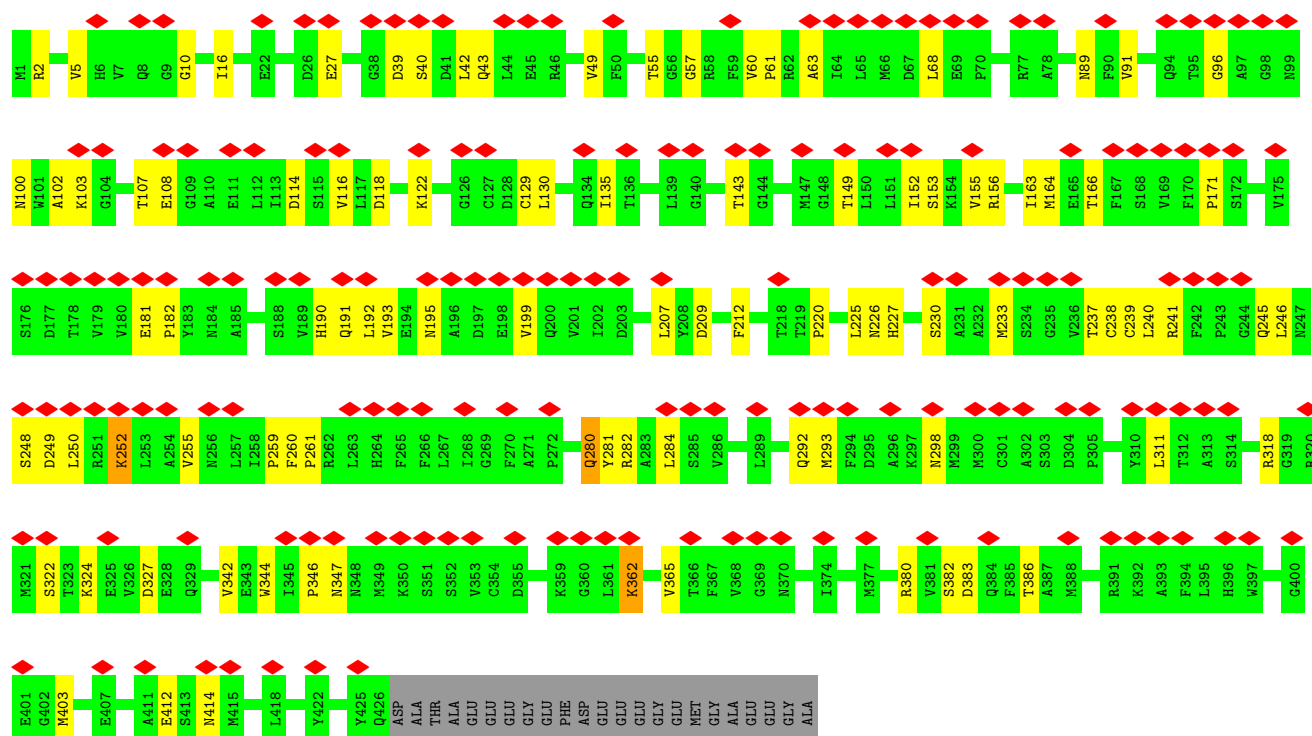
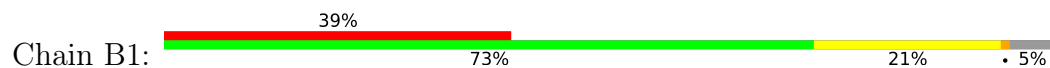


• Molecule 3: Tubulin beta chain

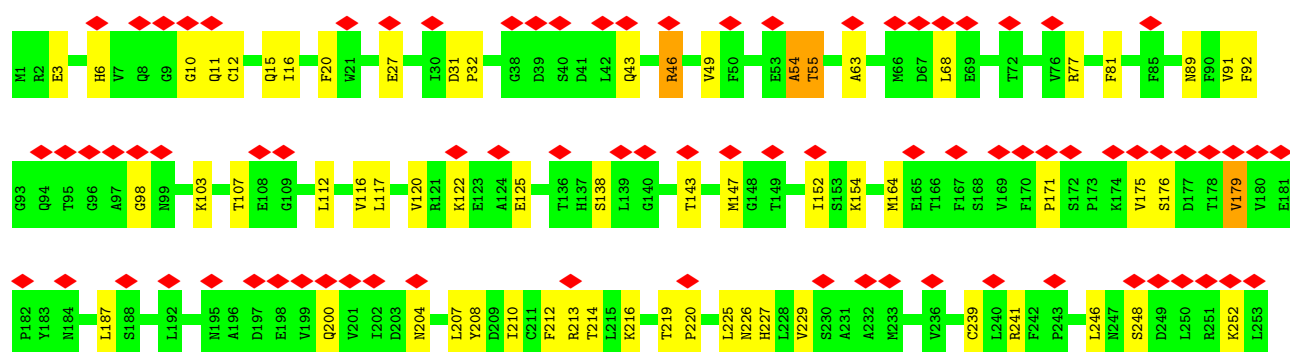
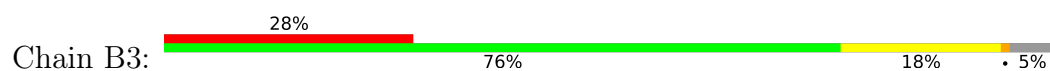


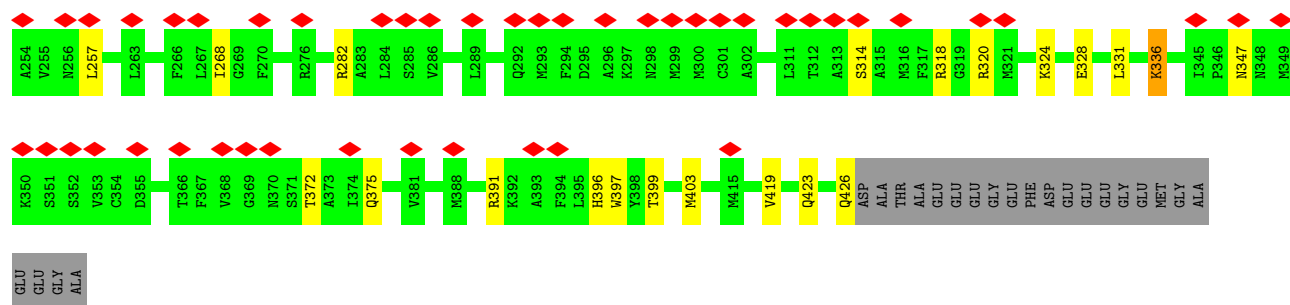


• Molecule 3: Tubulin beta chain

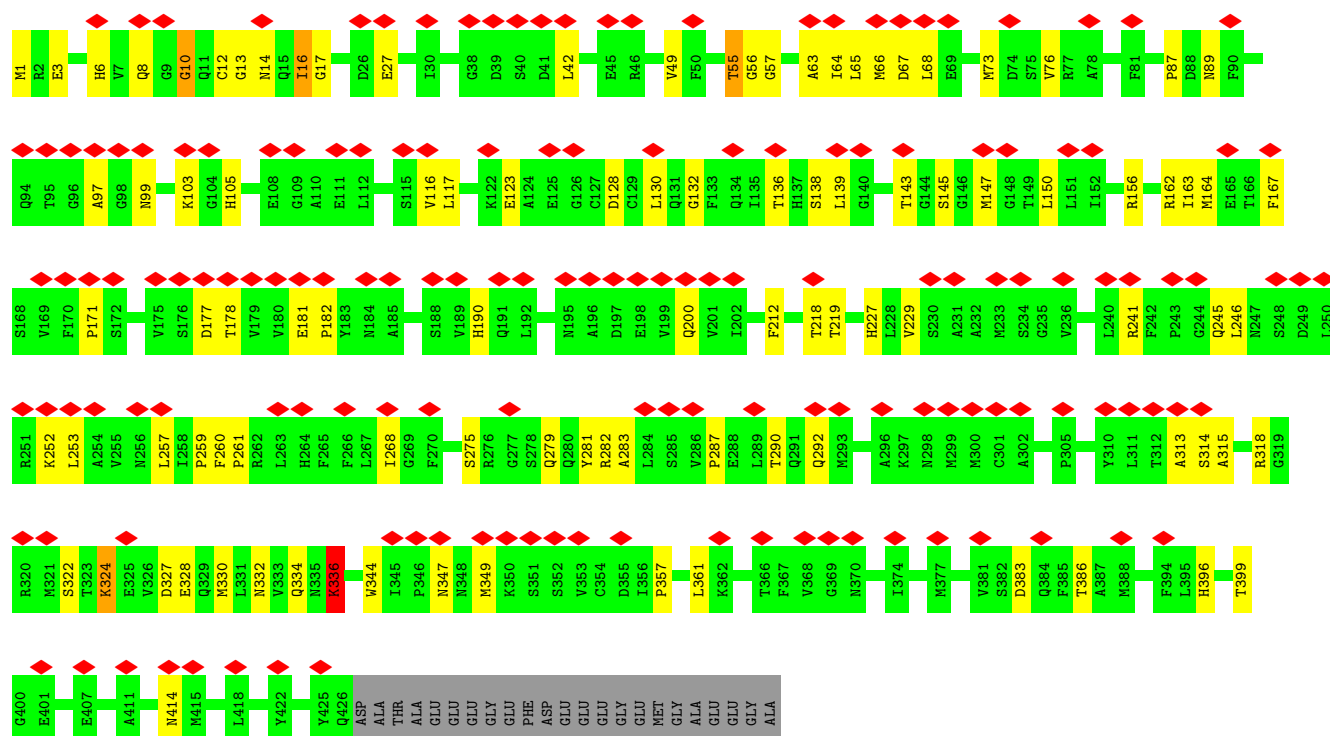
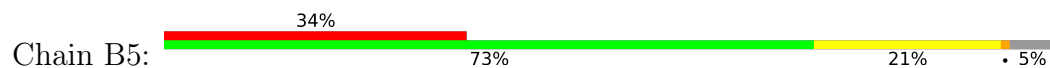


• Molecule 3: Tubulin beta chain

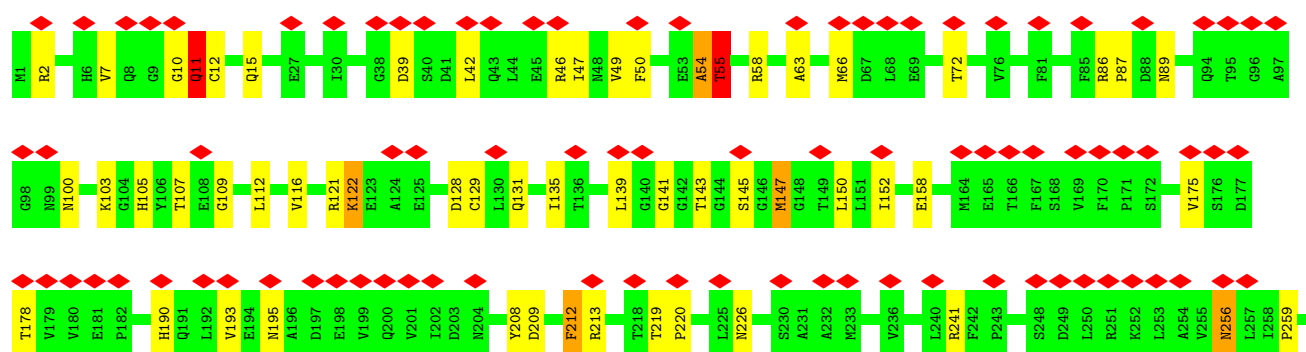
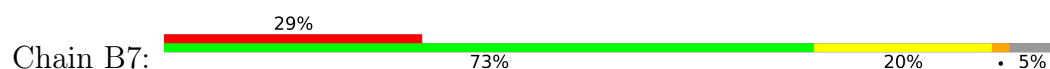


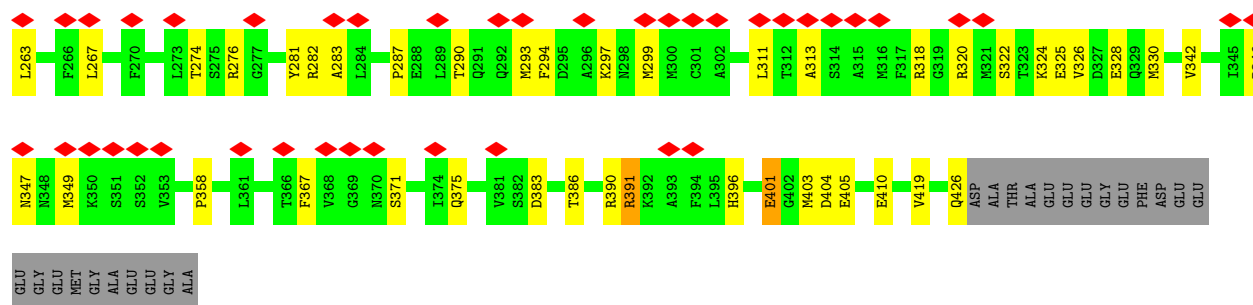


• Molecule 3: Tubulin beta chain

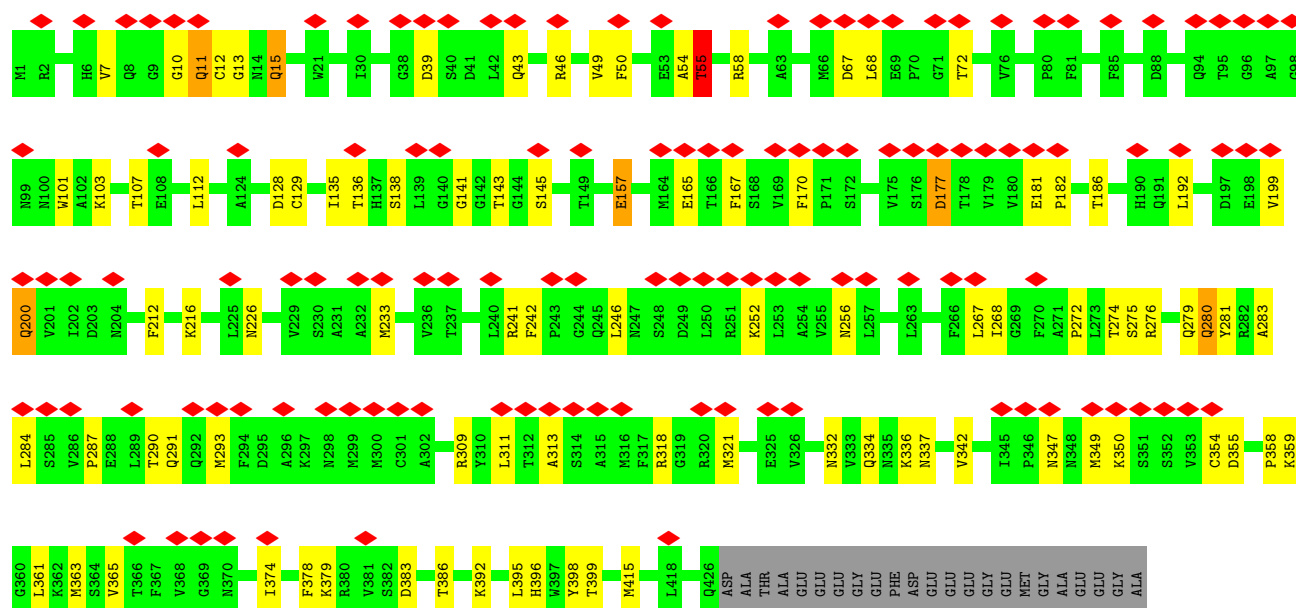
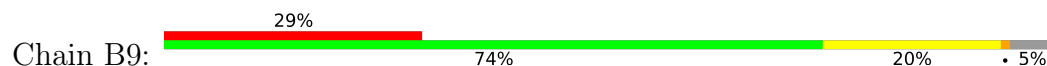


• Molecule 3: Tubulin beta chain

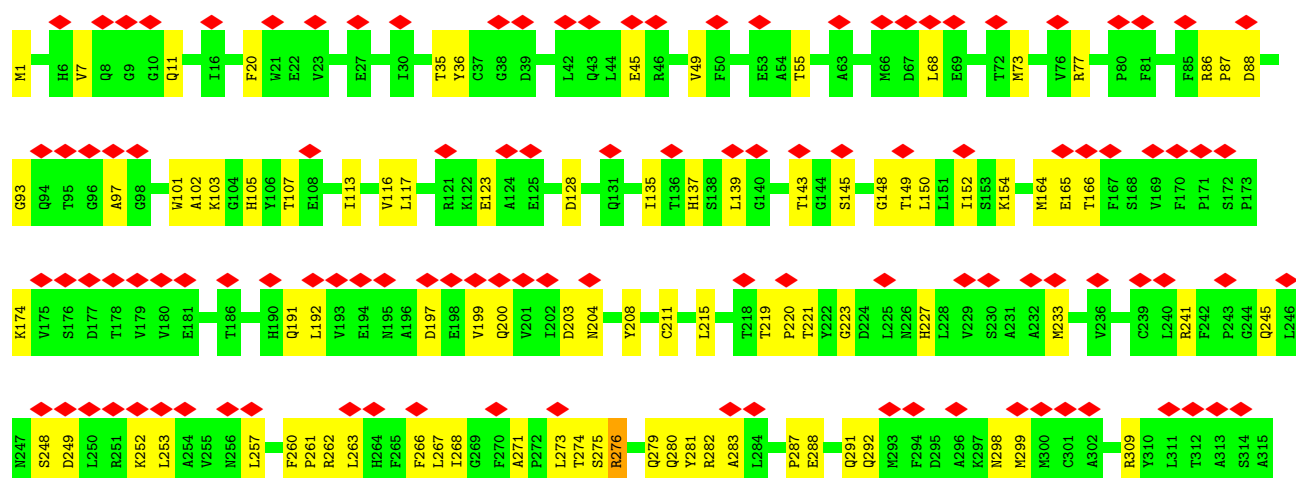


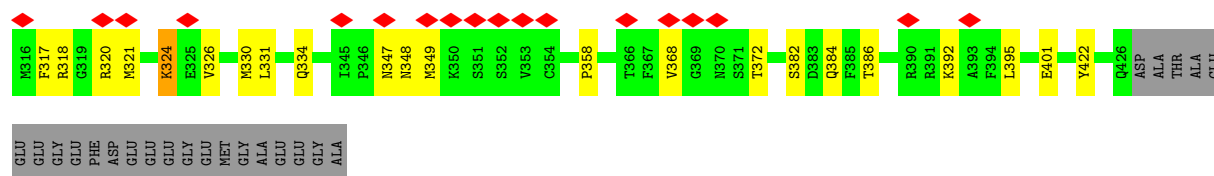


• Molecule 3: Tubulin beta chain

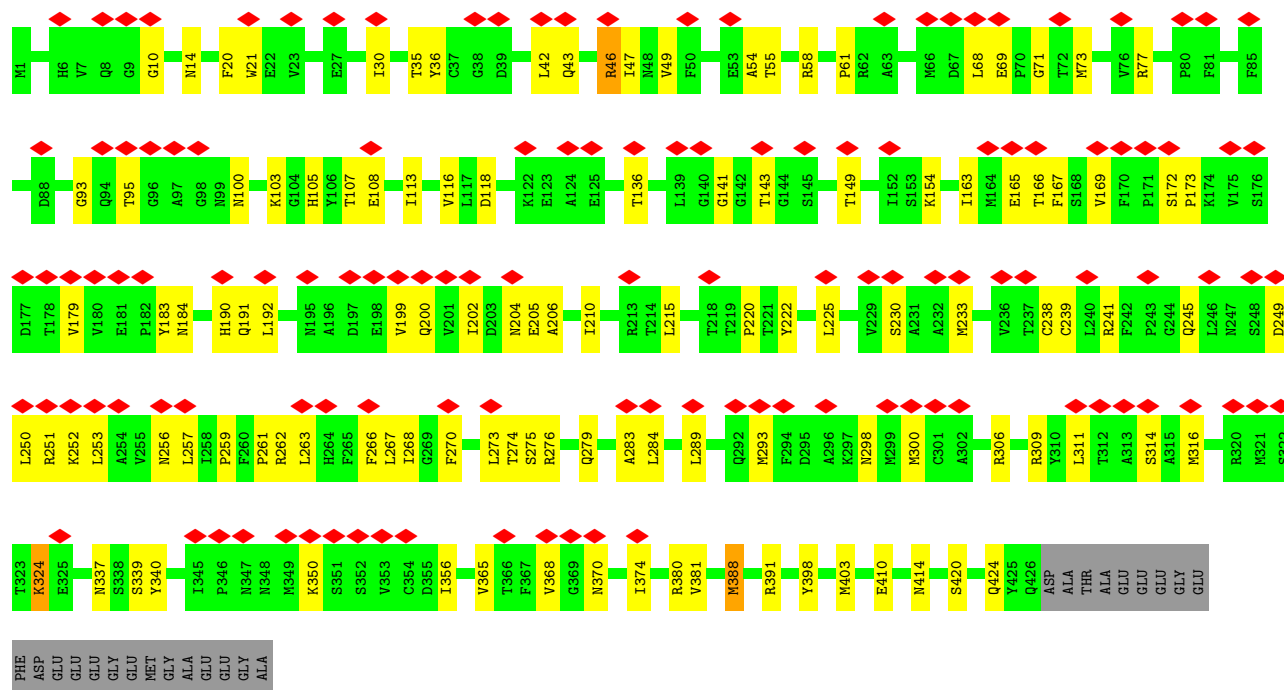


• Molecule 3: Tubulin beta chain

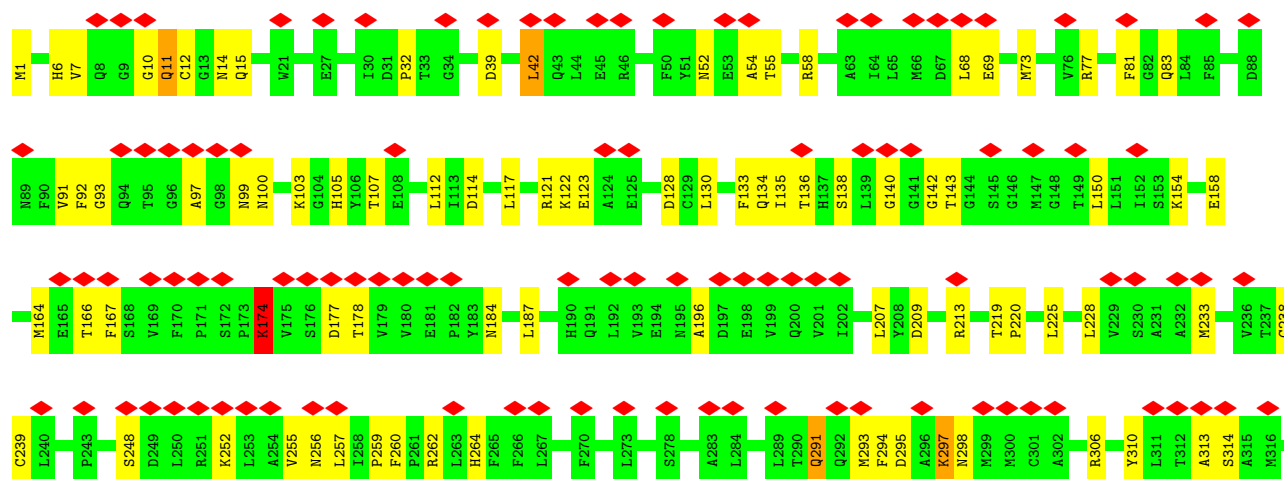
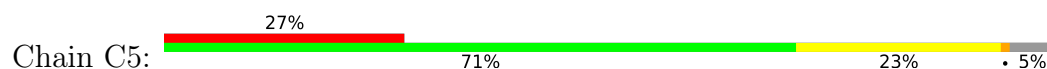


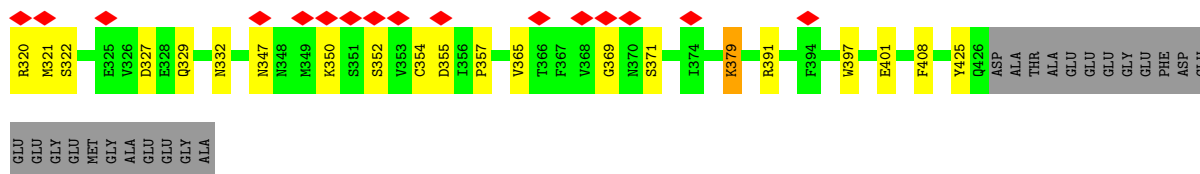


• Molecule 3: Tubulin beta chain

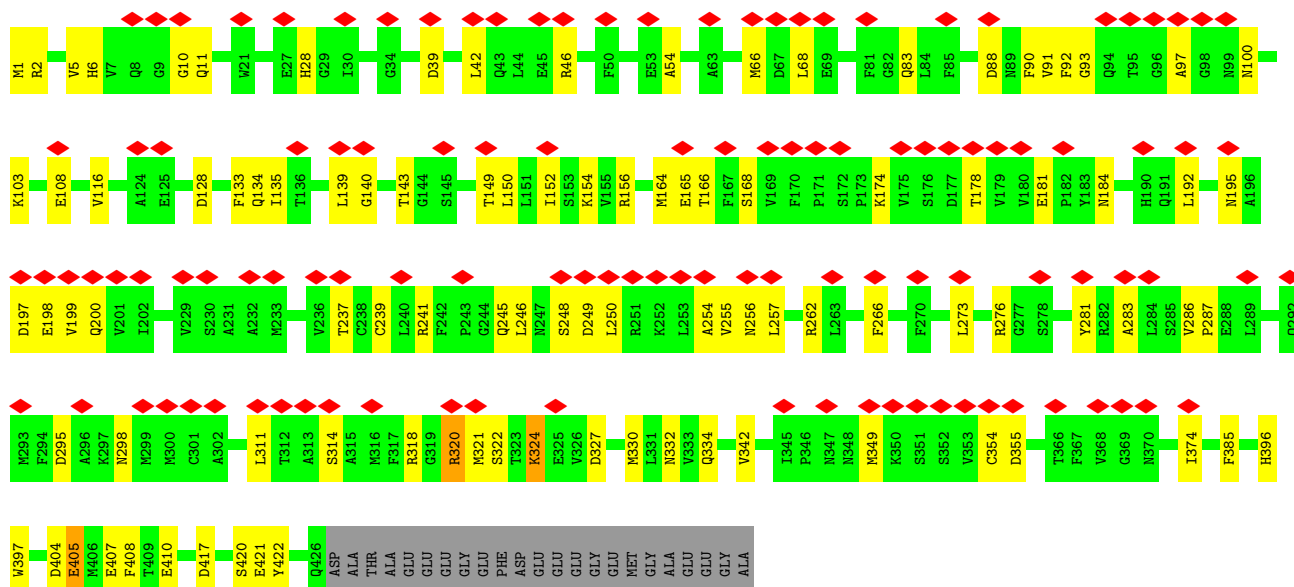
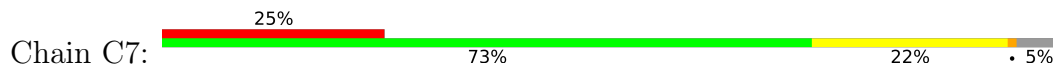


• Molecule 3: Tubulin beta chain

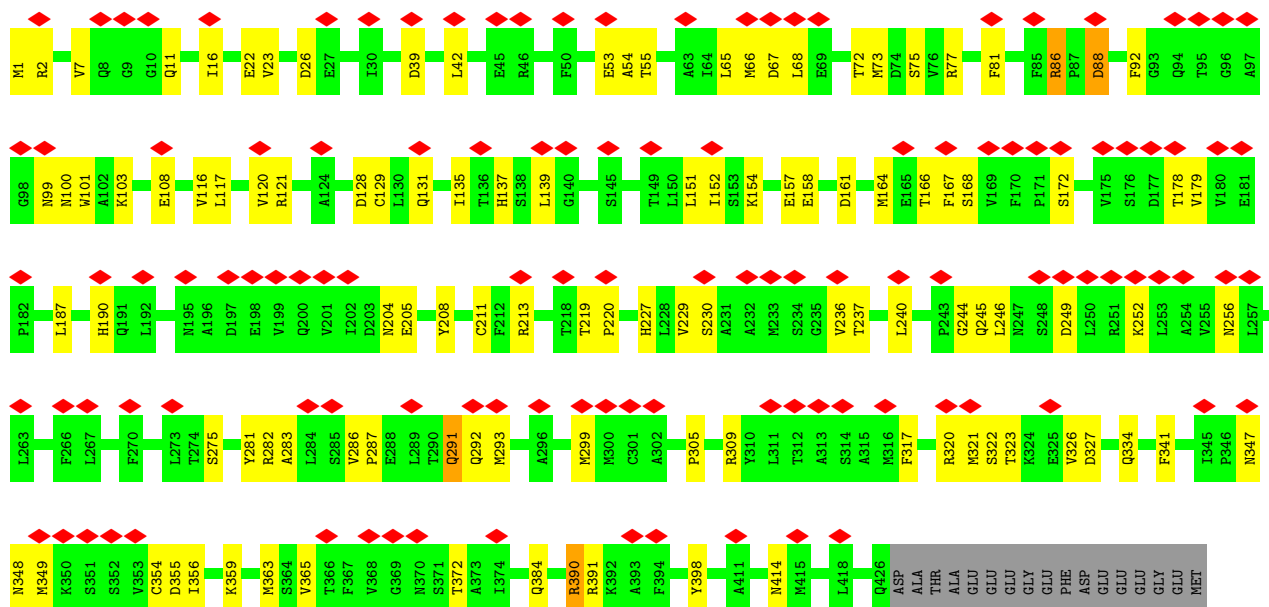




• Molecule 3: Tubulin beta chain



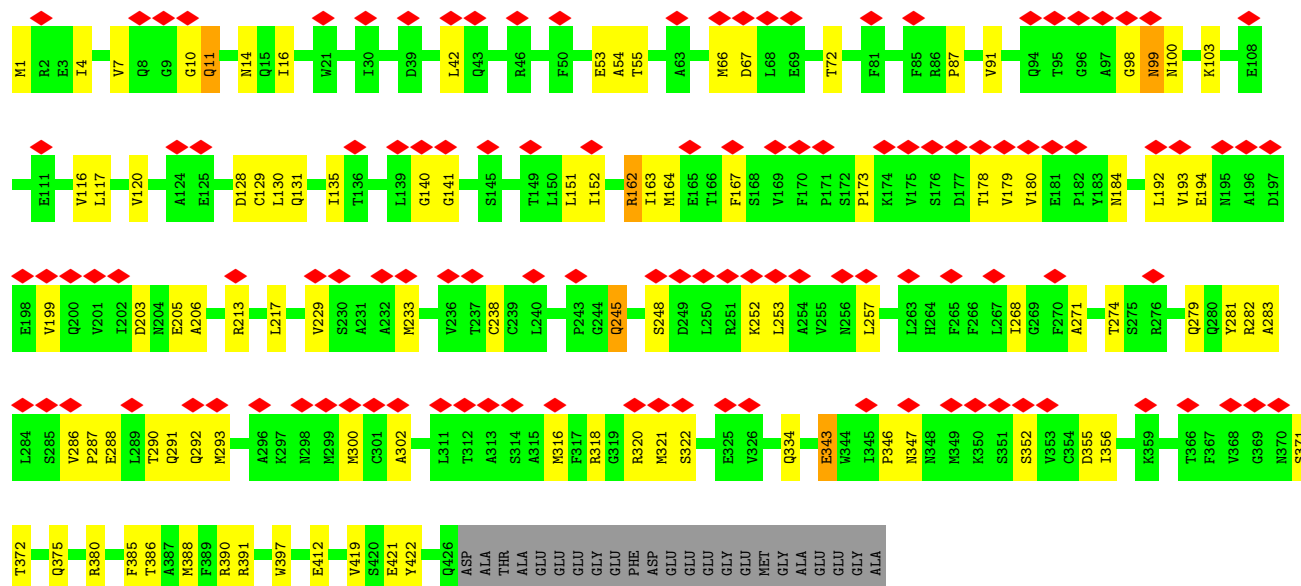
• Molecule 3: Tubulin beta chain



GLY
ALA
GLU
GLY
GLY
ALA

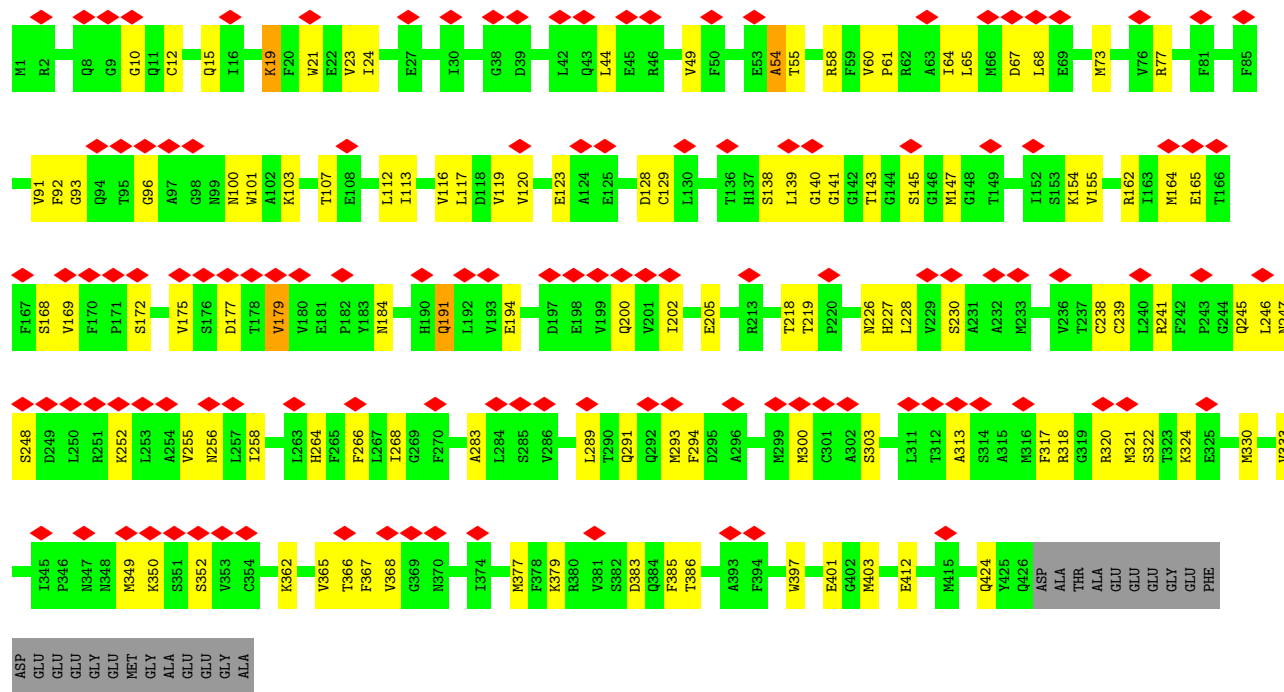
• Molecule 3: Tubulin beta chain

Chain D1: 26% 73% 21% • 5%



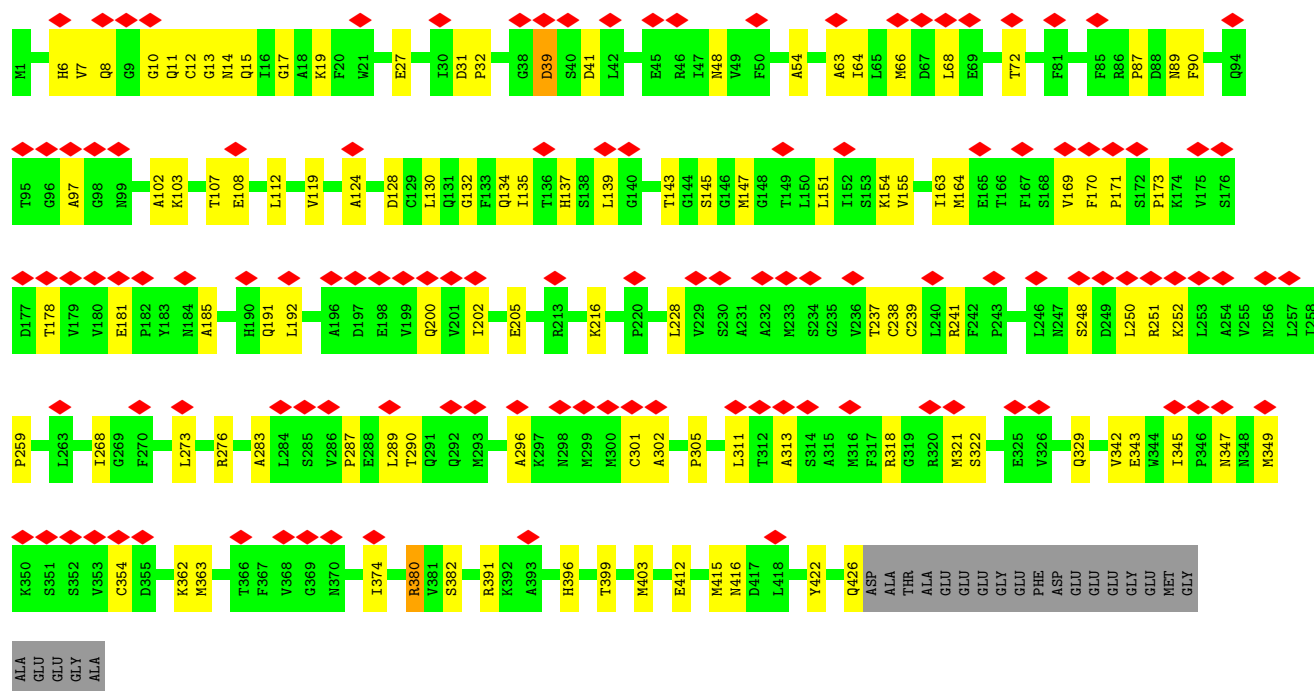
• Molecule 3: Tubulin beta chain

Chain D3: 27% 69% 25% • 5%

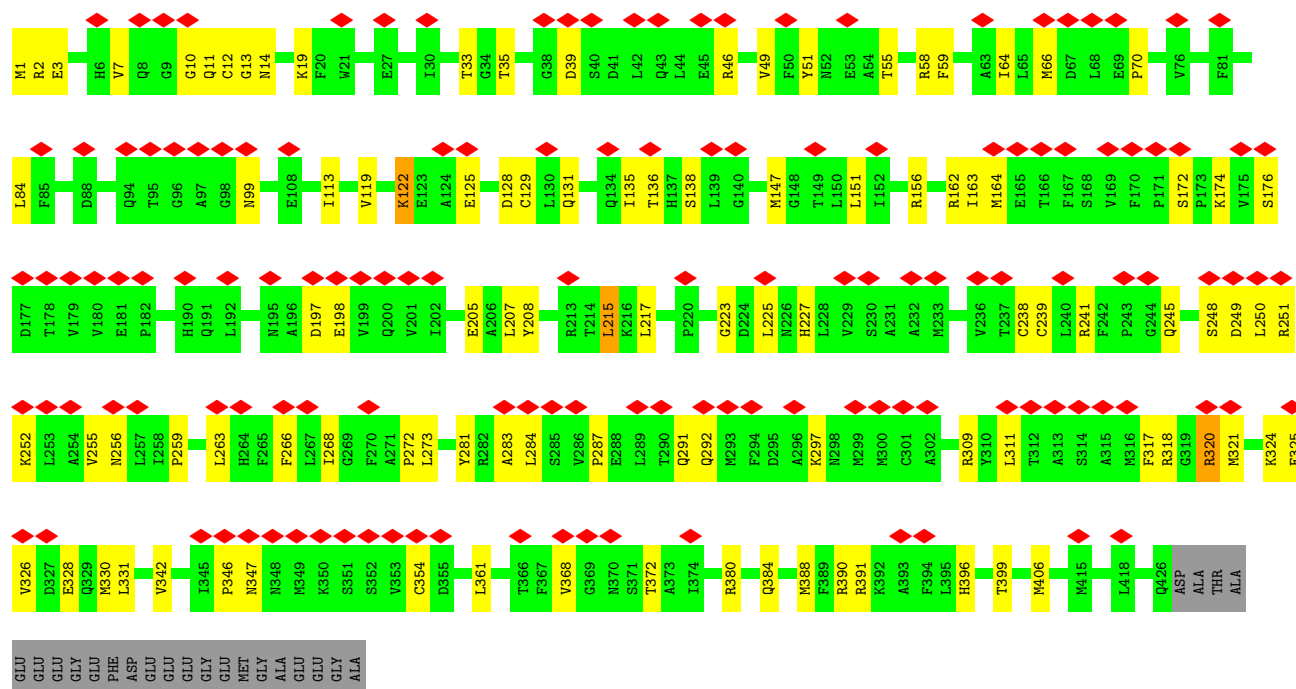
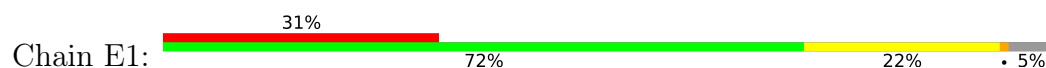


• Molecule 3: Tubulin beta chain

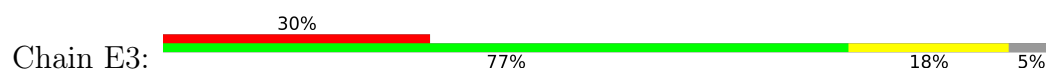


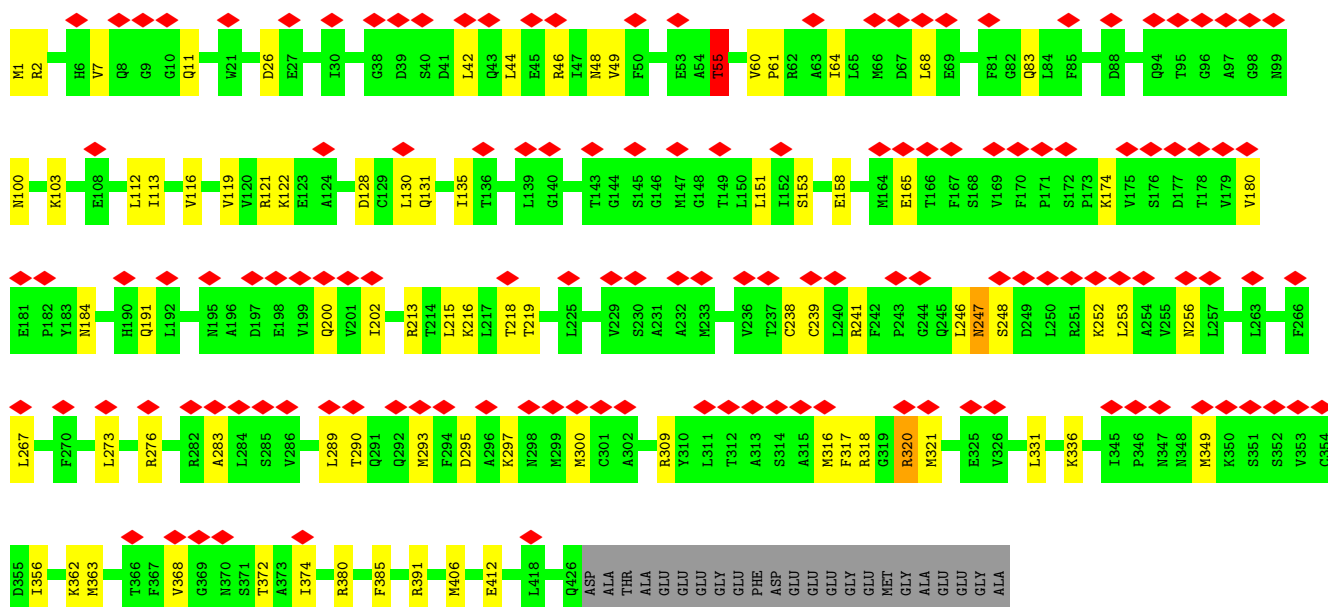


- Molecule 3: Tubulin beta chain

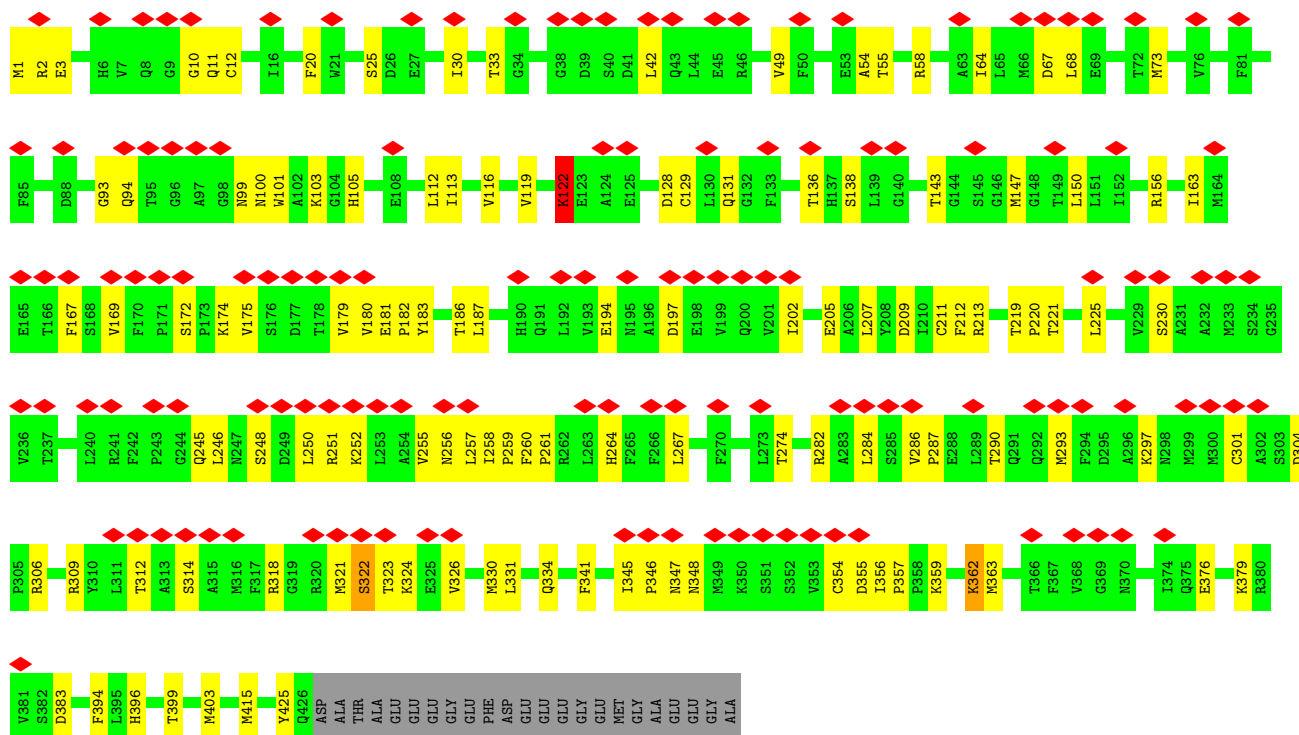


- Molecule 3: Tubulin beta chain

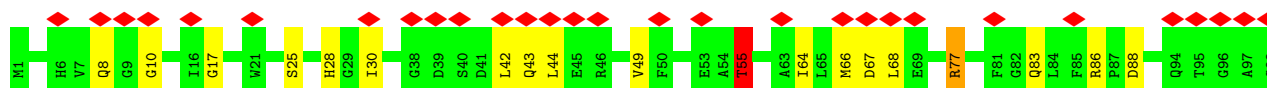
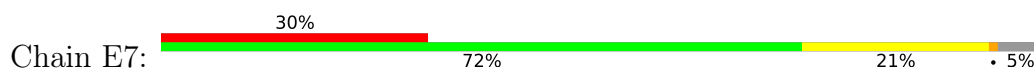




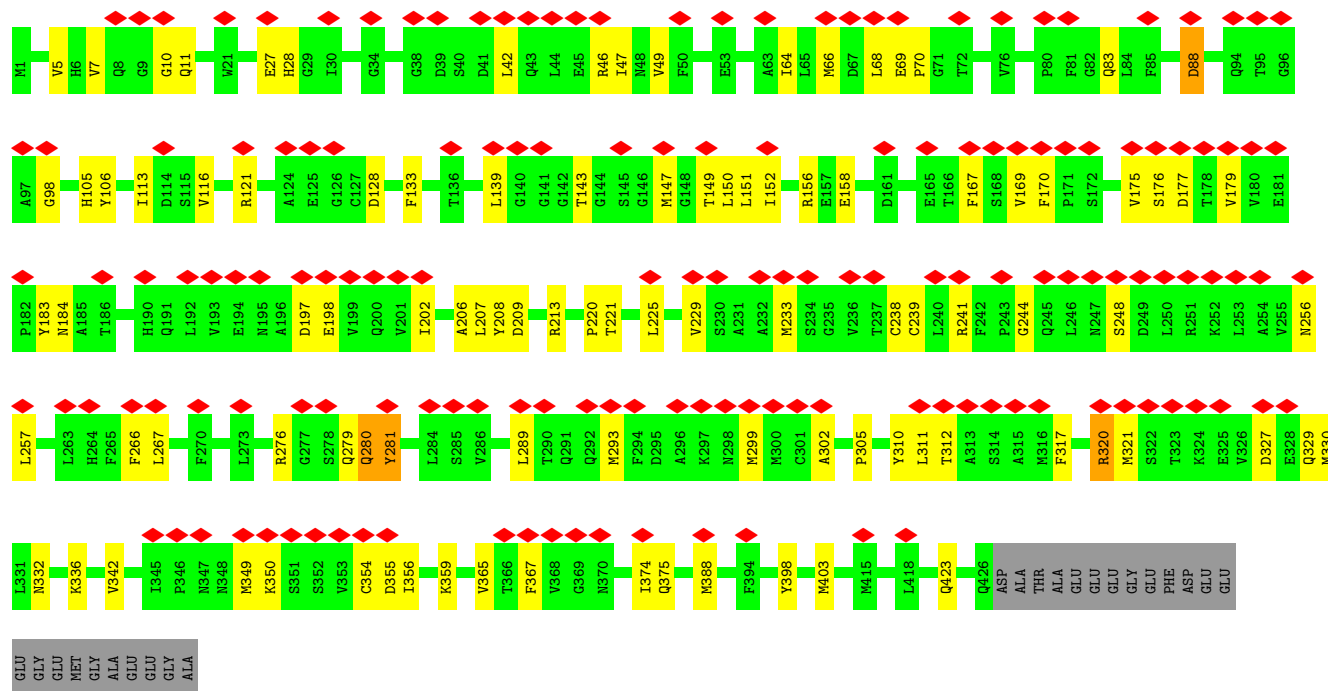
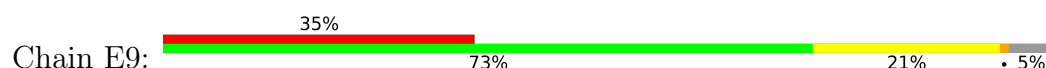
• Molecule 3: Tubulin beta chain



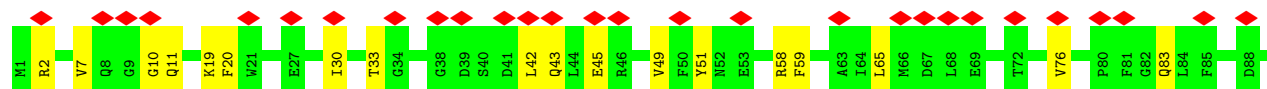
• Molecule 3: Tubulin beta chain

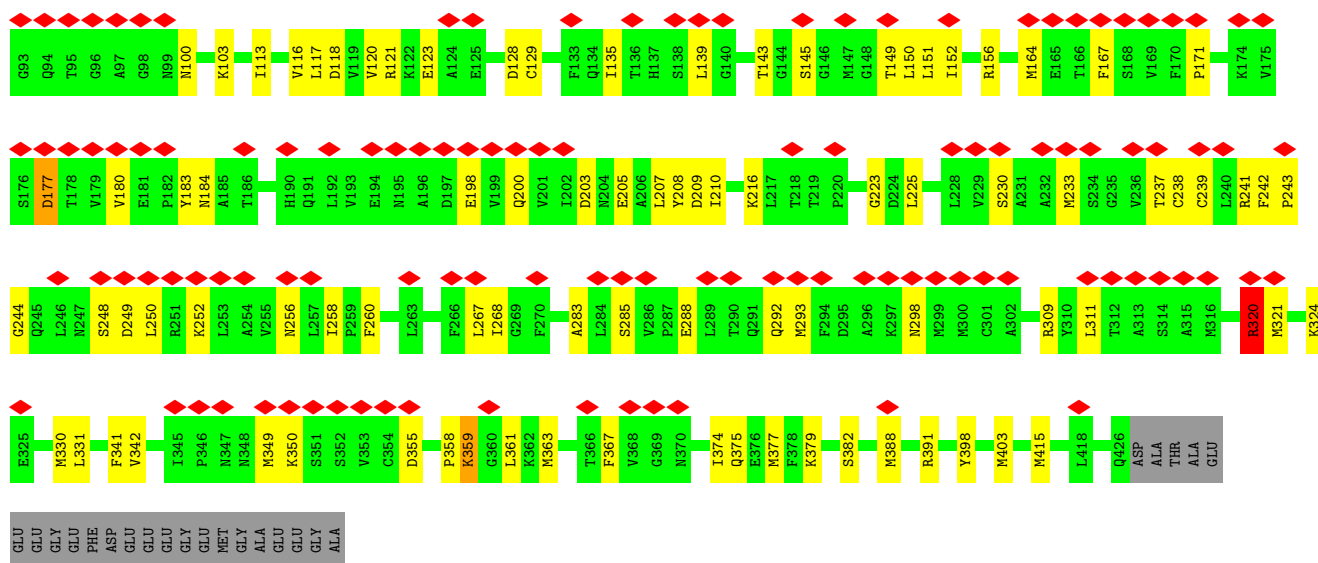


- Molecule 3: Tubulin beta chain

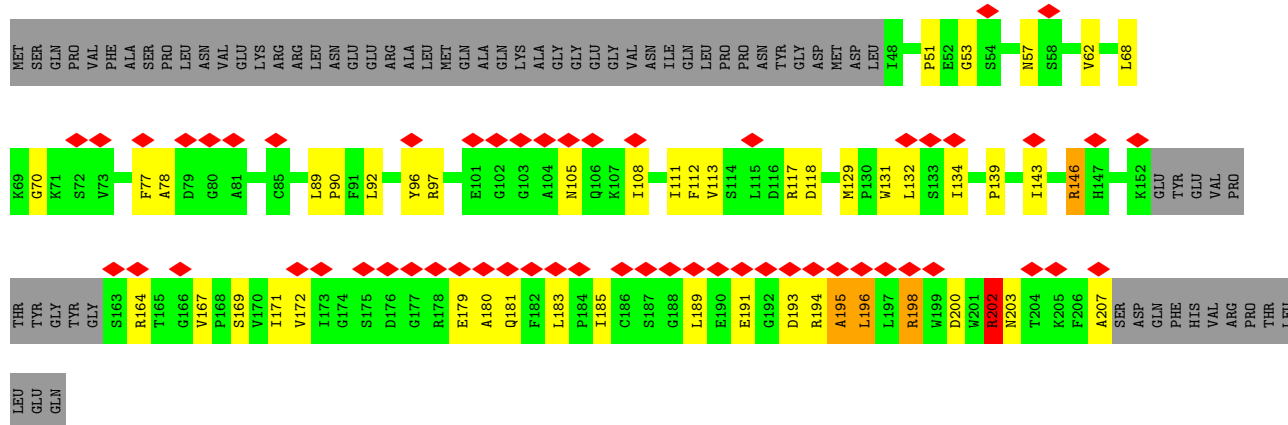


- Molecule 3: Tubulin beta chain

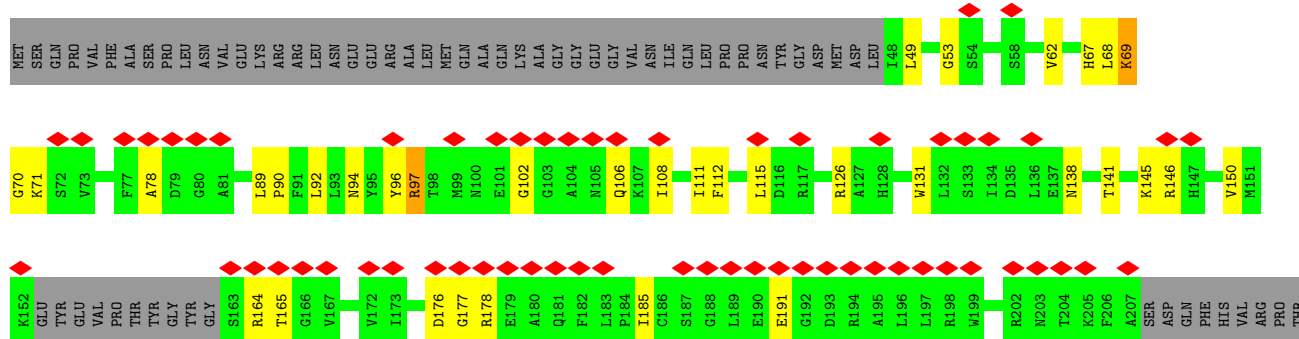




• Molecule 4: PDI family protein



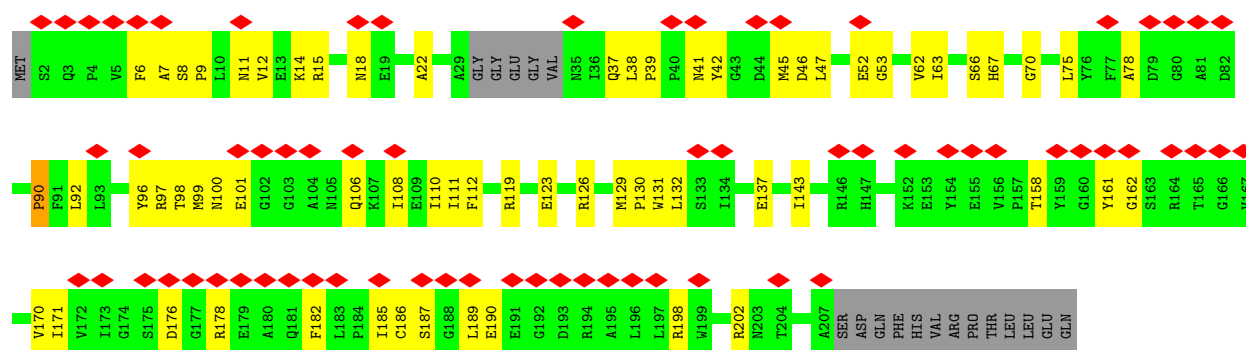
• Molecule 4: PDI family protein



LEU
LEU
GLU
GLN

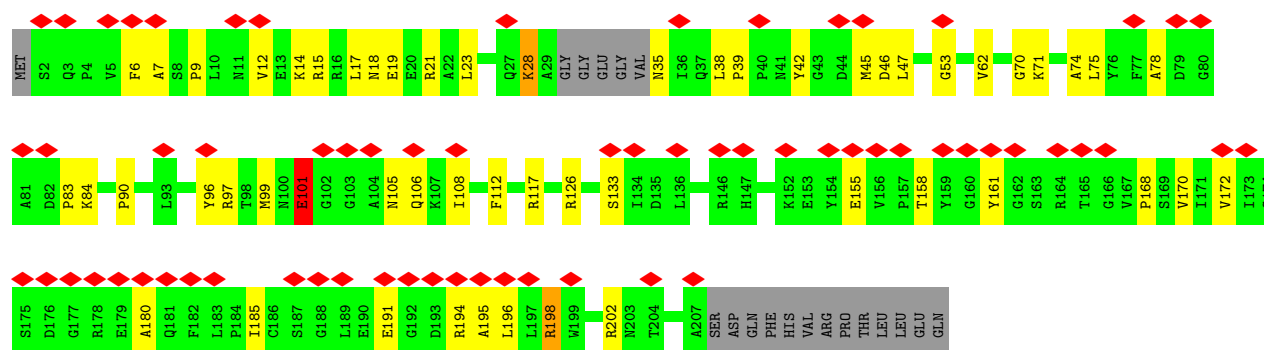
• Molecule 4: PDI family protein

Chain c: 31% 62% 29% 9%



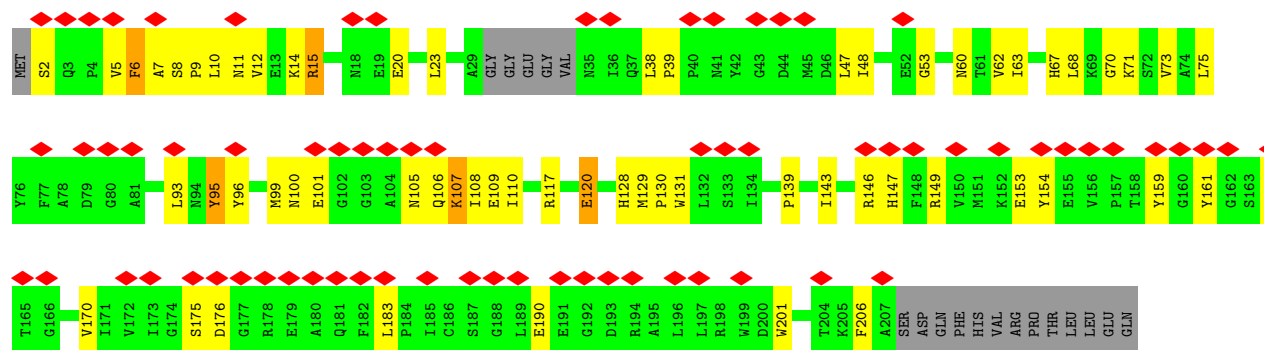
• Molecule 4: PDI family protein

Chain d: 30% 67% 23% 9%



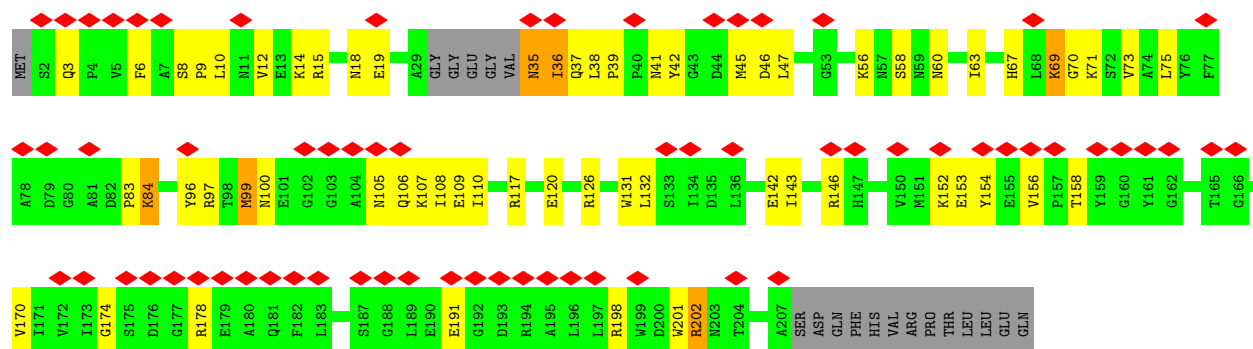
• Molecule 4: PDI family protein

Chain e: 32% 63% 26% 9%

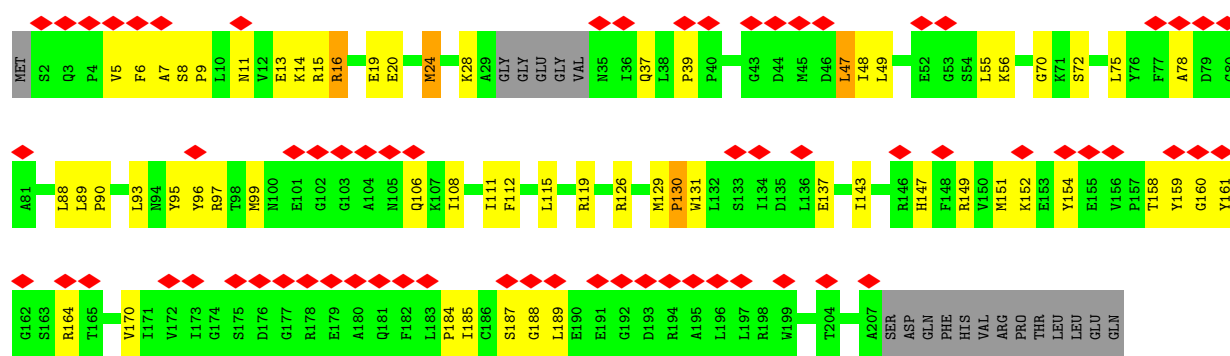


• Molecule 4: PDI family protein

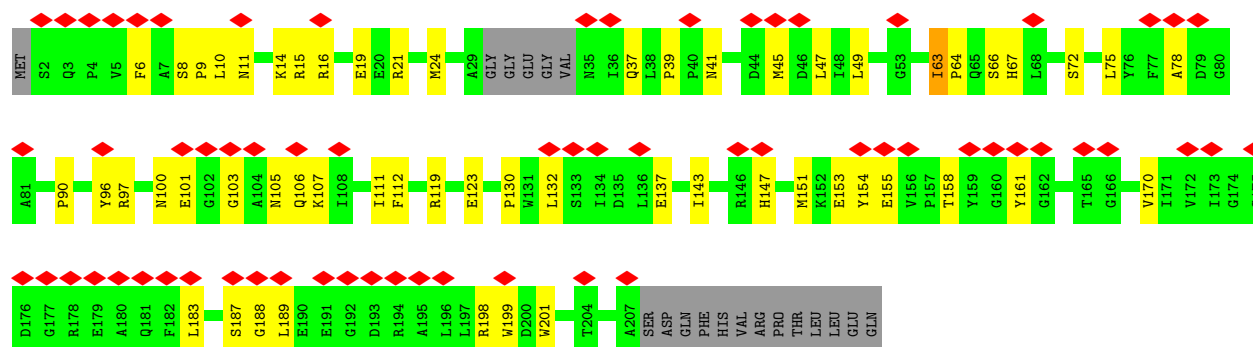
Chain f: 30% 63% 25% 9%



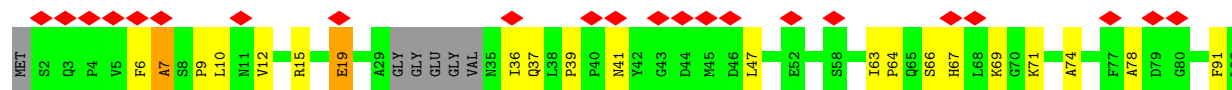
• Molecule 4: PDI family protein

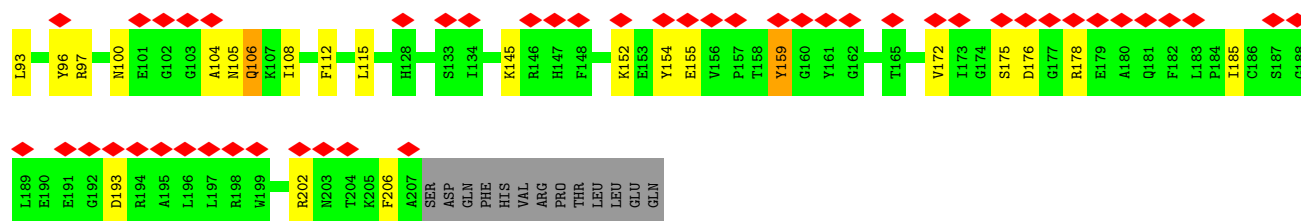


• Molecule 4: PDI family protein

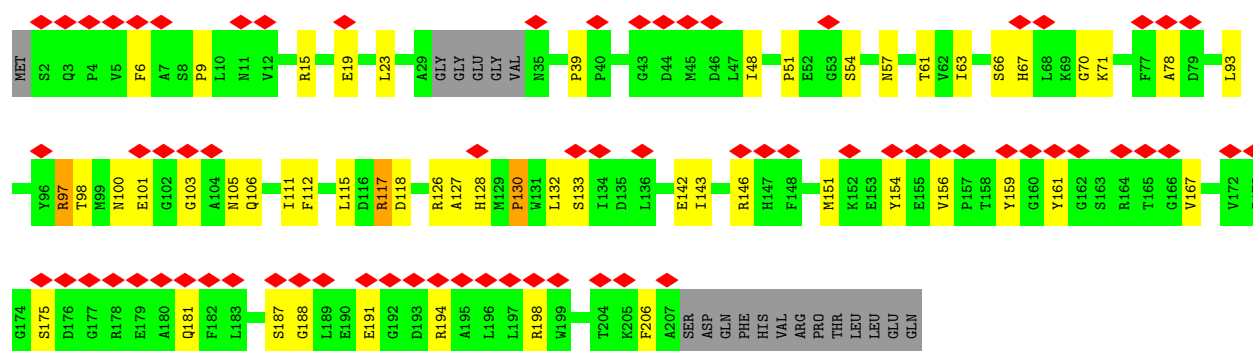


• Molecule 4: PDI family protein

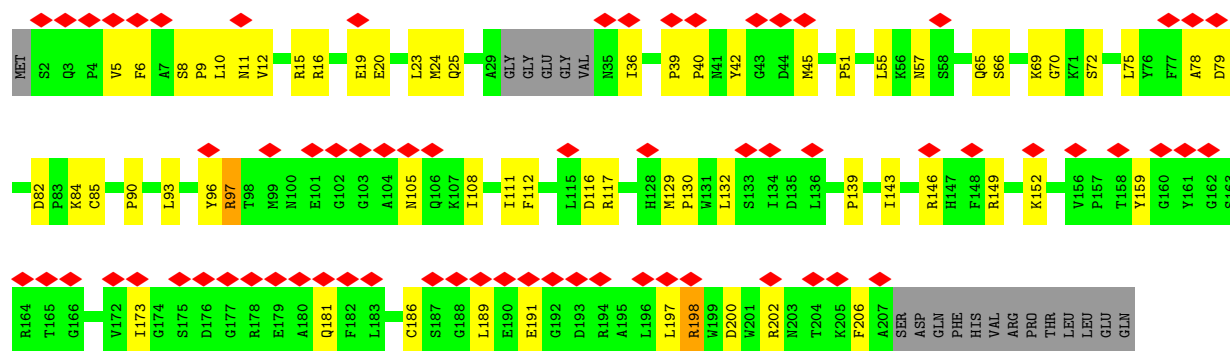




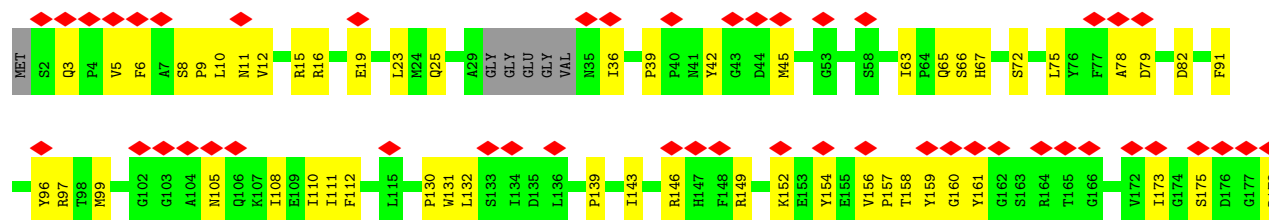
• Molecule 4: PDI family protein



• Molecule 4: PDI family protein

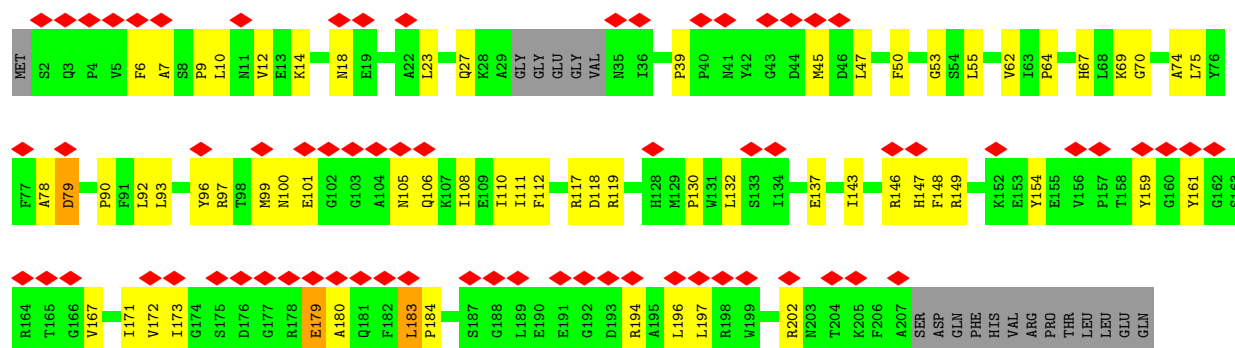


• Molecule 4: PDI family protein

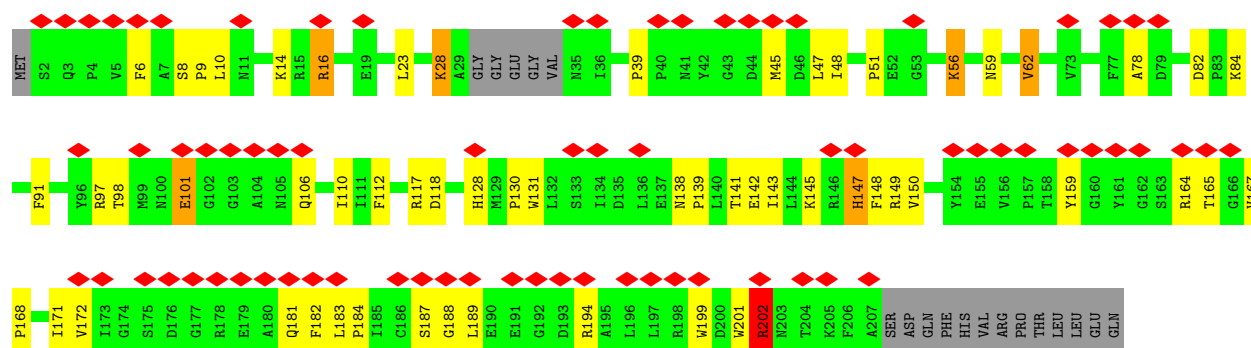




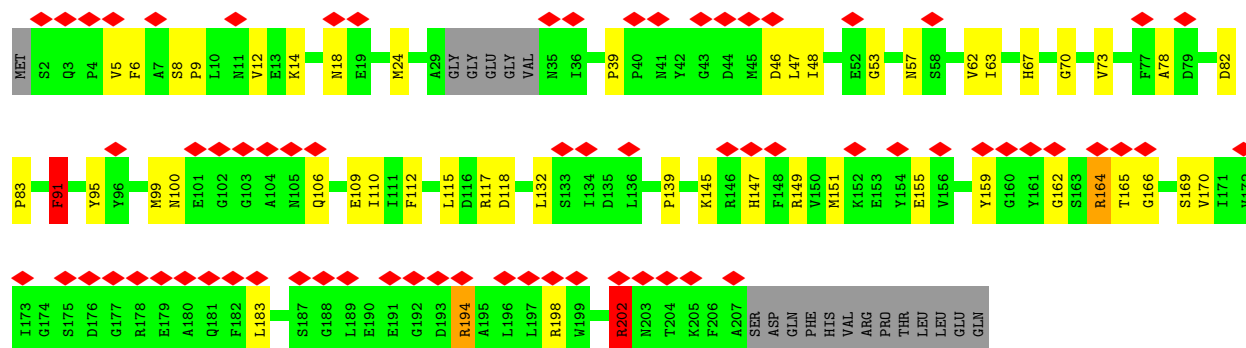
• Molecule 4: PDI family protein



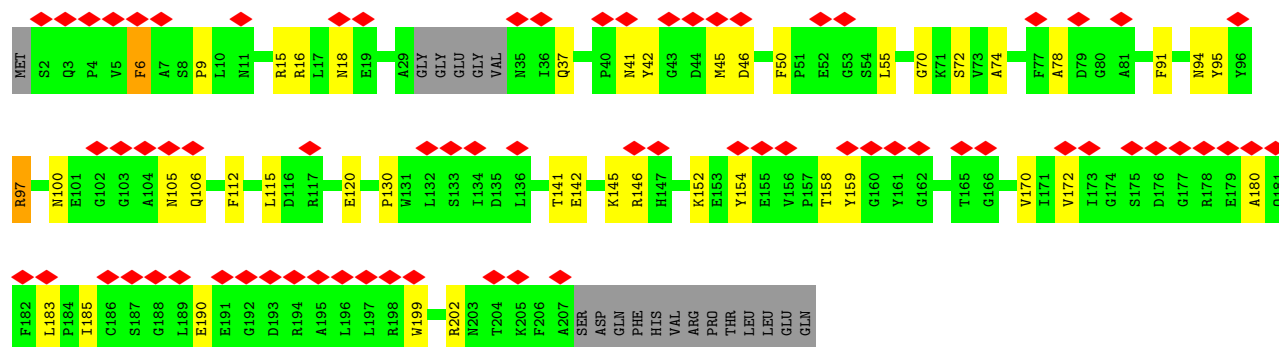
• Molecule 4: PDI family protein



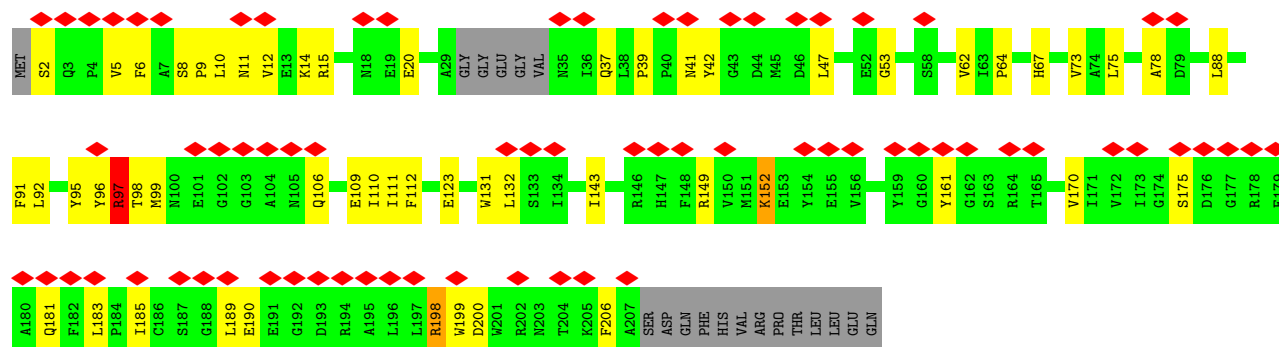
• Molecule 4: PDI family protein



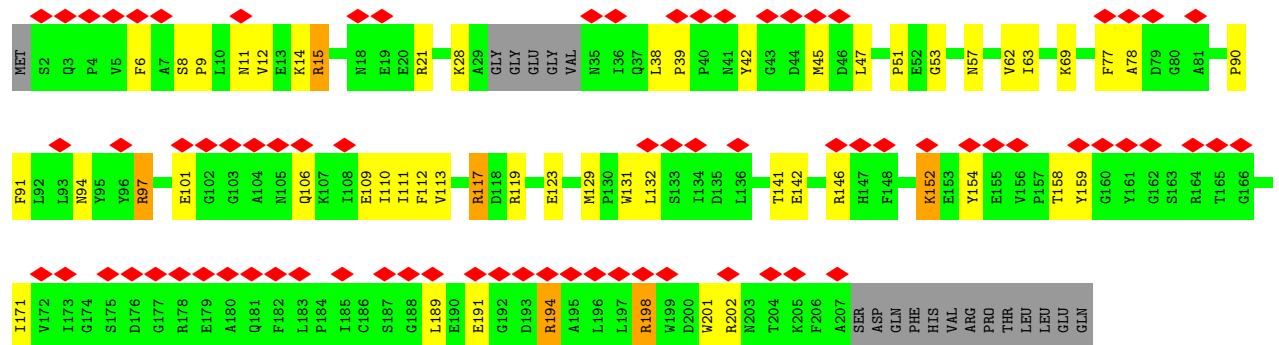
• Molecule 4: PDI family protein



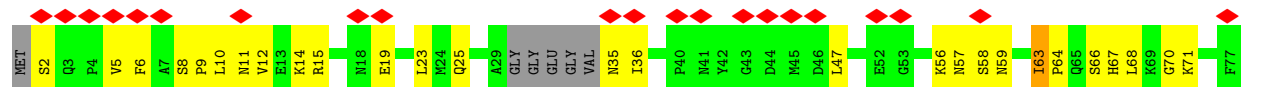
• Molecule 4: PDI family protein

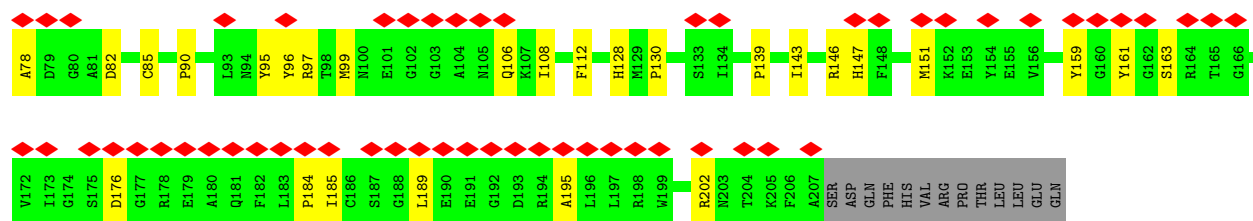


• Molecule 4: PDI family protein

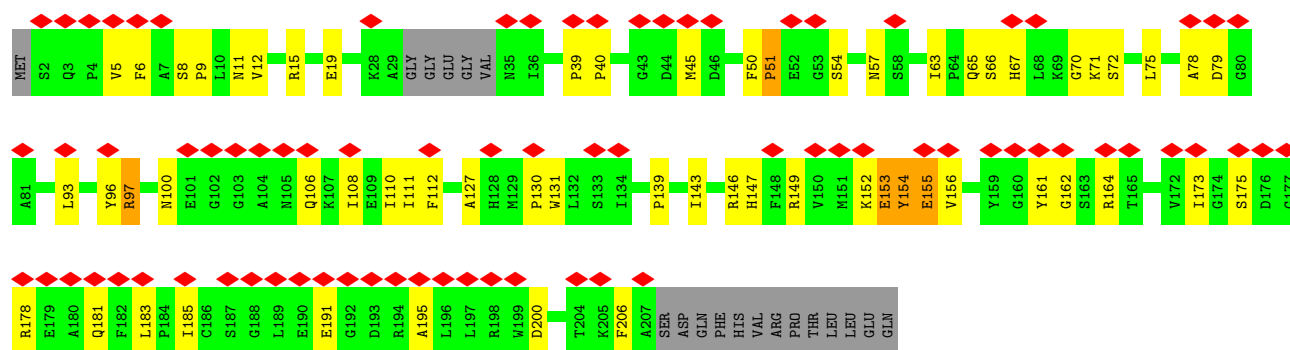


• Molecule 4: PDI family protein

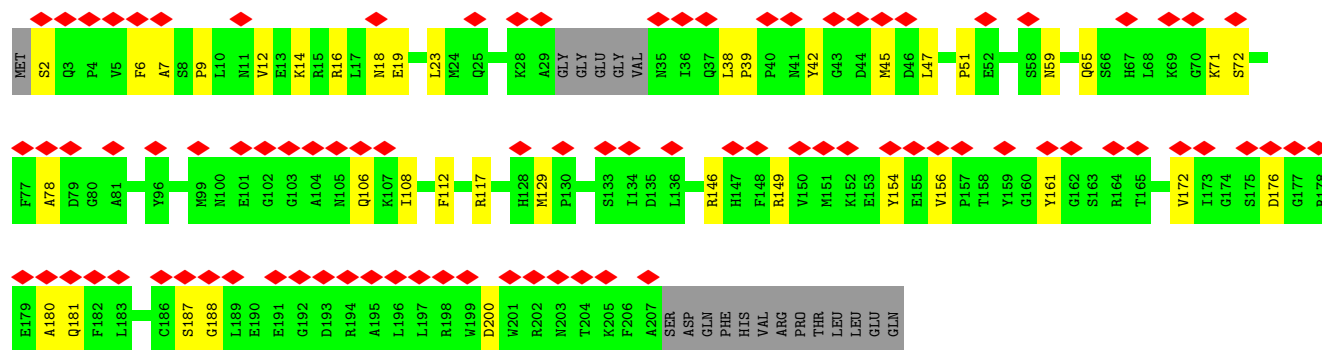
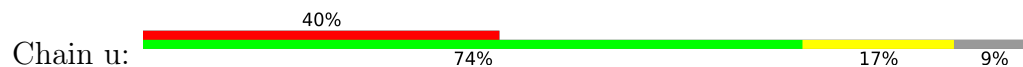




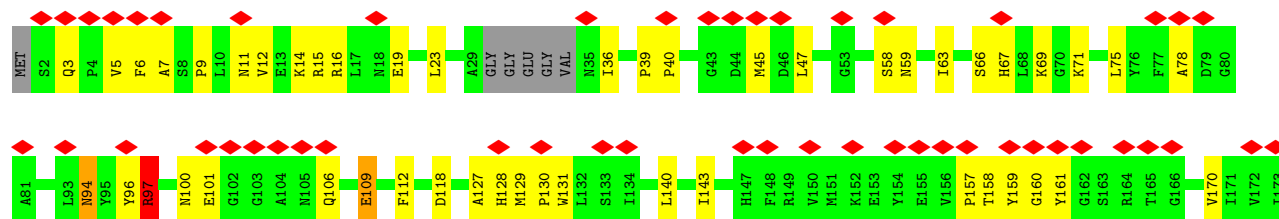
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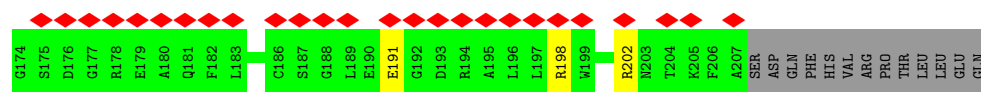


• Molecule 4: PDI family protein

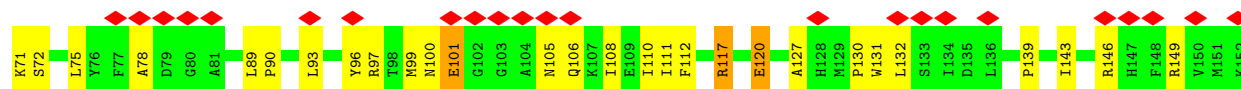
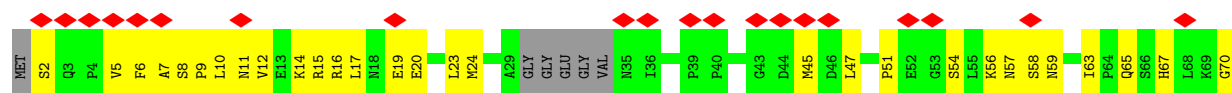


• Molecule 4: PDI family protein

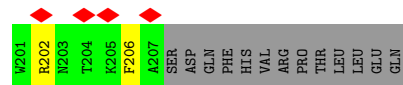
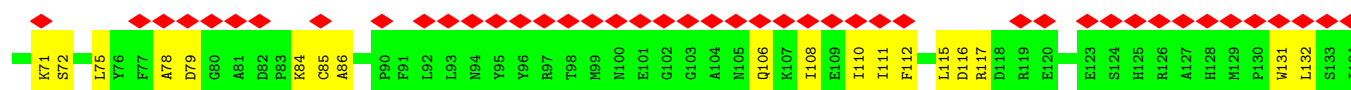
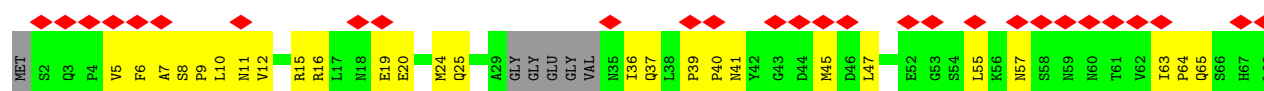




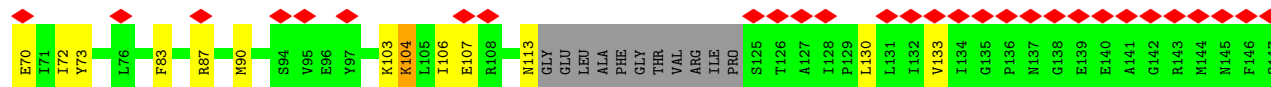
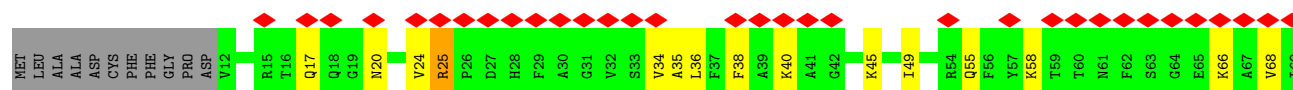
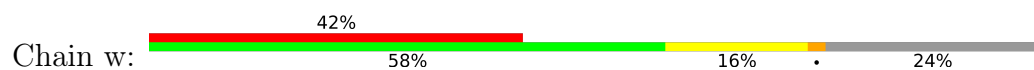
• Molecule 4: PDI family protein



• Molecule 4: PDI family protein



• Molecule 5: PDI family protein



Q148	S149	D150	E151	F152	V153	L154	Q155	R156	W157	D158	Y159	R160	F161	N162	K163	W164	P165	GLY	SER	ALA	GLN	ARG	LEU	ARG	THR	LEU	ASN	ASP	ALA	THR	ASP	PRO	TRP	LYS	LYS	ARG	LEU	PRO	GLN	ASN	VAL
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	HELICAL, twist=27.7°, rise=80 Å, axial sym=C13	Depositor
Number of subtomograms used	39122	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	132	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.064	Depositor
Minimum map value	-13.513	Depositor
Average map value	0.056	Depositor
Map value standard deviation	0.986	Depositor
Recommended contour level	2	Depositor
Map size (Å)	447.444, 447.444, 447.444	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.0715, 2.0715, 2.0715	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	0	0.69	0/181	1.31	2/248 (0.8%)
1	1	0.62	0/181	1.12	0/248
1	10	0.61	0/181	1.41	3/248 (1.2%)
1	11	0.70	0/181	1.62	4/248 (1.6%)
1	12	0.58	0/181	1.36	3/248 (1.2%)
1	13	0.63	0/181	1.37	1/248 (0.4%)
1	14	0.59	0/181	1.07	0/248
1	15	0.64	0/181	1.73	8/248 (3.2%)
1	16	0.60	0/181	1.26	1/248 (0.4%)
1	17	1.00	2/181 (1.1%)	1.66	7/248 (2.8%)
1	18	0.64	0/181	1.08	0/248
1	19	0.76	0/181	1.41	0/248
1	2	0.66	0/181	1.43	2/248 (0.8%)
1	20	0.61	0/181	1.04	0/248
1	21	0.74	0/181	1.22	0/248
1	22	0.92	1/166 (0.6%)	1.51	3/227 (1.3%)
1	23	0.66	0/166	1.40	0/227
1	3	0.63	0/181	1.21	0/248
1	4	0.66	0/181	1.48	3/248 (1.2%)
1	5	0.60	0/181	1.44	3/248 (1.2%)
1	6	0.55	0/181	1.40	4/248 (1.6%)
1	7	0.60	0/181	1.23	1/248 (0.4%)
1	8	0.67	0/181	1.33	2/248 (0.8%)
1	9	0.71	0/181	1.21	1/248 (0.4%)
2	A0	0.64	0/3398	1.17	11/4606 (0.2%)
2	A2	0.62	0/3398	1.12	8/4606 (0.2%)
2	A4	0.70	3/3398 (0.1%)	1.24	7/4606 (0.2%)
2	A6	0.61	1/3398 (0.0%)	1.14	16/4606 (0.3%)
2	A8	0.69	2/3398 (0.1%)	1.24	11/4606 (0.2%)
2	B0	0.63	1/3398 (0.0%)	1.16	14/4606 (0.3%)
2	B2	0.64	2/3398 (0.1%)	1.13	4/4606 (0.1%)
2	B4	0.59	1/3398 (0.0%)	1.05	2/4606 (0.0%)
2	B6	0.57	0/3398	1.06	6/4606 (0.1%)
2	B8	0.57	0/3398	1.05	6/4606 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	C0	0.62	3/3398 (0.1%)	1.06	7/4606 (0.2%)
2	C2	0.61	1/3398 (0.0%)	1.04	2/4606 (0.0%)
2	C4	0.78	2/3398 (0.1%)	1.15	8/4606 (0.2%)
2	C6	0.62	0/3398	1.14	12/4606 (0.3%)
2	C8	0.61	0/3398	1.10	9/4606 (0.2%)
2	D0	0.61	0/3398	1.15	14/4606 (0.3%)
2	D2	0.57	0/3398	1.09	13/4606 (0.3%)
2	D4	0.61	0/3398	1.13	12/4606 (0.3%)
2	D6	0.58	1/3398 (0.0%)	1.04	13/4606 (0.3%)
2	D8	0.61	0/3398	1.13	9/4606 (0.2%)
2	E0	0.53	0/3398	0.96	5/4606 (0.1%)
2	E2	0.58	0/3398	1.05	7/4606 (0.2%)
2	E4	0.53	0/3398	1.01	4/4606 (0.1%)
2	E6	0.56	0/3398	1.04	7/4606 (0.2%)
2	E8	0.49	0/3398	0.89	0/4606
2	F0	0.60	1/3398 (0.0%)	1.06	9/4606 (0.2%)
3	A1	0.59	0/3404	1.12	5/4606 (0.1%)
3	A3	0.52	0/3404	1.02	6/4606 (0.1%)
3	A5	0.63	0/3404	1.19	8/4606 (0.2%)
3	A7	0.57	1/3404 (0.0%)	1.07	8/4606 (0.2%)
3	A9	0.61	1/3404 (0.0%)	1.13	9/4606 (0.2%)
3	B1	0.60	0/3404	1.12	5/4606 (0.1%)
3	B3	0.56	0/3404	1.13	12/4606 (0.3%)
3	B5	0.59	0/3404	1.12	9/4606 (0.2%)
3	B7	0.57	0/3404	1.11	10/4606 (0.2%)
3	B9	0.56	0/3404	1.07	8/4606 (0.2%)
3	C1	0.60	2/3404 (0.1%)	1.09	9/4606 (0.2%)
3	C3	0.59	0/3404	1.10	7/4606 (0.2%)
3	C5	0.60	0/3404	1.10	10/4606 (0.2%)
3	C7	0.59	0/3404	1.11	8/4606 (0.2%)
3	C9	0.59	0/3404	1.16	15/4606 (0.3%)
3	D1	0.63	0/3404	1.16	15/4606 (0.3%)
3	D3	0.60	3/3404 (0.1%)	1.10	5/4606 (0.1%)
3	D5	0.68	0/3404	1.28	19/4606 (0.4%)
3	D7	0.59	0/3404	1.06	4/4606 (0.1%)
3	D9	0.60	2/3404 (0.1%)	1.13	15/4606 (0.3%)
3	E1	0.55	0/3404	1.02	5/4606 (0.1%)
3	E3	0.63	2/3404 (0.1%)	1.09	8/4606 (0.2%)
3	E5	0.56	0/3404	1.05	4/4606 (0.1%)
3	E7	0.60	0/3404	1.10	12/4606 (0.3%)
3	E9	0.56	0/3404	1.07	10/4606 (0.2%)
3	F1	0.61	1/3404 (0.0%)	1.14	10/4606 (0.2%)
4	a	0.72	2/1225 (0.2%)	1.28	9/1654 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	b	0.68	2/1225 (0.2%)	1.14	7/1654 (0.4%)
4	c	0.85	2/1645 (0.1%)	1.41	13/2225 (0.6%)
4	d	0.67	0/1645	1.23	7/2225 (0.3%)
4	e	0.67	0/1645	1.25	5/2225 (0.2%)
4	f	0.70	2/1645 (0.1%)	1.16	6/2225 (0.3%)
4	g	0.62	1/1645 (0.1%)	1.23	8/2225 (0.4%)
4	h	0.62	1/1645 (0.1%)	1.15	4/2225 (0.2%)
4	i	0.60	0/1645	1.18	7/2225 (0.3%)
4	j	0.61	0/1645	1.14	2/2225 (0.1%)
4	k	0.65	1/1645 (0.1%)	1.17	1/2225 (0.0%)
4	l	0.59	0/1645	1.13	4/2225 (0.2%)
4	m	0.76	3/1645 (0.2%)	1.23	13/2225 (0.6%)
4	n	0.70	1/1645 (0.1%)	1.30	8/2225 (0.4%)
4	o	0.61	0/1645	1.25	10/2225 (0.4%)
4	p	0.70	0/1645	1.33	11/2225 (0.5%)
4	q	0.69	2/1645 (0.1%)	1.20	6/2225 (0.3%)
4	r	0.68	0/1645	1.27	10/2225 (0.4%)
4	s	0.58	0/1645	1.14	2/2225 (0.1%)
4	t	0.63	0/1645	1.24	7/2225 (0.3%)
4	u	0.62	0/1645	1.13	3/2225 (0.1%)
4	v	0.61	0/1645	1.14	2/2225 (0.1%)
4	x	0.57	1/1645 (0.1%)	1.15	5/2225 (0.2%)
4	y	0.54	0/1645	1.09	1/2225 (0.0%)
5	w	0.58	0/1201	1.13	8/1623 (0.5%)
All	All	0.61	51/221007 (0.0%)	1.13	659/299303 (0.2%)

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	12	0	1
1	19	0	1
1	2	0	1
1	20	0	2
1	21	0	1
1	23	0	1
1	7	0	1
1	8	0	1
2	A0	0	1
2	A2	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	A4	0	1
2	A8	0	1
2	B4	0	1
2	B6	0	2
2	C4	0	1
2	C8	0	1
2	D2	0	2
2	D8	0	1
2	E4	0	1
2	F0	0	1
3	B3	0	1
3	B9	0	1
3	E5	0	2
3	E9	0	1
4	o	0	1
4	s	0	1
All	All	0	31

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C4	2	ARG	NE-CZ	22.48	1.57	1.33
2	C4	2	ARG	CD-NE	19.88	1.74	1.46
4	c	178	ARG	NE-CZ	17.46	1.52	1.33
2	C2	221	ARG	NE-CZ	12.31	1.46	1.33
4	m	202	ARG	NE-CZ	11.61	1.45	1.33
2	C0	221	ARG	NE-CZ	11.55	1.45	1.33
3	E3	391	ARG	NE-CZ	11.54	1.45	1.33
4	c	178	ARG	CD-NE	10.87	1.61	1.46
4	m	202	ARG	CD-NE	10.27	1.60	1.46
4	f	202	ARG	CD-NE	10.24	1.60	1.46
3	E3	391	ARG	CD-NE	10.21	1.60	1.46
2	A4	254	GLU	CD-OE2	9.56	1.43	1.25
3	F1	391	ARG	NE-CZ	9.56	1.43	1.33
4	q	97	ARG	NE-CZ	9.15	1.43	1.33
4	q	97	ARG	CD-NE	8.84	1.58	1.46
4	f	202	ARG	NE-CZ	8.41	1.42	1.33
2	C0	221	ARG	CZ-NH1	7.75	1.43	1.32
2	C0	221	ARG	CD-NE	7.57	1.56	1.46
1	17	248	ARG	CD-NE	7.45	1.56	1.46
2	F0	284	GLU	CD-OE1	7.34	1.39	1.25
3	A9	227	HIS	CE1-NE2	7.22	1.39	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A4	254	GLU	CG-CD	7.16	1.70	1.52
4	a	207	ALA	C-O	7.11	1.37	1.23
3	C1	276	ARG	NE-CZ	6.85	1.40	1.33
3	D3	227	HIS	CE1-NE2	6.75	1.39	1.32
1	17	248	ARG	NE-CZ	6.67	1.40	1.33
3	D3	227	HIS	CG-ND1	6.59	1.45	1.38
4	b	178	ARG	CD-NE	6.48	1.55	1.46
2	A8	433	GLU	CD-OE2	-6.43	1.13	1.25
2	A8	162	GLY	C-O	-6.21	1.16	1.24
2	A4	2	ARG	CZ-NH2	6.15	1.41	1.33
4	m	202	ARG	CZ-NH2	6.10	1.41	1.33
4	k	202	ARG	NE-CZ	6.06	1.39	1.33
3	A7	384	GLN	CD-NE2	5.96	1.45	1.33
2	A6	163	LYS	CE-NZ	5.92	1.67	1.49
2	B2	393	HIS	CE1-NE2	5.91	1.38	1.32
3	C1	227	HIS	CE1-NE2	5.81	1.38	1.32
4	b	178	ARG	NE-CZ	5.78	1.39	1.33
2	D6	393	HIS	CE1-NE2	5.72	1.38	1.32
3	D9	276	ARG	CD-NE	5.62	1.54	1.46
2	B4	61	HIS	CE1-NE2	5.42	1.38	1.32
2	B2	61	HIS	CE1-NE2	5.40	1.38	1.32
3	D9	276	ARG	NE-CZ	5.31	1.38	1.33
4	n	147	HIS	CE1-NE2	5.28	1.37	1.32
4	a	146	ARG	NE-CZ	5.24	1.38	1.33
4	g	24	MET	CG-SD	5.22	1.93	1.80
1	22	248	ARG	CD-NE	5.20	1.53	1.46
2	B0	8	HIS	CE1-NE2	5.18	1.37	1.32
4	x	54	SER	CA-CB	-5.11	1.47	1.53
4	h	147	HIS	CE1-NE2	5.02	1.37	1.32
3	D3	264	HIS	CE1-NE2	5.01	1.37	1.32

All (659) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C4	2	ARG	CD-NE-CZ	20.03	152.44	124.40
4	c	178	ARG	CD-NE-CZ	17.47	148.85	124.40
2	C4	2	ARG	NE-CZ-NH1	17.38	138.88	121.50
2	D2	85	HIS	CA-CB-CG	13.45	127.25	113.80
2	C4	2	ARG	CG-CD-NE	13.44	141.57	112.00
4	n	202	ARG	CB-CG-CD	12.94	141.06	111.30
2	A8	85	HIS	CA-CB-CG	12.92	126.72	113.80
4	o	202	ARG	CB-CG-CD	12.29	139.57	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A4	85	HIS	CA-CB-CG	12.21	126.01	113.80
3	C5	291	GLN	CB-CG-CD	12.18	133.31	112.60
3	E7	394	PHE	CA-CB-CG	-12.15	101.65	113.80
3	E3	391	ARG	CG-CD-NE	11.82	138.00	112.00
3	F1	177	ASP	CA-CB-CG	11.45	124.05	112.60
2	C4	2	ARG	NH1-CZ-NH2	-11.11	104.86	119.30
3	C9	384	GLN	CB-CG-CD	10.84	131.03	112.60
3	D1	291	GLN	CB-CA-C	-10.71	94.06	110.88
3	D1	213	ARG	CG-CD-NE	-10.39	89.14	112.00
2	A8	285	GLN	CB-CG-CD	10.33	130.16	112.60
3	B7	11	GLN	CB-CG-CD	10.24	130.02	112.60
4	r	117	ARG	CG-CD-NE	10.23	134.51	112.00
2	C8	85	HIS	CA-CB-CG	10.20	124.00	113.80
4	m	202	ARG	NE-CZ-NH2	10.19	128.37	119.20
3	A5	125	GLU	CB-CG-CD	10.18	129.90	112.60
2	D0	85	HIS	CA-CB-CG	10.16	123.97	113.80
4	h	198	ARG	CG-CD-NE	10.14	134.30	112.00
4	n	91	PHE	CA-CB-CG	-10.10	103.70	113.80
4	o	202	ARG	CG-CD-NE	9.95	133.90	112.00
4	x	97	ARG	CB-CG-CD	9.84	133.94	111.30
3	B3	227	HIS	CA-CB-CG	9.68	123.48	113.80
3	B9	11	GLN	CB-CG-CD	9.57	128.88	112.60
4	a	202	ARG	CG-CD-NE	9.52	132.95	112.00
4	c	178	ARG	NE-CZ-NH1	9.41	130.91	121.50
3	A3	177	ASP	CA-CB-CG	9.30	121.90	112.60
3	C9	291	GLN	CB-CG-CD	9.27	128.36	112.60
3	D5	391	ARG	CA-CB-CG	9.25	132.60	114.10
3	B1	280	GLN	CB-CG-CD	9.16	128.17	112.60
4	t	153	GLU	CB-CG-CD	9.10	128.07	112.60
4	d	117	ARG	CB-CG-CD	9.05	132.12	111.30
2	C8	420	GLU	CB-CG-CD	9.02	127.94	112.60
3	A5	227	HIS	CA-CB-CG	9.01	122.81	113.80
3	D5	276	ARG	CB-CG-CD	8.87	131.70	111.30
2	E2	220	GLU	CB-CG-CD	8.75	127.47	112.60
3	E3	391	ARG	NE-CZ-NH2	8.75	127.08	119.20
2	B2	156	ARG	NE-CZ-NH2	8.73	127.05	119.20
3	C5	15	GLN	CB-CG-CD	8.73	127.44	112.60
2	A6	214	ARG	CG-CD-NE	8.71	131.16	112.00
2	D4	85	HIS	CA-CB-CG	8.71	122.51	113.80
2	A8	285	GLN	N-CA-CB	8.60	123.05	110.06
2	D2	162	GLY	CA-C-N	8.60	137.97	121.54
2	D2	162	GLY	C-N-CA	8.60	137.97	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E1	390	ARG	CB-CG-CD	8.55	130.98	111.30
3	F1	391	ARG	NE-CZ-NH1	8.51	130.01	121.50
1	16	248	ARG	CG-CD-NE	-8.38	93.57	112.00
4	m	27	GLN	CB-CG-CD	8.36	126.81	112.60
2	C8	393	HIS	CA-CB-CG	8.34	122.14	113.80
3	C9	245	GLN	CB-CG-CD	8.34	126.78	112.60
4	c	123	GLU	CB-CG-CD	8.33	126.76	112.60
4	x	101	GLU	CB-CG-CD	-8.32	98.46	112.60
3	D5	48	ASN	CA-CB-CG	8.21	120.81	112.60
3	D1	388	MET	CB-CG-SD	8.21	137.32	112.70
2	D0	156	ARG	NE-CZ-NH2	8.14	126.52	119.20
2	A4	286	LEU	N-CA-CB	-8.12	98.93	110.46
4	p	94	ASN	CA-CB-CG	8.10	120.70	112.60
3	B9	15	GLN	CB-CG-CD	8.10	126.37	112.60
4	f	202	ARG	CD-NE-CZ	8.02	135.63	124.40
2	D8	35	GLN	CB-CG-CD	-8.00	99.00	112.60
4	a	198	ARG	CB-CG-CD	7.95	129.58	111.30
2	D4	219	ILE	CA-C-N	7.94	131.71	120.28
2	D4	219	ILE	C-N-CA	7.94	131.71	120.28
3	C3	391	ARG	CB-CG-CD	-7.91	93.10	111.30
2	D0	221	ARG	CG-CD-NE	7.86	129.29	112.00
2	E6	97	GLU	CB-CG-CD	7.86	125.96	112.60
2	A2	221	ARG	CG-CD-NE	7.83	129.22	112.00
2	A4	218	ASP	CA-CB-CG	7.83	120.43	112.60
3	D5	77	ARG	CG-CD-NE	7.82	129.20	112.00
3	C9	390	ARG	CG-CD-NE	7.82	129.20	112.00
3	F1	391	ARG	CD-NE-CZ	7.78	135.29	124.40
3	D5	343	GLU	CB-CG-CD	7.77	125.81	112.60
3	B9	157	GLU	CB-CG-CD	7.75	125.77	112.60
2	D6	218	ASP	CA-CB-CG	7.75	120.35	112.60
2	D2	163	LYS	CB-CG-CD	-7.73	93.52	111.30
2	D4	96	LYS	CB-CG-CD	7.67	128.94	111.30
4	j	130	PRO	N-CA-C	7.64	123.43	114.03
1	4	241	PHE	CA-CB-CG	7.64	121.44	113.80
4	p	91	PHE	CA-CB-CG	-7.63	106.17	113.80
2	D2	163	LYS	N-CA-CB	-7.62	97.61	110.49
3	B3	213	ARG	CG-CD-NE	7.57	128.65	112.00
2	A6	96	LYS	CB-CG-CD	7.55	128.67	111.30
2	B0	85	HIS	CB-CA-C	-7.55	96.86	109.55
4	p	95	TYR	CB-CA-C	7.55	123.69	110.85
3	B1	129	CYS	CB-CA-C	7.54	121.62	110.62
2	A8	155	GLU	CB-CG-CD	7.53	125.40	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B0	85	HIS	CA-CB-CG	7.53	121.33	113.80
1	17	248	ARG	CB-CG-CD	7.50	128.56	111.30
4	f	202	ARG	NE-CZ-NH2	7.49	125.94	119.20
2	D4	96	LYS	N-CA-CB	7.48	121.06	110.67
3	D5	56	GLY	CA-C-N	7.47	134.44	121.07
3	D5	56	GLY	C-N-CA	7.47	134.44	121.07
3	E7	77	ARG	NE-CZ-NH1	-7.46	114.04	121.50
3	E7	291	GLN	CB-CG-CD	7.46	125.28	112.60
4	i	36	ILE	CA-C-N	7.46	131.42	120.90
4	i	36	ILE	C-N-CA	7.46	131.42	120.90
5	w	156	ARG	CB-CG-CD	-7.45	94.17	111.30
2	C8	33	ASP	CB-CA-C	7.42	122.39	110.96
3	E5	345	ILE	O-C-N	-7.42	116.70	121.37
3	D5	212	PHE	CA-CB-CG	-7.41	106.39	113.80
3	B9	177	ASP	CA-CB-CG	7.36	119.95	112.60
2	D0	11	GLN	CB-CG-CD	-7.35	100.11	112.60
2	E2	156	ARG	CB-CG-CD	7.34	128.19	111.30
3	B3	391	ARG	CB-CG-CD	7.34	128.19	111.30
2	B8	156	ARG	CG-CD-NE	-7.33	95.87	112.00
3	C1	320	ARG	CG-CD-NE	7.33	128.13	112.00
2	A4	18	ASN	CA-CB-CG	7.32	119.92	112.60
4	d	194	ARG	CG-CD-NE	7.30	128.06	112.00
3	E3	391	ARG	CD-NE-CZ	7.28	134.60	124.40
3	C5	174	LYS	CB-CG-CD	7.28	128.04	111.30
1	15	256	LEU	CA-C-N	7.26	127.86	120.38
1	15	256	LEU	C-N-CA	7.26	127.86	120.38
2	D4	33	ASP	CA-CB-CG	7.26	119.86	112.60
4	o	194	ARG	CG-CD-NE	-7.25	96.05	112.00
3	A9	174	LYS	CG-CD-CE	7.24	127.95	111.30
3	B1	227	HIS	CA-CB-CG	7.17	120.97	113.80
4	p	97	ARG	CB-CG-CD	7.17	127.79	111.30
2	A8	263	PRO	CB-CA-C	-7.17	101.03	112.21
3	C3	388	MET	CB-CG-SD	7.13	134.09	112.70
2	B0	162	GLY	CA-C-N	7.13	131.15	120.31
2	B0	162	GLY	C-N-CA	7.13	131.15	120.31
3	E9	11	GLN	CB-CG-CD	-7.11	100.52	112.60
4	q	97	ARG	NE-CZ-NH2	7.09	125.58	119.20
3	E3	320	ARG	CB-CA-C	7.08	121.43	110.67
3	D1	421	GLU	CB-CG-CD	7.08	124.63	112.60
3	A7	282	ARG	NE-CZ-NH2	7.07	125.57	119.20
2	E0	156	ARG	CB-CG-CD	7.06	127.54	111.30
3	A3	391	ARG	CB-CG-CD	7.05	127.52	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B7	212	PHE	CA-CB-CG	7.03	120.83	113.80
3	D5	391	ARG	CG-CD-NE	7.01	127.42	112.00
2	C0	221	ARG	CG-CD-NE	7.00	127.40	112.00
2	F0	285	GLN	CB-CA-C	6.98	121.28	110.67
3	E9	280	GLN	CB-CG-CD	6.97	124.45	112.60
4	f	84	LYS	CB-CG-CD	6.97	127.34	111.30
4	e	95	TYR	CB-CA-C	6.97	122.69	110.85
2	C6	101	ASN	OD1-CG-ND2	-6.96	115.64	122.60
3	B7	122	LYS	CB-CG-CD	6.94	127.26	111.30
4	x	120	GLU	CB-CG-CD	6.94	124.40	112.60
2	C0	254	GLU	CB-CG-CD	6.93	124.39	112.60
1	2	257	PRO	O-C-N	-6.93	117.89	121.15
3	F1	118	ASP	CA-CB-CG	6.93	119.53	112.60
2	A0	96	LYS	CB-CG-CD	6.92	127.22	111.30
2	D6	2	ARG	CG-CD-NE	-6.92	96.77	112.00
2	A8	284	GLU	CB-CG-CD	6.92	124.36	112.60
3	E1	320	ARG	CB-CG-CD	6.88	127.12	111.30
3	B3	81	PHE	CA-CB-CG	6.88	120.68	113.80
4	d	101	GLU	CB-CG-CD	6.86	124.26	112.60
3	D1	391	ARG	CB-CG-CD	6.86	127.07	111.30
2	B4	221	ARG	CG-CD-NE	6.85	127.07	112.00
2	D0	32	PRO	CA-C-N	6.85	130.14	120.28
2	D0	32	PRO	C-N-CA	6.85	130.14	120.28
4	t	155	GLU	CB-CG-CD	6.85	124.24	112.60
4	c	178	ARG	NH1-CZ-NH2	-6.84	110.41	119.30
2	C8	358	GLN	CB-CA-C	6.83	118.50	108.87
5	w	25	ARG	CB-CG-CD	6.83	127.00	111.30
4	j	117	ARG	CG-CD-NE	6.82	127.00	112.00
2	C4	220	GLU	CB-CG-CD	6.82	124.19	112.60
4	r	194	ARG	CG-CD-NE	6.82	127.00	112.00
2	A6	214	ARG	CD-NE-CZ	6.81	133.94	124.40
2	E0	96	LYS	CG-CD-CE	6.80	126.95	111.30
3	E7	399	THR	CA-C-N	6.78	127.51	119.98
3	E7	399	THR	C-N-CA	6.78	127.51	119.98
4	l	97	ARG	CB-CG-CD	6.77	126.88	111.30
1	4	248	ARG	CG-CD-NE	6.76	126.88	112.00
2	D2	339	ARG	N-CA-CB	6.75	121.19	110.73
4	b	146	ARG	CG-CD-NE	6.75	126.85	112.00
4	m	202	ARG	CD-NE-CZ	6.74	133.83	124.40
3	C9	391	ARG	CB-CG-CD	6.72	126.76	111.30
3	C3	118	ASP	CA-CB-CG	6.72	119.32	112.60
3	A3	125	GLU	CB-CG-CD	6.71	124.01	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	i	106	GLN	CB-CA-C	-6.71	98.19	109.53
2	E4	404	PHE	CA-CB-CG	6.70	120.50	113.80
3	D5	177	ASP	CB-CA-C	6.68	123.05	109.76
4	q	152	LYS	CG-CD-CE	6.67	126.64	111.30
1	11	241	PHE	CA-CB-CG	6.67	120.47	113.80
3	E3	380	ARG	CB-CG-CD	6.67	126.63	111.30
1	22	248	ARG	NE-CZ-NH2	6.65	125.19	119.20
4	v	109	GLU	CB-CG-CD	6.65	123.91	112.60
2	D8	214	ARG	CB-CG-CD	-6.65	96.01	111.30
4	l	91	PHE	CA-CB-CG	-6.65	107.15	113.80
2	A8	214	ARG	CG-CD-NE	6.64	126.61	112.00
1	17	248	ARG	NE-CZ-NH2	6.64	125.17	119.20
2	B6	49	PHE	N-CA-CB	6.63	120.08	110.47
2	E2	416	GLY	N-CA-C	-6.62	106.50	113.58
1	22	248	ARG	CB-CG-CD	6.61	126.51	111.30
1	5	248	ARG	CG-CD-NE	6.61	126.53	112.00
2	B8	113	GLU	CB-CG-CD	6.60	123.83	112.60
2	C2	221	ARG	CG-CD-NE	6.59	126.51	112.00
4	n	56	LYS	CG-CD-CE	6.59	126.45	111.30
3	B9	309	ARG	CG-CD-NE	-6.58	97.53	112.00
4	o	91	PHE	CA-CB-CG	-6.57	107.23	113.80
3	D9	380	ARG	CD-NE-CZ	6.57	133.60	124.40
5	w	156	ARG	CG-CD-NE	6.55	126.41	112.00
2	A6	85	HIS	CA-CB-CG	6.54	120.34	113.80
4	c	158	THR	CA-CB-OG1	-6.53	99.80	109.60
2	B0	336	LYS	CB-CG-CD	6.53	126.31	111.30
4	m	202	ARG	CG-CD-NE	6.52	126.35	112.00
2	A0	279	GLU	CB-CG-CD	6.51	123.67	112.60
3	C9	227	HIS	CA-CB-CG	6.51	120.31	113.80
3	B7	320	ARG	CB-CG-CD	6.50	126.25	111.30
5	w	107	GLU	CB-CG-CD	6.49	123.63	112.60
2	C8	33	ASP	CA-CB-CG	6.49	119.09	112.60
3	D1	291	GLN	CA-CB-CG	6.49	127.08	114.10
3	B9	337	ASN	N-CA-CB	6.47	117.60	110.35
4	o	139	PRO	CB-CA-C	-6.47	101.46	112.26
3	D3	177	ASP	CA-CB-CG	6.45	119.05	112.60
2	C4	326	LYS	CG-CD-CE	6.45	126.12	111.30
1	17	256	LEU	CA-C-N	6.44	124.36	119.66
1	17	256	LEU	C-N-CA	6.44	124.36	119.66
2	B2	311	LYS	CB-CG-CD	6.44	126.11	111.30
2	D6	229	ARG	CB-CA-C	-6.44	100.77	110.88
3	C9	291	GLN	CB-CA-C	6.43	121.79	110.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	120	GLU	CB-CG-CD	6.43	123.53	112.60
3	E9	320	ARG	NE-CZ-NH1	-6.42	115.08	121.50
2	D8	85	HIS	CA-CB-CG	6.41	120.21	113.80
4	b	97	ARG	CB-CG-CD	6.41	126.04	111.30
4	p	16	ARG	CG-CD-NE	6.41	126.09	112.00
2	A2	214	ARG	NE-CZ-NH2	6.39	124.95	119.20
3	A9	280	GLN	CB-CG-CD	6.38	123.44	112.60
3	D9	380	ARG	NE-CZ-NH2	6.38	124.94	119.20
4	q	97	ARG	CD-NE-CZ	6.38	133.33	124.40
2	C6	101	ASN	CB-CG-ND2	6.37	125.95	116.40
4	k	97	ARG	CB-CG-CD	6.36	125.93	111.30
3	C1	204	ASN	CA-CB-CG	6.35	118.95	112.60
3	E9	88	ASP	CA-CB-CG	6.35	118.95	112.60
1	5	248	ARG	CB-CG-CD	6.34	125.89	111.30
3	F1	320	ARG	CG-CD-NE	6.34	125.95	112.00
3	B5	275	SER	CA-C-N	6.34	129.06	120.38
3	B5	275	SER	C-N-CA	6.34	129.06	120.38
3	C1	227	HIS	CA-CB-CG	6.33	120.13	113.80
4	c	198	ARG	CB-CG-CD	6.33	125.86	111.30
2	A0	2	ARG	CG-CD-NE	6.32	125.91	112.00
4	n	202	ARG	CG-CD-NE	6.32	125.91	112.00
1	6	245	SER	CA-C-N	6.29	129.03	120.54
1	6	245	SER	C-N-CA	6.29	129.03	120.54
3	C7	320	ARG	CG-CD-NE	6.28	125.82	112.00
4	r	91	PHE	CB-CA-C	-6.26	100.39	110.79
2	D0	298	PRO	CB-CA-C	-6.26	102.54	111.68
2	D0	344	VAL	CA-C-N	6.25	128.99	120.54
2	D0	344	VAL	C-N-CA	6.25	128.99	120.54
3	D7	380	ARG	CB-CG-CD	6.25	125.67	111.30
5	w	104	LYS	CB-CG-CD	6.25	125.67	111.30
3	B3	122	LYS	CB-CG-CD	6.24	125.65	111.30
3	A5	383	ASP	CA-CB-CG	6.23	118.83	112.60
3	F1	45	GLU	CB-CG-CD	6.23	123.19	112.60
2	D8	80	THR	CA-CB-CG2	6.22	121.07	110.50
4	i	155	GLU	CB-CG-CD	6.22	123.17	112.60
2	B8	123	ARG	CB-CG-CD	6.22	125.60	111.30
3	E7	10	GLY	CA-C-N	6.22	129.43	120.79
3	E7	10	GLY	C-N-CA	6.22	129.43	120.79
3	E3	320	ARG	CG-CD-NE	6.21	125.66	112.00
4	e	15	ARG	NE-CZ-NH2	6.21	124.79	119.20
4	l	178	ARG	CG-CD-NE	6.21	125.65	112.00
2	E0	206	ASN	CB-CA-C	6.20	121.21	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B7	410	GLU	CB-CA-C	-6.19	100.32	110.85
4	p	95	TYR	N-CA-CB	-6.19	101.00	110.16
3	B3	125	GLU	CA-C-N	6.19	126.98	119.99
3	B3	125	GLU	C-N-CA	6.19	126.98	119.99
4	m	194	ARG	CG-CD-NE	6.18	125.60	112.00
1	17	248	ARG	CG-CD-NE	6.18	125.59	112.00
2	C6	112	LYS	CB-CG-CD	6.18	125.50	111.30
4	r	97	ARG	CG-CD-NE	6.17	125.58	112.00
4	h	63	ILE	O-C-N	-6.17	117.48	121.37
2	B6	339	ARG	CG-CD-NE	6.17	125.56	112.00
3	C9	157	GLU	CB-CG-CD	6.17	123.08	112.60
2	D6	162	GLY	CA-C-N	6.16	129.14	120.28
2	D6	162	GLY	C-N-CA	6.16	129.14	120.28
3	A5	212	PHE	CA-CB-CG	-6.15	107.65	113.80
3	B5	227	HIS	CA-CB-CG	6.15	119.95	113.80
1	15	241	PHE	CA-CB-CG	6.15	119.95	113.80
3	A7	227	HIS	CA-CB-CG	6.11	119.91	113.80
3	A5	276	ARG	CB-CG-CD	6.09	125.31	111.30
2	D2	370	LYS	CB-CG-CD	6.08	125.30	111.30
3	C3	204	ASN	CB-CA-C	-6.07	101.34	110.88
2	D6	85	HIS	CA-CB-CG	6.07	119.87	113.80
2	A6	156	ARG	CB-CG-CD	6.07	125.26	111.30
3	B5	332	ASN	CA-CB-CG	6.07	118.67	112.60
3	D1	162	ARG	NE-CZ-NH1	-6.05	115.45	121.50
4	r	198	ARG	CG-CD-NE	6.04	125.29	112.00
3	D9	276	ARG	CB-CG-CD	6.04	125.18	111.30
2	B0	277	SER	CA-C-N	6.03	129.19	120.38
2	B0	277	SER	C-N-CA	6.03	129.19	120.38
2	C0	85	HIS	CA-CB-CG	6.03	119.83	113.80
3	E3	276	ARG	CB-CG-CD	6.03	125.17	111.30
2	A6	370	LYS	N-CA-CB	6.02	118.98	109.71
3	D5	291	GLN	CB-CA-C	-6.02	101.43	110.88
2	D2	285	GLN	CB-CG-CD	-6.01	102.38	112.60
4	r	117	ARG	CD-NE-CZ	6.01	132.81	124.40
4	i	7	ALA	N-CA-CB	6.01	120.50	110.53
2	D8	76	ASP	CA-CB-CG	6.00	118.60	112.60
2	D4	85	HIS	N-CA-C	-6.00	106.29	113.97
2	D6	33	ASP	CA-CB-CG	6.00	118.60	112.60
3	C9	391	ARG	CG-CD-NE	6.00	125.19	112.00
3	E3	26	ASP	CA-CB-CG	5.99	118.59	112.60
2	A2	85	HIS	CA-CB-CG	5.98	119.78	113.80
2	A2	84	ARG	CA-C-N	5.98	128.78	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A2	84	ARG	C-N-CA	5.98	128.78	120.29
3	E5	122	LYS	CB-CG-CD	5.98	125.05	111.30
2	E2	284	GLU	CB-CG-CD	5.97	122.75	112.60
3	D1	355	ASP	CA-CB-CG	5.97	118.57	112.60
3	C5	11	GLN	N-CA-CB	-5.95	101.37	110.12
4	h	123	GLU	CB-CG-CD	5.95	122.71	112.60
4	e	6	PHE	CA-CB-CG	-5.94	107.86	113.80
3	F1	83	GLN	CB-CG-CD	-5.94	102.50	112.60
4	d	195	ALA	CA-C-N	5.94	129.05	120.38
4	d	195	ALA	C-N-CA	5.94	129.05	120.38
3	D9	380	ARG	NE-CZ-NH1	-5.93	115.56	121.50
3	A5	10	GLY	CA-C-N	5.93	129.71	120.82
3	A5	10	GLY	C-N-CA	5.93	129.71	120.82
2	B0	343	PHE	CA-CB-CG	-5.92	107.88	113.80
4	u	117	ARG	CG-CD-NE	5.92	125.03	112.00
3	A5	128	ASP	CB-CA-C	5.90	120.10	110.95
4	x	51	PRO	CA-C-N	5.89	129.66	120.82
4	x	51	PRO	C-N-CA	5.89	129.66	120.82
4	c	198	ARG	CB-CA-C	5.89	120.61	110.01
3	D3	54	ALA	CA-C-N	5.89	132.79	121.54
3	D3	54	ALA	C-N-CA	5.89	132.79	121.54
2	C8	11	GLN	CB-CG-CD	-5.88	102.61	112.60
4	m	202	ARG	CB-CG-CD	5.88	124.81	111.30
1	7	237	PRO	CB-CA-C	5.87	121.26	110.10
1	15	256	LEU	N-CA-C	5.87	116.79	109.57
1	12	245	SER	CA-C-N	5.86	128.41	120.38
1	12	245	SER	C-N-CA	5.86	128.41	120.38
2	B6	286	LEU	N-CA-CB	-5.86	102.14	110.58
2	E0	162	GLY	CA-C-N	5.86	132.72	121.54
2	E0	162	GLY	C-N-CA	5.86	132.72	121.54
3	E1	320	ARG	CG-CD-NE	5.85	124.88	112.00
4	o	155	GLU	CB-CG-CD	5.85	122.55	112.60
4	o	151	MET	CA-C-N	5.85	128.59	120.29
4	o	151	MET	C-N-CA	5.85	128.59	120.29
3	C5	291	GLN	CA-CB-CG	-5.84	102.42	114.10
2	B6	285	GLN	CB-CA-C	5.84	119.97	110.22
3	B5	177	ASP	CA-CB-CG	5.83	118.43	112.60
3	D1	11	GLN	OE1-CD-NE2	-5.82	116.78	122.60
2	B0	390	ARG	CG-CD-NE	5.82	124.81	112.00
3	D9	343	GLU	CB-CG-CD	5.82	122.49	112.60
4	m	79	ASP	CA-C-N	5.82	126.40	119.94
4	m	79	ASP	C-N-CA	5.82	126.40	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A6	18	ASN	CA-CB-CG	5.82	118.42	112.60
4	s	128	HIS	CA-CB-CG	5.81	119.61	113.80
4	u	65	GLN	CB-CA-C	-5.81	99.52	110.67
1	15	255	PRO	CA-C-N	5.80	129.13	120.83
1	15	255	PRO	C-N-CA	5.80	129.13	120.83
4	t	178	ARG	CG-CD-NE	5.80	124.76	112.00
3	D9	251	ARG	CB-CG-CD	5.80	124.63	111.30
3	C5	77	ARG	CG-CD-NE	5.78	124.71	112.00
3	C5	122	LYS	CB-CG-CD	5.78	124.58	111.30
4	l	82	ASP	CB-CA-C	5.77	117.68	109.08
3	C5	357	PRO	N-CA-CB	5.77	106.22	103.22
2	D6	156	ARG	CG-CD-NE	-5.77	99.30	112.00
3	D5	391	ARG	NE-CZ-NH2	5.77	124.39	119.20
3	B3	216	LYS	CB-CG-CD	5.77	124.56	111.30
2	A4	2	ARG	CB-CG-CD	5.77	124.56	111.30
1	10	253	ALA	CA-C-N	5.76	129.44	120.68
1	10	253	ALA	C-N-CA	5.76	129.44	120.68
2	C0	221	ARG	CD-NE-CZ	5.76	132.46	124.40
3	C3	46	ARG	CB-CG-CD	5.74	124.50	111.30
3	D5	343	GLU	CB-CA-C	5.74	118.71	109.07
1	9	248	ARG	CD-NE-CZ	5.74	132.43	124.40
3	C3	410	GLU	CB-CA-C	-5.74	101.10	110.85
2	A4	393	HIS	CB-CA-C	-5.73	101.89	110.88
2	D8	275	ILE	CB-CA-C	5.72	117.44	111.09
3	A1	11	GLN	CB-CG-CD	-5.69	102.92	112.60
3	A3	128	ASP	CB-CA-C	5.69	119.77	110.95
1	12	242	ASN	CA-CB-CG	5.69	118.29	112.60
2	D4	373	ARG	CG-CD-NE	5.69	124.51	112.00
2	A0	326	LYS	CB-CG-CD	5.69	124.38	111.30
2	B2	297	GLU	CB-CG-CD	5.68	122.25	112.60
2	D4	229	ARG	CB-CA-C	-5.68	101.20	110.85
4	q	123	GLU	CB-CG-CD	5.68	122.25	112.60
1	5	240	PRO	CB-CA-C	-5.67	104.15	111.46
4	f	3	GLN	CB-CA-C	-5.66	102.63	110.16
2	A2	357	TYR	N-CA-CB	5.66	119.23	110.80
3	C1	203	ASP	CA-C-N	5.66	127.86	120.28
3	C1	203	ASP	C-N-CA	5.66	127.86	120.28
4	b	97	ARG	CG-CD-NE	5.66	124.44	112.00
2	D0	156	ARG	NE-CZ-NH1	-5.65	115.85	121.50
2	D6	393	HIS	CB-CA-C	5.65	120.46	110.85
4	t	164	ARG	CB-CG-CD	5.65	124.29	111.30
3	D9	276	ARG	NE-CZ-NH2	5.65	124.28	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	r	119	ARG	CG-CD-NE	5.65	124.42	112.00
1	15	257	PRO	CB-CA-C	-5.64	104.03	110.92
3	A7	162	ARG	CB-CG-CD	5.64	124.28	111.30
3	E5	376	GLU	CB-CG-CD	5.64	122.18	112.60
2	B8	221	ARG	NE-CZ-NH2	5.63	124.27	119.20
3	E9	280	GLN	CB-CA-C	5.63	121.87	110.38
3	B1	129	CYS	CA-C-O	5.63	127.35	120.25
3	D5	47	ILE	N-CA-C	-5.62	107.79	113.47
1	17	257	PRO	CB-CA-C	-5.62	106.11	111.39
3	F1	209	ASP	CA-CB-CG	-5.62	106.98	112.60
3	C7	108	GLU	CB-CG-CD	5.62	122.14	112.60
3	D9	41	ASP	CA-C-N	5.62	128.58	120.38
3	D9	41	ASP	C-N-CA	5.62	128.58	120.38
1	0	254	LYS	CB-CA-C	5.61	117.51	109.26
4	b	178	ARG	CD-NE-CZ	5.61	132.25	124.40
3	B5	130	LEU	N-CA-CB	-5.61	101.93	110.45
3	A7	276	ARG	CB-CG-CD	5.60	124.17	111.30
4	a	179	GLU	CB-CA-C	5.60	118.63	109.90
3	B1	209	ASP	CA-CB-CG	5.60	118.20	112.60
2	D2	340	THR	CA-CB-OG1	-5.60	101.21	109.60
2	D6	264	ARG	NE-CZ-NH1	-5.60	115.90	121.50
3	B7	401	GLU	CB-CA-C	5.59	118.47	109.07
3	E9	276	ARG	CG-CD-NE	5.59	124.31	112.00
3	D9	31	ASP	CA-CB-CG	5.59	118.19	112.60
4	v	97	ARG	CB-CG-CD	5.59	124.16	111.30
3	D5	72	THR	CA-CB-CG2	5.58	119.99	110.50
3	C9	213	ARG	CG-CD-NE	5.58	124.28	112.00
3	B5	10	GLY	CA-C-N	5.58	128.02	120.38
3	B5	10	GLY	C-N-CA	5.58	128.02	120.38
1	11	245	SER	CA-C-N	5.58	128.07	120.54
1	11	245	SER	C-N-CA	5.58	128.07	120.54
1	22	248	ARG	N-CA-CB	5.57	118.41	110.16
4	m	146	ARG	CG-CD-NE	5.57	124.26	112.00
3	E9	279	GLN	CB-CG-CD	5.57	122.06	112.60
3	C9	245	GLN	CB-CA-C	5.57	119.53	110.96
2	F0	285	GLN	N-CA-CB	5.56	118.72	109.60
4	g	48	ILE	CA-CB-CG2	-5.56	101.04	110.50
2	A0	217	LEU	CA-C-N	5.56	130.30	122.46
2	A0	217	LEU	C-N-CA	5.56	130.30	122.46
4	r	117	ARG	N-CA-CB	5.56	117.99	110.59
3	C5	379	LYS	CB-CG-CD	5.56	124.09	111.30
2	E6	363	VAL	O-C-N	-5.53	117.62	121.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	d	198	ARG	CB-CG-CD	5.53	124.01	111.30
3	D9	391	ARG	CG-CD-NE	5.51	124.13	112.00
2	A6	173	PRO	CB-CA-C	-5.51	104.80	111.46
3	C9	88	ASP	CA-CB-CG	5.50	118.11	112.60
3	A1	309	ARG	CG-CD-NE	-5.50	99.91	112.00
4	p	42	TYR	CA-C-N	5.50	127.06	120.13
4	p	42	TYR	C-N-CA	5.50	127.06	120.13
3	D5	268	ILE	CA-C-N	5.50	125.84	121.61
3	D5	268	ILE	C-N-CA	5.50	125.84	121.61
3	C5	130	LEU	CD1-CG-CD2	-5.49	98.72	110.80
2	A8	214	ARG	N-CA-CB	-5.49	102.04	110.16
2	C8	225	THR	CA-CB-OG1	-5.49	101.37	109.60
2	B0	58	ALA	CA-C-N	5.48	132.16	121.41
2	B0	58	ALA	C-N-CA	5.48	132.16	121.41
3	E5	194	GLU	CB-CG-CD	5.48	121.92	112.60
4	g	16	ARG	CG-CD-NE	5.48	124.06	112.00
2	A8	120	ASP	CA-CB-CG	5.48	118.08	112.60
2	D4	255	PHE	CA-CB-CG	5.48	119.28	113.80
2	A4	214	ARG	NE-CZ-NH1	-5.48	116.02	121.50
3	B7	47	ILE	N-CA-C	-5.48	108.16	113.53
3	C9	86	ARG	CG-CD-NE	-5.47	99.95	112.00
4	u	18	ASN	CA-CB-CG	-5.47	107.13	112.60
3	B7	426	GLN	CB-CA-C	5.47	120.48	110.10
3	A7	410	GLU	CB-CG-CD	5.46	121.89	112.60
3	B3	54	ALA	CA-C-N	5.46	131.97	121.54
3	B3	54	ALA	C-N-CA	5.46	131.97	121.54
2	D6	221	ARG	CG-CD-NE	5.46	124.01	112.00
3	D3	424	GLN	CB-CG-CD	5.46	121.88	112.60
3	C1	123	GLU	CB-CG-CD	5.46	121.87	112.60
3	D7	3	GLU	CB-CG-CD	5.45	121.87	112.60
4	g	16	ARG	N-CA-CB	5.45	118.06	109.94
3	E9	281	TYR	CB-CA-C	5.44	119.42	110.88
3	D1	397	TRP	N-CA-CB	5.43	118.59	110.22
4	g	49	LEU	N-CA-C	-5.43	104.77	111.40
2	B6	218	ASP	N-CA-CB	-5.43	104.22	112.47
2	B4	339	ARG	CB-CG-CD	5.42	123.77	111.30
4	a	195	ALA	CA-C-N	5.42	128.30	120.38
4	a	195	ALA	C-N-CA	5.42	128.30	120.38
3	C7	332	ASN	CA-CB-CG	5.42	118.02	112.60
3	C9	275	SER	CA-C-N	5.42	131.89	121.54
3	C9	275	SER	C-N-CA	5.42	131.89	121.54
3	D7	391	ARG	CG-CD-NE	-5.42	100.08	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	m	179	GLU	CB-CA-C	5.42	118.39	110.26
2	D8	218	ASP	CB-CA-C	5.41	119.11	111.86
3	D1	291	GLN	CB-CG-CD	-5.41	103.40	112.60
2	D0	18	ASN	CA-CB-CG	5.40	118.00	112.60
2	D4	11	GLN	CA-CB-CG	-5.40	103.30	114.10
4	f	99	MET	CB-CG-SD	-5.39	96.52	112.70
2	D2	163	LYS	CA-C-N	-5.39	114.85	122.94
2	D2	163	LYS	C-N-CA	-5.39	114.85	122.94
2	B0	221	ARG	CG-CD-NE	-5.39	100.15	112.00
3	A9	174	LYS	CB-CG-CD	5.38	123.68	111.30
2	E4	156	ARG	CB-CG-CD	5.38	123.67	111.30
4	g	24	MET	CA-CB-CG	-5.38	103.34	114.10
2	E4	221	ARG	CB-CG-CD	-5.38	98.93	111.30
3	A9	383	ASP	CA-CB-CG	5.38	117.98	112.60
3	A9	83	GLN	CB-CG-CD	5.37	121.74	112.60
4	c	98	THR	CA-C-N	-5.37	112.22	122.53
4	c	98	THR	C-N-CA	-5.37	112.22	122.53
4	i	19	GLU	CB-CA-C	5.37	120.03	109.72
3	A7	54	ALA	CA-C-N	5.36	131.78	121.54
3	A7	54	ALA	C-N-CA	5.36	131.78	121.54
2	D0	85	HIS	N-CA-CB	-5.36	102.65	110.53
2	D8	156	ARG	NE-CZ-NH2	5.36	124.02	119.20
4	s	56	LYS	CG-CD-CE	5.36	123.63	111.30
3	E7	394	PHE	CB-CA-C	5.36	122.44	110.76
3	D9	276	ARG	CD-NE-CZ	5.35	131.90	124.40
2	A2	214	ARG	CG-CD-NE	-5.35	100.22	112.00
4	b	138	ASN	CA-CB-CG	5.35	117.95	112.60
2	C6	83	TYR	CB-CA-C	5.35	119.07	111.74
4	n	128	HIS	CA-CB-CG	5.34	119.14	113.80
2	D0	36	MET	CB-CG-SD	5.34	128.72	112.70
3	A3	324	LYS	N-CA-CB	5.34	117.81	110.07
2	E6	85	HIS	CA-CB-CG	5.34	119.14	113.80
3	D1	178	THR	CA-C-N	5.33	131.57	121.97
3	D1	178	THR	C-N-CA	5.33	131.57	121.97
2	F0	336	LYS	CB-CG-CD	5.33	123.55	111.30
3	C7	397	TRP	CB-CG-CD1	5.31	134.87	126.90
2	E6	77	GLU	CB-CA-C	5.31	121.09	109.99
4	a	193	ASP	N-CA-CB	-5.31	104.50	113.15
4	p	120	GLU	CB-CG-CD	5.31	121.62	112.60
1	10	241	PHE	CB-CA-C	5.30	118.88	110.19
4	d	155	GLU	CB-CG-CD	5.30	121.61	112.60
3	E7	77	ARG	CB-CG-CD	5.30	123.48	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D8	163	LYS	CB-CG-CD	5.29	123.48	111.30
3	B5	212	PHE	CA-CB-CG	5.29	119.09	113.80
4	m	69	LYS	CB-CG-CD	5.29	123.47	111.30
2	A6	390	ARG	CG-CD-NE	5.29	123.63	112.00
4	m	69	LYS	CB-CA-C	5.29	118.69	109.65
5	w	24	VAL	CA-C-N	5.29	127.74	120.39
5	w	24	VAL	C-N-CA	5.29	127.74	120.39
2	A0	196	GLU	CB-CG-CD	5.29	121.59	112.60
2	E6	129	CYS	CA-C-N	5.28	130.35	120.95
2	E6	129	CYS	C-N-CA	5.28	130.35	120.95
4	a	164	ARG	CG-CD-NE	5.27	123.60	112.00
3	D3	366	THR	CA-CB-CG2	5.27	119.46	110.50
2	B2	218	ASP	CB-CA-C	5.27	119.80	112.11
3	A9	390	ARG	CG-CD-NE	5.26	123.57	112.00
4	g	47	LEU	N-CA-CB	-5.26	103.11	111.62
3	B3	204	ASN	CA-CB-CG	5.25	117.86	112.60
4	b	94	ASN	CA-CB-CG	5.25	117.86	112.60
3	D5	227	HIS	CA-CB-CG	5.25	119.05	113.80
4	c	126	ARG	NE-CZ-NH1	-5.25	116.25	121.50
3	A9	81	PHE	CA-CB-CG	5.25	119.05	113.80
3	D1	271	ALA	O-C-N	-5.25	118.15	121.88
4	m	183	LEU	CA-C-O	5.24	123.50	119.46
2	E4	221	ARG	CG-CD-NE	5.24	123.53	112.00
4	b	191	GLU	CB-CA-C	5.24	119.46	111.76
4	q	198	ARG	CG-CD-NE	5.23	123.51	112.00
2	B8	284	GLU	CA-C-N	5.23	129.78	121.99
2	B8	284	GLU	C-N-CA	5.23	129.78	121.99
2	A8	285	GLN	OE1-CD-NE2	-5.23	117.37	122.60
2	D4	71	GLU	CB-CA-C	5.22	115.94	108.68
3	C7	397	TRP	CB-CG-CD2	-5.22	119.49	126.80
4	n	82	ASP	CA-CB-CG	5.22	117.82	112.60
4	c	52	GLU	CB-CG-CD	5.22	121.47	112.60
4	t	50	PHE	CB-CA-C	-5.22	105.01	110.17
3	D9	205	GLU	CB-CG-CD	5.21	121.45	112.60
3	E1	125	GLU	CA-C-N	5.21	126.69	120.13
3	E1	125	GLU	C-N-CA	5.21	126.69	120.13
4	c	90	PRO	N-CD-CG	-5.20	95.40	103.20
2	F0	282	TYR	N-CA-CB	5.20	119.15	110.41
3	C7	276	ARG	CB-CG-CD	5.20	123.25	111.30
2	D2	340	THR	CA-CB-CG2	5.20	119.33	110.50
4	n	28	LYS	CB-CG-CD	5.20	123.25	111.30
2	C4	85	HIS	CA-CB-CG	5.19	118.99	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	p	105	ASN	CA-C-O	-5.19	115.64	121.40
2	E6	326	LYS	N-CA-CB	5.19	117.84	110.16
4	q	91	PHE	CA-CB-CG	-5.19	108.61	113.80
4	a	194	ARG	CB-CA-C	-5.18	102.47	109.16
3	A9	83	GLN	OE1-CD-NE2	-5.18	117.42	122.60
3	B9	212	PHE	CA-CB-CG	5.18	118.98	113.80
4	c	99	MET	N-CA-CB	5.18	118.34	110.42
4	g	97	ARG	CG-CD-NE	-5.18	100.61	112.00
3	E7	139	LEU	CA-C-N	5.18	125.83	120.03
3	E7	139	LEU	C-N-CA	5.18	125.83	120.03
4	i	202	ARG	CB-CG-CD	-5.17	99.40	111.30
2	C6	282	TYR	N-CA-CB	-5.17	102.26	110.22
2	E2	254	GLU	CB-CG-CD	5.17	121.39	112.60
2	A6	280	LYS	CB-CG-CD	5.17	123.18	111.30
2	C4	401	LYS	CB-CA-C	5.17	122.25	111.97
3	B3	227	HIS	CB-CG-CD2	5.17	137.91	131.20
3	C1	271	ALA	O-C-N	-5.16	118.22	121.88
3	A3	252	LYS	CB-CG-CD	5.16	123.17	111.30
3	E9	320	ARG	CD-NE-CZ	-5.16	117.17	124.40
3	C7	396	HIS	CA-C-N	5.16	127.71	120.28
3	C7	396	HIS	C-N-CA	5.16	127.71	120.28
3	D9	191	GLN	CB-CG-CD	5.16	121.37	112.60
2	D0	85	HIS	N-CA-C	-5.15	107.16	113.50
4	h	155	GLU	CB-CG-CD	5.15	121.36	112.60
4	o	118	ASP	CA-C-N	5.15	127.50	120.54
4	o	118	ASP	C-N-CA	5.15	127.50	120.54
3	F1	11	GLN	CB-CG-CD	-5.15	103.85	112.60
3	F1	123	GLU	CB-CG-CD	5.15	121.35	112.60
3	B7	54	ALA	N-CA-C	5.15	117.47	110.88
3	A7	282	ARG	CD-NE-CZ	5.14	131.60	124.40
3	D7	26	ASP	CA-CB-CG	5.14	117.74	112.60
2	C6	218	ASP	CA-CB-CG	5.14	117.74	112.60
2	B0	214	ARG	CG-CD-NE	-5.14	100.70	112.00
2	C2	430	LYS	CB-CA-C	-5.13	102.27	110.79
2	C6	372	MET	CB-CG-SD	5.13	128.10	112.70
4	r	123	GLU	CB-CG-CD	5.13	121.32	112.60
3	C3	251	ARG	CG-CD-NE	-5.12	100.73	112.00
2	C6	156	ARG	CB-CG-CD	5.12	123.09	111.30
4	t	97	ARG	CG-CD-NE	-5.12	100.73	112.00
3	D1	343	GLU	CB-CG-CD	5.12	121.30	112.60
2	D2	297	GLU	CB-CG-CD	5.12	121.30	112.60
2	B0	11	GLN	CB-CG-CD	-5.12	103.90	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C0	221	ARG	CB-CA-C	5.11	117.76	110.96
2	E2	77	GLU	CB-CA-C	5.11	119.92	109.55
3	C1	11	GLN	CB-CG-CD	-5.11	103.92	112.60
2	C6	322	ASP	CA-CB-CG	5.11	117.71	112.60
2	F0	47	ASP	CA-C-N	5.11	127.08	120.44
2	F0	47	ASP	C-N-CA	5.11	127.08	120.44
2	A6	370	LYS	CB-CA-C	5.10	117.91	110.26
1	2	246	CYS	O-C-N	5.10	127.39	122.09
1	15	247	TYR	CB-CA-C	5.10	118.81	110.96
2	A0	163	LYS	CG-CD-CE	5.10	123.03	111.30
2	C0	282	TYR	CA-CB-CG	-5.10	104.72	113.90
2	C6	176	GLN	CB-CG-CD	5.10	121.27	112.60
3	E7	83	GLN	CB-CG-CD	-5.10	103.94	112.60
3	D5	213	ARG	CG-CD-NE	5.09	123.21	112.00
2	C6	370	LYS	CB-CG-CD	5.09	123.01	111.30
2	C8	390	ARG	CG-CD-NE	5.09	123.19	112.00
3	A9	45	GLU	CB-CG-CD	5.08	121.25	112.60
2	F0	221	ARG	CB-CA-C	5.08	117.87	111.21
2	C0	221	ARG	NE-CZ-NH2	5.08	123.77	119.20
2	D6	11	GLN	CB-CG-CD	-5.08	103.97	112.60
3	B9	309	ARG	CB-CG-CD	5.07	122.97	111.30
4	p	6	PHE	CA-CB-CG	-5.07	108.73	113.80
1	8	255	PRO	CA-C-N	5.07	127.46	120.67
1	8	255	PRO	C-N-CA	5.07	127.46	120.67
3	A1	379	LYS	CB-CG-CD	-5.07	99.64	111.30
3	B7	391	ARG	CB-CG-CD	5.07	122.95	111.30
4	n	16	ARG	CB-CG-CD	5.06	122.94	111.30
2	A0	35	GLN	CB-CG-CD	5.06	121.20	112.60
2	A8	433	GLU	CB-CG-CD	5.06	121.20	112.60
2	A0	224	TYR	N-CA-C	5.06	117.45	111.33
4	y	155	GLU	CB-CG-CD	5.06	121.20	112.60
2	B6	48	ALA	CA-C-O	-5.05	113.16	119.38
2	A6	124	LYS	CB-CG-CD	5.05	122.92	111.30
2	A6	71	GLU	CB-CA-C	5.05	115.43	109.47
1	6	248	ARG	CB-CG-CD	5.05	122.91	111.30
3	C1	384	GLN	CB-CG-CD	5.05	121.18	112.60
2	A6	370	LYS	CB-CG-CD	5.04	122.90	111.30
1	11	246	CYS	CA-CB-SG	5.04	125.99	114.40
1	17	248	ARG	CD-NE-CZ	5.04	131.45	124.40
1	6	237	PRO	CA-N-CD	-5.04	104.95	112.00
2	D6	60	LYS	CB-CG-CD	5.04	122.89	111.30
2	F0	85	HIS	CA-CB-CG	5.04	118.84	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	120	GLU	CB-CG-CD	5.04	121.17	112.60
3	A1	355	ASP	CA-CB-CG	5.04	117.64	112.60
2	A0	121	ARG	CG-CD-NE	5.04	123.08	112.00
2	A6	96	LYS	CB-CA-C	5.04	119.78	110.56
1	0	257	PRO	N-CA-CB	5.03	105.83	103.22
4	t	155	GLU	CB-CA-C	5.03	118.62	110.37
3	D9	426	GLN	CB-CA-C	5.03	119.65	110.10
1	4	240	PRO	CB-CA-C	5.03	117.46	110.17
2	C6	339	ARG	CB-CG-CD	5.02	122.85	111.30
2	F0	280	LYS	CG-CD-CE	5.02	122.86	111.30
4	e	95	TYR	N-CA-CB	-5.02	102.73	110.16
2	A2	218	ASP	CA-CB-CG	5.02	117.62	112.60
3	A1	177	ASP	CA-CB-CG	5.01	117.61	112.60
2	E2	11	GLN	CB-CG-CD	-5.01	104.08	112.60
3	E9	336	LYS	CA-CB-CG	5.01	124.13	114.10
5	w	55	GLN	CB-CG-CD	5.01	121.12	112.60
4	r	15	ARG	NE-CZ-NH2	5.01	123.71	119.20
4	g	13	GLU	CB-CG-CD	5.01	121.11	112.60
1	13	242	ASN	CB-CA-C	5.00	120.06	111.45
2	A6	211	ASP	CA-CB-CG	5.00	117.60	112.60
4	a	202	ARG	N-CA-C	-5.00	105.91	111.36

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	12	255	PRO	Peptide
1	19	257	PRO	Peptide
1	2	239	LEU	Peptide
1	20	238	THR	Peptide
1	20	239	LEU	Peptide
1	21	239	LEU	Peptide
1	23	255	PRO	Peptide
1	7	237	PRO	Peptide
1	8	240	PRO	Peptide
2	A0	163	LYS	Peptide
2	A2	284	GLU	Peptide
2	A2	401	LYS	Peptide
2	A4	401	LYS	Peptide
2	A8	284	GLU	Peptide
3	B3	43	GLN	Peptide
2	B4	284	GLU	Peptide

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Mol	Chain	Res	Type	Group
2	B6	284	GLU	Peptide
2	B6	338	LYS	Peptide
3	B9	200	GLN	Peptide
2	C4	401	LYS	Peptide
2	C8	284	GLU	Peptide
2	D2	163	LYS	Peptide
2	D2	284	GLU	Peptide
2	D8	163	LYS	Peptide
2	E4	163	LYS	Peptide
3	E5	321	MET	Peptide
3	E5	322	SER	Peptide
3	E9	354	CYS	Peptide
2	F0	162	GLY	Peptide
4	o	91	PHE	Sidechain
4	s	35	ASN	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	0	174	0	171	17	0
1	1	174	0	171	6	0
1	10	174	0	171	16	0
1	11	174	0	171	9	0
1	12	174	0	171	4	0
1	13	174	0	171	7	0
1	14	174	0	171	0	0
1	15	174	0	171	11	0
1	16	174	0	171	10	0
1	17	174	0	171	5	0
1	18	174	0	171	28	0
1	19	174	0	171	28	0
1	2	174	0	171	10	0
1	20	174	0	171	8	0
1	21	174	0	171	25	0
1	22	160	0	156	6	0
1	23	160	0	156	13	0
1	3	174	0	171	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	4	174	0	171	19	0
1	5	174	0	171	7	0
1	6	174	0	171	15	0
1	7	174	0	171	7	0
1	8	174	0	171	10	0
1	9	174	0	171	8	0
2	A0	3325	0	3252	87	0
2	A2	3325	0	3252	89	0
2	A4	3325	0	3252	60	0
2	A6	3325	0	3252	85	0
2	A8	3325	0	3252	78	0
2	B0	3325	0	3252	92	0
2	B2	3325	0	3252	54	0
2	B4	3325	0	3252	84	0
2	B6	3325	0	3252	71	0
2	B8	3325	0	3252	75	0
2	C0	3325	0	3252	73	0
2	C2	3325	0	3252	73	0
2	C4	3325	0	3252	88	0
2	C6	3325	0	3252	104	0
2	C8	3325	0	3252	59	0
2	D0	3325	0	3252	81	0
2	D2	3325	0	3252	71	0
2	D4	3325	0	3252	97	0
2	D6	3325	0	3252	60	0
2	D8	3325	0	3252	63	0
2	E0	3325	0	3252	95	0
2	E2	3325	0	3252	68	0
2	E4	3325	0	3252	153	0
2	E6	3325	0	3252	94	0
2	E8	3325	0	3252	76	0
2	F0	3325	0	3252	111	0
3	A1	3331	0	3207	88	0
3	A3	3331	0	3209	70	0
3	A5	3331	0	3207	66	0
3	A7	3331	0	3207	62	0
3	A9	3331	0	3207	86	0
3	B1	3331	0	3209	95	0
3	B3	3331	0	3207	59	0
3	B5	3331	0	3207	84	0
3	B7	3331	0	3209	80	0
3	B9	3331	0	3209	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C1	3331	0	3209	86	0
3	C3	3331	0	3209	82	0
3	C5	3331	0	3209	80	0
3	C7	3331	0	3209	70	0
3	C9	3331	0	3209	88	0
3	D1	3331	0	3209	72	0
3	D3	3331	0	3207	96	0
3	D5	3331	0	3207	91	0
3	D7	3331	0	3207	79	0
3	D9	3331	0	3207	75	0
3	E1	3331	0	3207	96	0
3	E3	3331	0	3209	55	0
3	E5	3331	0	3207	159	0
3	E7	3331	0	3207	74	0
3	E9	3331	0	3207	70	0
3	F1	3331	0	3207	71	0
4	a	1198	0	1194	35	0
4	b	1198	0	1194	42	0
4	c	1608	0	1590	71	0
4	d	1608	0	1590	68	0
4	e	1608	0	1590	75	0
4	f	1608	0	1590	79	0
4	g	1608	0	1590	73	0
4	h	1608	0	1590	71	0
4	i	1608	0	1590	67	0
4	j	1608	0	1590	84	0
4	k	1608	0	1590	82	0
4	l	1608	0	1590	90	0
4	m	1608	0	1590	57	0
4	n	1608	0	1590	57	0
4	o	1608	0	1590	39	0
4	p	1608	0	1590	33	0
4	q	1608	0	1590	43	0
4	r	1608	0	1590	44	0
4	s	1608	0	1590	61	0
4	t	1608	0	1590	68	0
4	u	1608	0	1590	49	0
4	v	1608	0	1590	88	0
4	x	1608	0	1590	109	0
4	y	1608	0	1590	86	0
5	w	1172	0	1171	20	0
All	All	216148	0	210569	4710	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (4710) 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)
4:b:97:ARG:NH1	4:d:6:PHE:HB3	1.24	1.50
2:C4:2:ARG:NE	2:C4:2:ARG:CD	1.74	1.46
1:4:240:PRO:CB	4:g:154:TYR:HB3	1.50	1.38
4:i:63:ILE:CD1	4:k:16:ARG:HG3	1.53	1.38
1:4:240:PRO:HB2	4:g:154:TYR:CB	1.56	1.35
2:A0:37:PRO:O	4:y:86:ALA:HB1	1.31	1.30
4:v:128:HIS:O	4:x:159:TYR:CD1	1.86	1.27
1:13:247:TYR:OH	2:D4:81:GLY:HA3	1.22	1.27
4:i:106:GLN:NE2	4:k:15:ARG:HD2	1.52	1.23
3:A1:219:THR:CG2	2:A2:324:VAL:HG21	1.69	1.21
4:v:128:HIS:O	4:x:159:TYR:HD1	1.15	1.21
1:0:244:GLN:NE2	4:c:162:GLY:HA2	1.54	1.20
1:15:247:TYR:OH	2:D8:81:GLY:CA	1.88	1.20
1:15:247:TYR:OH	2:D8:81:GLY:HA3	1.09	1.19
2:E4:403:ALA:HA	3:E5:260:PHE:CE1	1.77	1.19
4:x:93:LEU:HD21	4:y:159:TYR:C	1.67	1.19
2:E4:222:PRO:HG2	3:E5:324:LYS:HB2	1.21	1.18
2:E4:222:PRO:HG2	3:E5:324:LYS:CB	1.72	1.17
2:E4:100:ALA:CB	3:E5:251:ARG:HG2	1.75	1.16
4:x:100:ASN:ND2	4:y:6:PHE:CE1	2.14	1.16
2:B0:222:PRO:HD2	3:B1:324:LYS:HB3	1.28	1.16
4:i:106:GLN:NE2	4:k:15:ARG:CD	2.09	1.15
4:v:67:HIS:HD2	4:x:19:GLU:CD	1.54	1.15
2:B0:73:THR:HB	3:B1:2:ARG:NH2	1.58	1.15
4:j:106:GLN:HG3	4:l:6:PHE:HE1	1.05	1.15
3:B5:57:GLY:HA3	4:f:83:PRO:CB	1.76	1.15
4:i:71:LYS:HZ3	4:k:39:PRO:HG3	1.03	1.14
2:A4:221:ARG:NH2	4:c:189:LEU:O	1.81	1.13
4:s:66:SER:O	4:u:23:LEU:HD11	1.49	1.12
2:B0:221:ARG:HB2	3:B1:322:SER:CB	1.79	1.12
4:j:93:LEU:HD21	4:l:159:TYR:O	1.48	1.12
4:x:93:LEU:HD21	4:y:159:TYR:O	1.46	1.12
3:B5:57:GLY:HA3	4:f:83:PRO:HB2	1.15	1.12
1:0:244:GLN:HE21	4:c:162:GLY:CA	1.62	1.11
1:19:243:ALA:HB3	3:E7:356:ILE:HD12	1.32	1.11
4:i:63:ILE:HD12	4:k:16:ARG:CG	1.80	1.11
1:0:244:GLN:NE2	4:c:162:GLY:CA	2.13	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A1:219:THR:HG23	2:A2:324:VAL:CG2	1.79	1.10
4:j:106:GLN:HG3	4:l:6:PHE:CE1	1.85	1.10
4:s:70:GLY:HA3	4:u:38:LEU:O	1.51	1.10
4:v:63:ILE:HD12	4:x:16:ARG:HG3	1.24	1.10
1:13:247:TYR:OH	2:D4:81:GLY:CA	1.98	1.10
4:s:96:TYR:OH	4:u:6:PHE:HE2	1.34	1.09
2:C4:404:PHE:HE1	3:C5:255:VAL:O	1.32	1.08
4:i:63:ILE:CD1	4:k:16:ARG:CG	2.31	1.08
4:j:106:GLN:HG2	4:l:6:PHE:CZ	1.90	1.07
2:A2:214:ARG:HD2	3:A3:324:LYS:NZ	1.66	1.07
1:19:243:ALA:HB1	3:E7:356:ILE:HD13	1.37	1.06
3:E9:69:GLU:OE1	2:F0:2:ARG:NH1	1.87	1.06
4:b:97:ARG:NH1	4:d:6:PHE:CB	2.18	1.06
2:E0:176:GLN:HB3	3:E1:331:LEU:HD13	1.35	1.06
4:v:67:HIS:CD2	4:x:19:GLU:OE2	2.09	1.06
4:l:96:TYR:HE2	4:n:6:PHE:CE2	1.73	1.05
2:B0:394:LYS:HD3	3:B1:346:PRO:HG3	1.34	1.05
4:i:106:GLN:HE22	4:k:15:ARG:HD2	1.02	1.05
2:E0:223:THR:OG1	3:E1:245:GLN:NE2	1.89	1.05
2:B0:221:ARG:HB2	3:B1:322:SER:OG	1.57	1.05
1:0:247:TYR:OH	2:A4:81:GLY:HA2	1.55	1.04
2:B0:222:PRO:HD2	3:B1:324:LYS:CB	1.87	1.04
3:C5:219:THR:HB	2:C6:324:VAL:HG11	1.39	1.04
1:21:257:PRO:HD2	2:F0:29:GLY:HA2	1.38	1.03
2:C6:407:TRP:CZ3	3:C7:255:VAL:HA	1.93	1.03
4:t:67:HIS:HE1	4:v:16:ARG:HG2	1.18	1.03
2:B0:223:THR:HB	3:B1:245:GLN:OE1	1.58	1.03
1:5:240:PRO:HB3	4:h:154:TYR:HB3	1.34	1.03
1:4:247:TYR:CZ	2:B2:81:GLY:HA3	1.93	1.02
4:e:9:PRO:HB2	4:e:143:ILE:HG23	1.39	1.02
1:21:256:LEU:HD13	2:F0:29:GLY:O	1.60	1.02
4:d:106:GLN:NE2	4:f:6:PHE:HZ	1.56	1.02
4:j:106:GLN:CG	4:l:6:PHE:CE1	2.43	1.02
1:23:257:PRO:HG3	2:C4:26:LEU:HD12	1.42	1.01
4:i:63:ILE:HD13	4:k:16:ARG:CD	1.89	1.01
4:r:97:ARG:HH22	4:t:161:TYR:HA	1.24	1.01
2:E4:214:ARG:HG3	3:E5:324:LYS:HZ1	1.25	1.01
1:0:247:TYR:OH	2:A4:81:GLY:CA	2.08	1.01
4:x:106:GLN:HE22	4:y:6:PHE:HZ	1.04	1.01
1:18:241:PHE:HE1	3:E5:356:ILE:HG23	1.26	1.00
3:B7:281:TYR:HE2	3:C1:87:PRO:HD3	1.26	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E4:181:VAL:CG1	3:E5:256:ASN:O	2.10	0.99
3:E5:175:VAL:HG11	2:E6:332:VAL:HG13	1.38	0.99
4:i:71:LYS:NZ	4:k:39:PRO:HG3	1.77	0.99
2:E4:222:PRO:CG	3:E5:324:LYS:CB	2.41	0.99
1:4:247:TYR:CE1	2:B2:81:GLY:HA3	1.96	0.99
2:A2:221:ARG:HB2	3:A3:322:SER:OG	1.60	0.99
1:23:240:PRO:HG2	4:m:154:TYR:HB3	1.42	0.99
2:E0:176:GLN:HB3	3:E1:331:LEU:CD1	1.93	0.99
4:v:63:ILE:CD1	4:x:16:ARG:CD	2.40	0.99
2:D4:214:ARG:HB2	3:D5:324:LYS:NZ	1.77	0.98
4:l:96:TYR:CE2	4:n:6:PHE:CE2	2.50	0.98
4:o:67:HIS:CE1	4:q:20:GLU:HB3	1.97	0.98
4:j:93:LEU:HD21	4:l:159:TYR:C	1.86	0.98
2:A2:214:ARG:HD2	3:A3:324:LYS:HZ2	1.28	0.98
3:B5:283:ALA:HA	3:B9:55:THR:HB	1.46	0.98
2:C2:73:THR:OG1	3:C3:46:ARG:NH1	1.97	0.98
2:C4:404:PHE:CE1	3:C5:255:VAL:O	2.15	0.97
4:j:106:GLN:NE2	4:l:42:TYR:HE1	1.62	0.97
4:j:67:HIS:CD2	4:l:19:GLU:OE2	2.17	0.97
4:l:96:TYR:HE2	4:n:6:PHE:HE2	1.08	0.97
2:B0:73:THR:CB	3:B1:2:ARG:NH2	2.27	0.97
4:v:67:HIS:CD2	4:x:19:GLU:CD	2.42	0.97
2:E4:403:ALA:HA	3:E5:260:PHE:HE1	1.12	0.97
3:C3:283:ALA:HB2	3:C7:54:ALA:HA	1.47	0.97
2:E4:101:ASN:HB2	3:E5:255:VAL:HG11	1.43	0.96
4:v:63:ILE:HD13	4:x:16:ARG:HD2	1.47	0.96
3:C9:283:ALA:HB2	3:D3:54:ALA:HA	1.48	0.96
4:v:63:ILE:HD12	4:x:16:ARG:CG	1.95	0.96
2:C6:168:ASN:HD21	2:C6:194:LEU:HD11	1.30	0.96
2:D0:283:HIS:CD2	2:D4:60:LYS:NZ	2.34	0.96
2:D0:283:HIS:CD2	2:D4:60:LYS:HZ1	1.83	0.96
1:19:243:ALA:CB	3:E7:356:ILE:CD1	2.44	0.95
3:B5:282:ARG:O	3:B9:55:THR:HG22	1.66	0.95
4:j:63:ILE:HD12	4:l:16:ARG:HG3	1.44	0.95
2:D4:96:LYS:HD2	3:D5:1:MET:HA	1.49	0.95
3:C9:11:GLN:HE22	2:D0:248:LEU:HD12	1.30	0.95
3:F1:267:LEU:HD21	3:F1:374:ILE:HD11	1.48	0.95
4:s:70:GLY:O	4:u:39:PRO:HD3	1.67	0.95
4:j:106:GLN:NE2	4:l:15:ARG:HD3	1.81	0.94
4:i:106:GLN:HE22	4:k:15:ARG:CD	1.76	0.94
4:m:106:GLN:HG3	4:o:6:PHE:HZ	1.30	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:i:93:LEU:HD21	4:k:159:TYR:O	1.66	0.94
4:t:67:HIS:CE1	4:v:16:ARG:HG2	2.01	0.94
4:j:106:GLN:NE2	4:l:42:TYR:CE1	2.36	0.94
3:B9:39:ASP:OD1	4:h:90:PRO:HG3	1.68	0.93
4:b:97:ARG:HH12	4:d:6:PHE:HB3	1.18	0.93
4:j:106:GLN:HG2	4:l:6:PHE:HZ	1.31	0.93
1:19:243:ALA:HB3	3:E7:356:ILE:CD1	1.97	0.93
4:v:67:HIS:HD2	4:x:19:GLU:OE2	1.47	0.93
2:E4:222:PRO:CG	3:E5:324:LYS:HB3	1.98	0.93
4:x:67:HIS:CE1	4:y:16:ARG:HG2	2.02	0.93
3:B7:281:TYR:CE2	3:C1:87:PRO:HD3	2.02	0.93
2:C6:407:TRP:HZ3	3:C7:255:VAL:HA	1.26	0.93
2:E2:283:HIS:HD2	2:E6:60:LYS:HZ2	1.12	0.93
4:s:67:HIS:HA	4:u:19:GLU:OE1	1.69	0.93
2:A6:222:PRO:HD2	3:A7:324:LYS:HB2	1.48	0.92
3:C9:11:GLN:HE22	2:D0:248:LEU:CD1	1.82	0.92
4:d:70:GLY:HA3	4:f:38:LEU:O	1.69	0.92
2:D6:176:GLN:O	3:D7:347:ASN:ND2	2.03	0.92
4:k:70:GLY:O	4:m:39:PRO:HD3	1.67	0.92
1:19:243:ALA:CB	3:E7:356:ILE:HD13	1.99	0.92
1:18:241:PHE:HE1	3:E5:356:ILE:CG2	1.83	0.92
3:A9:200:GLN:HB3	3:A9:268:ILE:HD11	1.51	0.92
1:4:247:TYR:OH	2:B2:81:GLY:HA3	1.68	0.92
4:d:71:LYS:NZ	4:f:19:GLU:OE2	2.01	0.91
3:E5:274:THR:HG21	3:E5:282:ARG:HD2	1.52	0.91
2:B2:119:LEU:HD13	2:B2:156:ARG:HD2	1.53	0.91
4:v:106:GLN:OE1	4:x:15:ARG:HD2	1.68	0.91
2:A0:279:GLU:OE2	4:a:198:ARG:HD3	1.71	0.91
4:u:59:ASN:ND2	5:w:104:LYS:HZ2	1.69	0.91
4:v:63:ILE:CD1	4:x:16:ARG:HD2	2.01	0.91
1:19:257:PRO:HD2	2:E6:26:LEU:O	1.70	0.91
4:a:97:ARG:HH22	4:c:7:ALA:HB3	1.35	0.91
4:n:9:PRO:HB2	4:n:143:ILE:HG23	1.50	0.91
4:i:63:ILE:HD13	4:k:16:ARG:HD2	1.52	0.90
1:9:240:PRO:HG3	4:l:154:TYR:HB3	1.54	0.90
4:e:67:HIS:NE2	4:g:20:GLU:HB3	1.85	0.90
1:18:248:ARG:HH12	3:E5:42:LEU:HD21	1.37	0.90
2:E4:403:ALA:CA	3:E5:260:PHE:HE1	1.83	0.90
1:21:256:LEU:HD11	2:F0:31:GLN:CG	2.02	0.90
3:A7:282:ARG:O	3:B1:55:THR:HG21	1.70	0.90
4:b:97:ARG:HH11	4:d:6:PHE:HB3	1.25	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:h:106:GLN:HG3	4:j:6:PHE:CZ	2.07	0.89
1:15:247:TYR:HH	2:D8:81:GLY:CA	1.76	0.89
1:18:241:PHE:CE1	3:E5:356:ILE:HG23	2.06	0.89
2:A8:262:TYR:HB3	2:A8:263:PRO:HD2	1.55	0.89
2:D4:214:ARG:HB2	3:D5:324:LYS:HZ3	1.35	0.89
4:a:105:ASN:ND2	4:c:41:ASN:OD1	2.06	0.89
4:h:106:GLN:HG3	4:j:6:PHE:HZ	1.37	0.89
1:23:244:GLN:O	3:C5:320:ARG:NH2	2.06	0.89
1:16:246:CYS:SG	3:E1:320:ARG:NH2	2.45	0.89
2:D0:283:HIS:HD2	2:D4:60:LYS:HZ1	1.17	0.88
2:D0:283:HIS:HD2	2:D4:60:LYS:NZ	1.69	0.88
2:E2:283:HIS:CD2	2:E6:60:LYS:NZ	2.41	0.88
3:D3:179:VAL:CG1	2:D4:258:ASN:HA	2.03	0.88
4:x:96:TYR:HH	4:y:6:PHE:HE2	0.90	0.88
4:a:97:ARG:NH2	4:c:7:ALA:HB3	1.88	0.88
4:t:9:PRO:HB2	4:t:143:ILE:HG23	1.55	0.88
1:10:257:PRO:HD3	2:C8:26:LEU:HD22	1.55	0.88
2:B4:285:GLN:HB3	2:B8:57:GLY:H	1.35	0.88
2:C0:176:GLN:O	3:C1:347:ASN:ND2	2.06	0.88
2:E4:221:ARG:CZ	3:E5:322:SER:OG	2.22	0.88
4:i:63:ILE:CD1	4:k:16:ARG:CD	2.52	0.87
2:D6:181:VAL:H	3:D7:256:ASN:ND2	1.70	0.87
4:r:154:TYR:HE1	4:r:158:THR:HG22	1.38	0.87
3:E1:66:MET:HE1	3:E1:151:LEU:HD22	1.56	0.87
2:E2:283:HIS:CD2	2:E6:60:LYS:HZ2	1.93	0.87
2:E4:223:THR:OG1	3:E5:245:GLN:NE2	2.09	0.86
4:j:106:GLN:CG	4:l:6:PHE:HE1	1.80	0.86
4:x:106:GLN:NE2	4:y:6:PHE:HZ	1.72	0.86
1:4:240:PRO:CG	4:g:154:TYR:H	1.87	0.86
2:D4:221:ARG:NH1	4:r:189:LEU:O	2.09	0.86
2:E0:283:HIS:ND1	2:E4:60:LYS:HE2	1.90	0.86
3:D5:135:ILE:HG13	3:D5:152:ILE:HD11	1.58	0.86
1:21:254:LYS:HD2	2:F0:364:PRO:HD2	1.56	0.86
2:E0:292:THR:HG21	2:E0:331:ALA:HB1	1.55	0.86
2:E4:181:VAL:HG12	3:E5:256:ASN:O	1.73	0.86
3:B7:274:THR:HG21	3:B7:282:ARG:HD2	1.58	0.86
2:E4:403:ALA:CA	3:E5:260:PHE:CE1	2.58	0.86
1:0:244:GLN:HE21	4:c:162:GLY:HA2	1.23	0.86
1:21:256:LEU:HD11	2:F0:31:GLN:HG3	1.56	0.86
2:E0:223:THR:HG1	3:E1:245:GLN:NE2	1.68	0.86
3:C1:281:TYR:O	3:C5:54:ALA:HB1	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F0:66:VAL:HG12	2:F0:91:GLN:HB2	1.56	0.85
2:B4:283:HIS:O	2:B8:56:THR:CB	2.23	0.85
2:C0:176:GLN:HB3	3:C1:331:LEU:HD21	1.59	0.85
3:C7:68:LEU:HD13	3:C7:93:GLY:HA3	1.57	0.85
4:j:67:HIS:HD2	4:l:19:GLU:OE2	1.59	0.85
4:j:130:PRO:HD3	4:l:159:TYR:CD1	2.11	0.85
4:o:67:HIS:HE1	4:q:20:GLU:HB3	1.42	0.85
4:t:66:SER:O	4:v:23:LEU:HD11	1.75	0.85
4:i:63:ILE:HD12	4:k:16:ARG:HG3	0.86	0.85
1:20:256:LEU:HD11	2:E8:31:GLN:HG3	1.57	0.85
4:j:63:ILE:HD12	4:l:16:ARG:CG	2.05	0.85
1:23:257:PRO:CG	2:C4:26:LEU:HD12	2.05	0.85
3:A5:219:THR:HB	2:A6:324:VAL:HG21	1.56	0.85
2:A2:406:HIS:CD2	3:A3:261:PRO:HD3	2.12	0.85
3:C9:220:PRO:HG2	2:D0:326:LYS:HE3	1.57	0.85
1:9:240:PRO:CG	4:l:154:TYR:HB3	2.06	0.85
4:t:96:TYR:CZ	4:v:6:PHE:HE2	1.94	0.85
4:b:49:LEU:HD11	4:b:177:GLY:HA2	1.58	0.84
4:d:106:GLN:NE2	4:f:6:PHE:CZ	2.44	0.84
4:u:59:ASN:HD22	5:w:104:LYS:NZ	1.75	0.84
1:4:247:TYR:CE1	2:B2:81:GLY:CA	2.61	0.84
2:D4:221:ARG:HG2	3:D5:322:SER:HB2	1.59	0.84
1:10:254:LYS:NZ	2:C8:22:GLU:HG2	1.92	0.84
2:E4:100:ALA:HB2	3:E5:251:ARG:HG2	1.57	0.84
4:e:14:LYS:HB2	4:e:47:LEU:HD22	1.59	0.84
1:18:241:PHE:CE1	3:E5:356:ILE:CG2	2.61	0.84
1:4:240:PRO:HG2	4:g:154:TYR:H	1.41	0.84
2:C8:279:GLU:OE2	4:o:198:ARG:HD3	1.77	0.84
4:u:59:ASN:HD22	5:w:104:LYS:HZ2	1.21	0.84
4:j:63:ILE:HD12	4:l:16:ARG:CD	2.07	0.83
1:18:250:GLU:OE1	2:E4:229:ARG:NH2	2.11	0.83
4:k:93:LEU:HD21	4:m:159:TYR:O	1.77	0.83
2:A2:214:ARG:CD	3:A3:324:LYS:NZ	2.40	0.83
2:A4:178:SER:H	3:A5:347:ASN:HD22	1.26	0.83
2:E4:222:PRO:HG2	3:E5:324:LYS:HB3	1.56	0.83
1:1:245:SER:OG	3:A7:42:LEU:HD11	1.77	0.83
1:2:240:PRO:CG	4:e:154:TYR:HB3	2.08	0.83
2:C0:223:THR:OG1	3:C1:245:GLN:OE1	1.96	0.83
4:b:97:ARG:HH22	4:d:7:ALA:HB2	1.43	0.83
4:x:67:HIS:HE1	4:y:16:ARG:HG2	1.41	0.83
1:10:238:THR:HG21	3:C9:26:ASP:OD1	1.79	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C6:221:ARG:HB3	3:C7:322:SER:CB	2.09	0.83
3:D1:66:MET:HE1	3:D1:151:LEU:HD22	1.61	0.83
3:D7:176:SER:HB2	2:D8:349:THR:OG1	1.77	0.83
1:19:256:LEU:HD22	2:E6:30:ILE:O	1.78	0.83
2:E4:214:ARG:HG3	3:E5:324:LYS:NZ	1.94	0.83
4:t:67:HIS:HA	4:v:19:GLU:OE1	1.79	0.83
3:A7:321:MET:HE2	3:A7:326:VAL:HG22	1.59	0.82
3:B5:99:ASN:HD22	3:B5:178:THR:HG23	1.43	0.82
1:15:257:PRO:HG2	2:D8:29:GLY:HA2	1.62	0.82
4:j:130:PRO:HG3	4:l:159:TYR:CG	2.14	0.82
3:A1:70:PRO:HD2	2:A2:2:ARG:HH21	1.44	0.82
1:19:241:PHE:HB2	3:E7:43:GLN:HE22	1.41	0.82
3:A7:282:ARG:O	3:B1:55:THR:CG2	2.28	0.82
2:E0:394:LYS:HG2	3:E1:346:PRO:HG3	1.61	0.82
2:D6:12:ALA:HB3	2:D6:140:ALA:HB2	1.61	0.82
2:E4:222:PRO:CG	3:E5:324:LYS:HB2	2.05	0.82
2:E4:100:ALA:HB1	3:E5:251:ARG:HG2	1.60	0.82
1:11:245:SER:OG	3:D1:42:LEU:HD22	1.80	0.81
3:C9:11:GLN:NE2	2:D0:248:LEU:HD12	1.96	0.81
3:E1:39:ASP:OD1	4:s:90:PRO:HG3	1.79	0.81
2:E4:285:GLN:HG3	2:E8:57:GLY:HA3	1.62	0.81
4:j:106:GLN:CG	4:l:6:PHE:CZ	2.61	0.81
2:A2:285:GLN:OE1	2:A6:57:GLY:O	1.99	0.81
2:B0:73:THR:CB	3:B1:2:ARG:HH22	1.93	0.81
2:B4:11:GLN:HE22	3:B5:246:LEU:HD12	1.45	0.81
1:15:242:ASN:ND2	4:t:153:GLU:OE2	2.13	0.81
1:0:244:GLN:NE2	4:c:162:GLY:HA3	1.95	0.81
2:D0:285:GLN:HB3	2:D4:57:GLY:H	1.45	0.81
3:D7:281:TYR:HE1	3:E1:58:ARG:NH2	1.77	0.81
2:A2:282:TYR:O	2:A6:60:LYS:NZ	2.13	0.81
2:E8:177:VAL:HG11	3:E9:327:ASP:OD2	1.79	0.81
1:18:244:GLN:O	3:E5:355:ASP:OD2	1.99	0.81
2:A4:178:SER:H	3:A5:347:ASN:ND2	1.77	0.81
2:D4:283:HIS:CD2	2:D8:60:LYS:HE2	2.16	0.80
4:b:69:LYS:O	4:d:39:PRO:HD3	1.81	0.80
2:E6:223:THR:OG1	3:E7:245:GLN:NE2	2.13	0.80
4:t:71:LYS:HE3	4:t:106:GLN:HG2	1.64	0.80
2:E4:151:CYS:SG	2:E4:193:SER:OG	2.38	0.80
4:k:198:ARG:HH11	4:k:198:ARG:HG2	1.44	0.80
1:4:240:PRO:HB3	4:g:154:TYR:HB3	1.60	0.80
3:A5:132:GLY:HA3	3:A5:163:ILE:HG22	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:i:106:GLN:NE2	4:k:15:ARG:HD3	1.94	0.80
4:x:93:LEU:CD2	4:y:159:TYR:C	2.54	0.80
1:2:240:PRO:HG3	4:e:154:TYR:HB3	1.63	0.80
2:B4:285:GLN:HB3	2:B8:57:GLY:N	1.97	0.80
4:s:96:TYR:CZ	4:u:6:PHE:HE2	1.99	0.80
1:6:257:PRO:HG2	2:B6:26:LEU:HG	1.64	0.80
3:A1:219:THR:HG23	2:A2:324:VAL:HG21	0.84	0.80
2:C4:12:ALA:HB3	2:C4:140:ALA:HB2	1.62	0.80
3:D5:7:VAL:HG11	3:D5:151:LEU:HD21	1.63	0.80
4:n:59:ASN:HD21	4:p:9:PRO:HB3	1.47	0.80
1:1:247:TYR:OH	2:A6:82:THR:N	2.12	0.80
3:B1:282:ARG:O	3:B5:55:THR:HG22	1.81	0.80
2:E4:222:PRO:CD	3:E5:324:LYS:HB3	2.11	0.80
1:22:246:CYS:HB3	3:C7:355:ASP:OD2	1.82	0.79
2:B4:178:SER:OG	3:B5:347:ASN:ND2	2.14	0.79
3:C3:259:PRO:HG2	3:C3:311:LEU:HD21	1.64	0.79
1:4:240:PRO:HB2	4:g:154:TYR:HB3	0.82	0.79
2:E4:223:THR:HG23	2:E4:225:THR:HG22	1.62	0.79
4:m:106:GLN:HG3	4:o:6:PHE:CZ	2.18	0.79
3:B1:49:VAL:HG21	3:B1:241:ARG:HG2	1.64	0.79
2:E0:229:ARG:HH11	2:E0:229:ARG:HG3	1.47	0.79
3:C9:211:CYS:HB2	2:D0:326:LYS:HZ1	1.47	0.79
3:C9:208:TYR:HA	2:D0:326:LYS:HE2	1.65	0.79
3:B7:281:TYR:HE2	3:C1:87:PRO:CD	1.95	0.79
1:8:257:PRO:HB2	2:C0:29:GLY:HA2	1.63	0.79
2:C8:12:ALA:HB3	2:C8:140:ALA:HB2	1.61	0.79
2:D0:85:HIS:NE2	4:n:98:THR:CG2	2.46	0.79
3:E5:219:THR:HB	2:E6:324:VAL:HG11	1.64	0.79
1:5:240:PRO:CB	4:h:154:TYR:HB3	2.12	0.79
2:A6:7:ILE:HD11	2:A6:137:MET:HE1	1.63	0.78
3:A9:100:ASN:HB2	3:A9:103:LYS:HG2	1.66	0.78
3:A3:267:LEU:HD21	3:A3:371:SER:HB3	1.64	0.78
3:D3:175:VAL:HG23	2:D4:329:ASN:OD1	1.84	0.78
2:E4:178:SER:HB3	3:E5:347:ASN:HB2	1.65	0.78
4:c:67:HIS:HA	4:e:23:LEU:HD11	1.64	0.78
4:g:14:LYS:HB2	4:g:47:LEU:HD12	1.64	0.78
2:B0:224:TYR:HE2	3:B1:246:LEU:HD13	1.48	0.78
4:k:97:ARG:HH11	4:m:161:TYR:HE1	1.32	0.78
3:E9:317:PHE:HB3	3:E9:321:MET:HE3	1.66	0.78
3:A1:10:GLY:HA2	3:A1:143:THR:HG23	1.64	0.78
2:A6:222:PRO:HD2	3:A7:324:LYS:CB	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D0:142:GLY:HA3	2:D0:183:GLU:HG2	1.66	0.78
2:E4:101:ASN:HB2	3:E5:255:VAL:CG1	2.13	0.78
3:A3:135:ILE:HG21	3:A3:152:ILE:HD11	1.64	0.77
4:x:93:LEU:CD2	4:y:159:TYR:O	2.29	0.77
4:x:106:GLN:NE2	4:y:6:PHE:CZ	2.49	0.77
3:D3:291:GLN:HB3	3:D7:122:LYS:NZ	2.00	0.77
2:D4:407:TRP:HH2	3:D5:258:ILE:HB	1.49	0.77
3:B7:281:TYR:CE2	3:C1:87:PRO:CD	2.67	0.77
3:D1:283:ALA:HB2	3:D5:54:ALA:HA	1.66	0.77
2:A2:372:MET:HA	2:A2:372:MET:HE3	1.65	0.77
3:D3:202:ILE:HD11	3:D3:268:ILE:HD12	1.68	0.77
4:t:106:GLN:HE22	4:v:6:PHE:HZ	1.32	0.76
3:A9:11:GLN:HB2	3:A9:72:THR:HG21	1.65	0.76
3:C5:391:ARG:O	2:C6:262:TYR:OH	2.03	0.76
4:b:97:ARG:HH22	4:d:7:ALA:CB	1.97	0.76
2:B2:119:LEU:CD1	2:B2:156:ARG:HD2	2.15	0.76
3:C7:281:TYR:CD2	3:D1:87:PRO:HD3	2.19	0.76
3:C9:211:CYS:HB2	2:D0:326:LYS:NZ	1.99	0.76
2:E2:11:GLN:HE22	3:E3:246:LEU:HD12	1.51	0.76
2:A2:214:ARG:CD	3:A3:324:LYS:HZ2	1.97	0.76
2:A4:285:GLN:HB2	2:A8:57:GLY:CA	2.15	0.76
1:10:254:LYS:HZ2	2:C8:22:GLU:HG2	1.50	0.76
2:A6:222:PRO:CD	3:A7:324:LYS:HB2	2.14	0.76
1:6:256:LEU:CD2	2:B6:31:GLN:HG2	2.15	0.76
2:E4:222:PRO:HD2	3:E5:324:LYS:HB3	1.66	0.76
4:h:96:TYR:HB3	4:j:159:TYR:OH	1.86	0.76
4:i:106:GLN:CD	4:k:15:ARG:HD2	2.10	0.76
3:A1:70:PRO:HD2	2:A2:2:ARG:NH2	2.01	0.76
4:j:97:ARG:HG3	4:l:161:TYR:CZ	2.21	0.76
1:21:254:LYS:HD2	2:F0:364:PRO:CD	2.16	0.75
3:B1:207:LEU:HB3	3:B1:225:LEU:HD22	1.69	0.75
2:E0:73:THR:CB	3:E1:46:ARG:HH22	1.99	0.75
4:g:130:PRO:HG3	4:i:159:TYR:CD1	2.21	0.75
4:i:64:PRO:HG2	4:k:20:GLU:OE1	1.87	0.75
4:v:128:HIS:O	4:x:159:TYR:CE1	2.38	0.75
2:B6:73:THR:HG22	3:B7:46:ARG:CZ	2.17	0.75
2:C4:241:SER:HB2	2:C4:249:ASN:HB2	1.68	0.75
2:C6:6:SER:HA	2:C6:136:LEU:HB2	1.68	0.75
3:D3:179:VAL:HG12	2:D4:258:ASN:HA	1.67	0.75
2:F0:407:TRP:CZ2	3:F1:258:ILE:HD11	2.22	0.75
4:l:146:ARG:HD3	4:l:156:VAL:HG21	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D2:12:ALA:HB3	2:D2:140:ALA:HB2	1.68	0.75
1:9:254:LYS:HB3	1:9:255:PRO:HD2	1.66	0.75
4:x:100:ASN:ND2	4:y:6:PHE:HE1	1.80	0.75
2:A0:282:TYR:HB2	4:a:202:ARG:NH2	2.01	0.75
4:a:70:GLY:C	4:c:39:PRO:HD3	2.11	0.75
3:F1:113:ILE:HG13	3:F1:150:LEU:HD22	1.68	0.75
3:D1:274:THR:HG21	3:D1:282:ARG:HD2	1.68	0.75
3:E9:208:TYR:CD1	2:F0:326:LYS:HB3	2.22	0.75
4:i:66:SER:O	4:k:23:LEU:HD22	1.87	0.75
1:4:247:TYR:HE1	2:B2:81:GLY:CA	1.98	0.74
3:C7:2:ARG:NH1	3:C7:249:ASP:OD2	2.20	0.74
3:B5:57:GLY:CA	4:f:83:PRO:HB2	2.09	0.74
2:E6:285:GLN:HG2	2:F0:57:GLY:H	1.52	0.74
4:d:106:GLN:HE21	4:f:6:PHE:HZ	1.28	0.74
1:0:244:GLN:HE21	4:c:162:GLY:HA3	1.49	0.74
1:6:256:LEU:HD21	2:B6:31:GLN:HG2	1.68	0.74
1:0:244:GLN:HE22	4:c:162:GLY:HA2	1.47	0.74
2:C0:403:ALA:HA	3:C1:260:PHE:HE1	1.52	0.74
3:C3:30:ILE:HD11	3:C3:47:ILE:HD11	1.70	0.74
2:C6:221:ARG:HB3	3:C7:322:SER:HB2	1.69	0.74
4:j:97:ARG:HG3	4:l:161:TYR:OH	1.85	0.74
4:s:9:PRO:HB2	4:s:143:ILE:HG23	1.68	0.74
3:B3:336:LYS:HE2	3:B3:336:LYS:HA	1.68	0.74
3:B5:281:TYR:O	3:B9:54:ALA:HB1	1.87	0.74
4:m:14:LYS:HB2	4:m:47:LEU:HD22	1.68	0.74
2:B2:241:SER:HB2	2:B2:249:ASN:HB2	1.69	0.74
3:E5:186:THR:HG22	3:E5:415:MET:HE1	1.68	0.74
2:F0:407:TRP:HZ2	3:F1:258:ILE:HD11	1.53	0.74
4:r:15:ARG:HG2	4:r:45:MET:HE1	1.68	0.74
1:16:256:LEU:CD1	2:E0:29:GLY:HA2	2.18	0.74
2:A6:339:ARG:HG2	2:A6:339:ARG:HH11	1.52	0.74
4:f:9:PRO:HB2	4:f:143:ILE:HG23	1.69	0.74
4:q:5:VAL:HG11	4:q:149:ARG:HD2	1.70	0.74
4:v:101:GLU:OE2	4:x:2:SER:OG	2.06	0.74
3:D5:381:VAL:HB	3:D5:415:MET:HE1	1.70	0.73
4:d:71:LYS:HG3	4:f:39:PRO:HD3	1.70	0.73
4:v:63:ILE:CD1	4:x:16:ARG:HG3	2.14	0.73
1:18:251:TYR:OH	2:E4:19:ALA:CA	2.37	0.73
3:B7:39:ASP:OD1	4:g:90:PRO:HG3	1.88	0.73
2:E0:96:LYS:HZ2	3:E1:1:MET:HA	1.52	0.73
1:21:257:PRO:HG2	2:F0:26:LEU:O	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C4:209:ILE:HG23	2:C4:227:LEU:HD22	1.69	0.73
2:D2:283:HIS:CD2	2:D6:60:LYS:HE2	2.23	0.73
4:h:10:LEU:HD21	4:h:49:LEU:CD1	2.19	0.73
1:19:256:LEU:HD13	2:E6:29:GLY:C	2.14	0.73
2:B4:96:LYS:HZ2	3:B5:1:MET:HA	1.54	0.73
2:D2:180:ALA:HB1	3:D3:256:ASN:HD21	1.52	0.73
4:r:14:LYS:HB2	4:r:47:LEU:HD12	1.70	0.73
3:A7:207:LEU:HB3	3:A7:225:LEU:HD12	1.71	0.73
2:B0:174:SER:OG	2:B0:177:VAL:O	2.05	0.73
2:E4:285:GLN:HG3	2:E8:57:GLY:CA	2.18	0.73
4:v:106:GLN:OE1	4:x:15:ARG:CD	2.36	0.73
2:C0:210:TYR:HB3	3:C1:324:LYS:CE	2.18	0.73
2:E4:96:LYS:HD2	3:E5:1:MET:HA	1.71	0.73
1:23:240:PRO:CG	4:m:154:TYR:HB3	2.16	0.73
3:C1:113:ILE:HG21	3:C1:154:LYS:HD2	1.71	0.73
3:A9:39:ASP:HB2	4:c:90:PRO:CG	2.19	0.72
3:C1:166:THR:HB	3:C1:199:VAL:HG12	1.71	0.72
3:D3:179:VAL:HG11	2:D4:258:ASN:HA	1.70	0.72
2:B6:238:LEU:HD11	2:B6:378:ILE:HD11	1.70	0.72
3:D3:291:GLN:HB3	3:D7:122:LYS:HZ1	1.54	0.72
4:v:130:PRO:HB3	4:x:7:ALA:HB1	1.69	0.72
1:1:245:SER:OG	3:A7:42:LEU:CD1	2.37	0.72
2:E6:133:GLN:HG3	2:E6:252:VAL:HG22	1.72	0.72
1:4:240:PRO:CG	4:g:154:TYR:N	2.52	0.72
2:A0:115:VAL:HG21	2:A0:152:LEU:HD22	1.69	0.72
2:D2:222:PRO:HD2	3:D3:324:LYS:HB2	1.71	0.72
4:e:71:LYS:HG2	4:g:39:PRO:HG3	1.72	0.72
4:j:63:ILE:CD1	4:l:16:ARG:HD2	2.20	0.72
4:s:70:GLY:C	4:u:39:PRO:HD3	2.15	0.72
2:B0:221:ARG:CB	3:B1:322:SER:OG	2.37	0.72
2:B4:269:LEU:HD21	2:B4:384:ILE:HD11	1.71	0.72
2:F0:70:LEU:HD12	2:F0:99:ALA:HB2	1.72	0.72
4:v:130:PRO:CB	4:x:7:ALA:HB1	2.19	0.72
4:o:5:VAL:HG11	4:o:149:ARG:HE	1.54	0.72
3:A9:192:LEU:HD21	3:A9:199:VAL:HG21	1.72	0.72
2:B0:397:LEU:HD21	3:B1:344:TRP:HB2	1.72	0.72
3:D7:208:TYR:O	2:D8:326:LYS:NZ	2.23	0.72
2:E0:176:GLN:OE1	3:E1:331:LEU:HD11	1.89	0.72
3:E7:213:ARG:HH22	3:E7:297:LYS:HB2	1.55	0.72
3:B5:56:GLY:O	4:f:83:PRO:HG2	1.90	0.72
3:C3:267:LEU:HD11	3:C3:374:ILE:HD13	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F0:223:THR:HG23	2:F0:225:THR:HG22	1.71	0.72
4:c:67:HIS:NE2	4:e:20:GLU:OE1	2.23	0.72
1:15:247:TYR:HH	2:D8:81:GLY:HA3	0.80	0.72
2:D2:230:LEU:HD21	2:D2:368:LEU:HD11	1.70	0.72
3:C9:66:MET:HE1	3:C9:151:LEU:HD22	1.72	0.71
4:t:93:LEU:HD21	4:v:159:TYR:O	1.90	0.71
4:v:63:ILE:HD12	4:x:16:ARG:CD	2.19	0.71
4:j:63:ILE:CD1	4:l:16:ARG:CD	2.67	0.71
4:c:111:ILE:HD13	4:c:132:LEU:HB2	1.72	0.71
4:y:198:ARG:HG2	4:y:198:ARG:HH11	1.55	0.71
2:B0:100:ALA:O	3:B1:255:VAL:HG21	1.90	0.71
3:B3:219:THR:HB	2:B4:324:VAL:HG21	1.71	0.71
3:D7:281:TYR:CE1	3:E1:58:ARG:CZ	2.73	0.71
2:E4:176:GLN:HB2	3:E5:331:LEU:HD13	1.72	0.71
2:E8:80:THR:HA	2:E8:84:ARG:HE	1.56	0.71
4:h:100:ASN:HB3	4:j:6:PHE:CD1	2.25	0.71
3:D3:175:VAL:CG2	2:D4:329:ASN:OD1	2.39	0.71
3:C3:166:THR:HB	3:C3:199:VAL:HG22	1.70	0.71
4:g:115:LEU:HD23	4:g:152:LYS:HG3	1.73	0.71
4:v:63:ILE:CD1	4:x:16:ARG:CG	2.68	0.71
3:B3:91:VAL:HG21	3:B3:116:VAL:HG22	1.73	0.71
2:C2:406:HIS:CD2	3:C3:261:PRO:HD3	2.25	0.71
3:A5:113:ILE:CG2	3:A5:154:LYS:HE2	2.21	0.71
4:p:18:ASN:HD21	4:p:46:ASP:H	1.37	0.71
2:C8:217:LEU:HB3	2:C8:219:ILE:HG13	1.71	0.71
3:D9:39:ASP:HB2	4:r:90:PRO:HG3	1.73	0.71
3:E1:176:SER:HB3	2:E2:351:PHE:HB2	1.73	0.71
3:E7:163:ILE:HD13	3:E7:250:LEU:HB3	1.73	0.71
1:21:254:LYS:HD2	2:F0:364:PRO:CG	2.21	0.70
3:B3:200:GLN:HB3	3:B3:268:ILE:HD11	1.72	0.70
2:E6:181:VAL:HG13	3:E7:350:LYS:NZ	2.06	0.70
4:q:96:TYR:HH	4:s:6:PHE:HE2	1.38	0.70
2:B0:210:TYR:HB3	3:B1:324:LYS:HZ2	1.55	0.70
2:D0:230:LEU:HD23	2:D0:368:LEU:HD21	1.72	0.70
3:C9:208:TYR:CD1	2:D0:326:LYS:HD3	2.25	0.70
3:D5:202:ILE:HD11	3:D5:268:ILE:HD12	1.71	0.70
3:A1:379:LYS:HB2	3:A1:379:LYS:NZ	2.05	0.70
3:B3:49:VAL:HG21	3:B3:241:ARG:HG2	1.73	0.70
2:B0:221:ARG:NH1	4:f:191:GLU:OE2	2.25	0.70
4:l:105:ASN:OD1	4:n:39:PRO:HG2	1.92	0.70
1:5:242:ASN:OD1	4:h:154:TYR:HB2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A6:283:HIS:HD2	2:B0:60:LYS:HE2	1.57	0.70
2:E4:210:TYR:CD1	3:E5:324:LYS:HB2	2.27	0.70
3:C5:39:ASP:OD1	4:k:90:PRO:HG3	1.91	0.70
4:a:96:TYR:HA	4:a:108:ILE:HD11	1.73	0.70
4:e:71:LYS:CG	4:g:39:PRO:HG3	2.22	0.70
4:l:96:TYR:CE2	4:n:6:PHE:HE2	1.98	0.70
2:A0:229:ARG:HD3	2:A0:363:VAL:HG21	1.74	0.70
2:C2:279:GLU:HG2	4:l:197:LEU:O	1.92	0.70
3:F1:10:GLY:HA2	3:F1:143:THR:HG23	1.73	0.70
1:13:247:TYR:CE1	2:D4:77:GLU:HB3	2.27	0.70
3:E5:179:VAL:HG22	2:E6:350:GLY:HA2	1.72	0.70
4:y:198:ARG:HH11	4:y:198:ARG:CG	2.04	0.70
2:D4:214:ARG:CB	3:D5:324:LYS:HZ3	2.05	0.70
1:16:247:TYR:CE2	2:E0:81:GLY:HA3	2.27	0.69
1:4:240:PRO:HB2	4:g:154:TYR:HB2	1.72	0.69
2:B8:250:VAL:HG23	2:B8:254:GLU:HG2	1.74	0.69
2:B8:269:LEU:HD12	2:B8:303:ALA:HB3	1.74	0.69
3:D9:283:ALA:HA	3:E3:55:THR:HB	1.74	0.69
2:B0:404:PHE:CE1	3:B1:259:PRO:HA	2.26	0.69
2:D6:285:GLN:HB2	2:E0:56:THR:HA	1.75	0.69
4:b:97:ARG:NH2	4:d:7:ALA:CB	2.55	0.69
4:t:96:TYR:CZ	4:v:6:PHE:CE2	2.78	0.69
2:C4:151:CYS:SG	2:C4:193:SER:OG	2.50	0.69
2:E0:223:THR:HG23	2:E0:225:THR:HG22	1.74	0.69
2:E4:214:ARG:CG	3:E5:324:LYS:HZ1	2.04	0.69
4:s:96:TYR:CZ	4:u:6:PHE:CE2	2.79	0.69
3:D5:127:CYS:SG	3:D5:128:ASP:N	2.65	0.69
3:D7:281:TYR:CE1	3:E1:58:ARG:NH2	2.60	0.69
3:B3:375:GLN:NE2	3:B3:423:GLN:OE1	2.26	0.69
3:D7:68:LEU:HB3	3:D7:96:GLY:HA2	1.74	0.69
3:E7:274:THR:HG21	3:E7:282:ARG:HD2	1.73	0.69
4:c:15:ARG:HG2	4:c:45:MET:HE1	1.75	0.69
3:B1:163:ILE:HD13	3:B1:250:LEU:HB3	1.75	0.69
3:B1:311:LEU:HD12	3:B1:342:VAL:HG11	1.73	0.69
2:E0:298:PRO:HG3	2:E0:308:ARG:HH22	1.58	0.69
4:t:19:GLU:HB3	4:t:40:PRO:HD2	1.75	0.69
2:D8:178:SER:H	3:D9:347:ASN:ND2	1.90	0.69
4:e:63:ILE:HG22	4:g:16:ARG:HD2	1.75	0.69
4:h:14:LYS:HB2	4:h:47:LEU:HD12	1.73	0.69
1:16:256:LEU:HD11	2:E0:29:GLY:HA2	1.75	0.69
2:A8:136:LEU:HD13	2:A8:235:ILE:HD11	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D1:390:ARG:HG2	3:D1:390:ARG:HH21	1.55	0.69
4:g:119:ARG:NH1	4:g:137:GLU:OE1	2.26	0.69
4:j:106:GLN:CD	4:l:42:TYR:HE1	2.01	0.69
3:B5:57:GLY:HA3	4:f:83:PRO:HB3	1.73	0.69
2:B6:73:THR:HG22	3:B7:46:ARG:NH1	2.08	0.69
2:F0:279:GLU:OE2	4:y:198:ARG:HG2	1.92	0.69
4:f:106:GLN:HG3	4:h:6:PHE:CZ	2.28	0.69
2:C0:10:GLY:HA2	2:C0:145:THR:HG23	1.74	0.69
2:E0:71:GLU:OE2	3:E1:2:ARG:NH1	2.25	0.69
4:j:63:ILE:HD12	4:l:16:ARG:HD2	1.75	0.69
4:j:93:LEU:CD2	4:l:160:GLY:HA3	2.23	0.69
4:t:70:GLY:O	4:v:39:PRO:HD3	1.93	0.69
2:B0:222:PRO:HD2	3:B1:324:LYS:HB2	1.75	0.68
3:D3:248:SER:HA	3:D3:252:LYS:HD3	1.73	0.68
2:E4:71:GLU:HB2	3:E5:2:ARG:NH2	2.08	0.68
2:E4:285:GLN:HG3	2:E8:57:GLY:N	2.08	0.68
4:l:75:LEU:HD23	4:l:111:ILE:HB	1.74	0.68
4:n:117:ARG:NH1	4:n:118:ASP:OD1	2.26	0.68
2:B0:214:ARG:HB2	3:B1:324:LYS:HE2	1.73	0.68
3:C5:1:MET:N	3:C5:128:ASP:OD2	2.25	0.68
2:D4:274:PRO:HG3	2:D4:286:LEU:HD23	1.76	0.68
3:E5:220:PRO:HG2	2:E6:326:LYS:HB2	1.75	0.68
2:E6:283:HIS:NE2	2:F0:85:HIS:HB3	2.08	0.68
2:E8:180:ALA:HB3	2:E8:183:GLU:HG2	1.75	0.68
2:B0:73:THR:HB	3:B1:2:ARG:HH22	1.54	0.68
3:B3:212:PHE:CZ	2:B4:326:LYS:HG2	2.29	0.68
4:k:75:LEU:HD23	4:k:111:ILE:HB	1.73	0.68
2:B8:11:GLN:HE22	3:B9:246:LEU:HD12	1.58	0.68
3:C7:237:THR:HG22	3:C7:250:LEU:HD11	1.74	0.68
4:c:70:GLY:HA3	4:e:38:LEU:O	1.94	0.68
4:q:14:LYS:HB2	4:q:47:LEU:HD12	1.75	0.68
1:6:247:TYR:CE2	2:B6:81:GLY:HA3	2.28	0.68
3:A1:222:TYR:HB2	2:A2:325:PRO:HG2	1.74	0.68
2:C4:2:ARG:HB3	2:C4:133:GLN:HE21	1.58	0.68
2:E4:394:LYS:HG2	3:E5:346:PRO:HG3	1.75	0.68
4:f:198:ARG:HG3	4:f:198:ARG:HH11	1.58	0.68
3:E1:70:PRO:HD2	2:E2:2:ARG:NH2	2.08	0.68
1:18:251:TYR:OH	2:E4:19:ALA:HA	1.94	0.68
2:D2:250:VAL:CG1	2:D2:318:MET:HE1	2.24	0.68
4:b:69:LYS:HD3	4:d:38:LEU:HD21	1.76	0.68
2:A0:142:GLY:O	2:A0:186:ASN:ND2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C6:168:ASN:ND2	2:C6:194:LEU:HD11	2.04	0.68
2:E4:283:HIS:CD2	2:E8:85:HIS:HB3	2.28	0.68
3:E7:236:VAL:HA	3:E7:316:MET:HE1	1.76	0.68
3:F1:2:ARG:NH2	3:F1:249:ASP:OD2	2.26	0.68
4:h:14:LYS:HD3	4:h:47:LEU:HD12	1.74	0.68
4:m:172:VAL:HG23	4:m:180:ALA:HB3	1.76	0.68
3:A9:248:SER:HA	3:A9:252:LYS:HG2	1.76	0.68
2:E4:274:PRO:HD3	2:E4:291:ILE:HD11	1.76	0.68
1:23:257:PRO:CG	2:C4:26:LEU:CD1	2.71	0.68
2:A0:37:PRO:O	4:y:86:ALA:CB	2.26	0.67
2:A8:22:GLU:OE2	2:A8:229:ARG:NH1	2.27	0.67
3:B7:391:ARG:O	2:B8:262:TYR:OH	2.11	0.67
2:C4:221:ARG:HB3	3:C5:322:SER:HB3	1.75	0.67
3:D9:169:VAL:HG12	3:D9:202:ILE:HB	1.76	0.67
4:e:95:TYR:CE2	4:e:99:MET:HE1	2.29	0.67
2:B0:221:ARG:HB2	3:B1:322:SER:HB2	1.73	0.67
2:D2:222:PRO:HD2	3:D3:324:LYS:CB	2.23	0.67
3:D7:70:PRO:HD2	2:D8:2:ARG:HH22	1.59	0.67
4:a:117:ARG:NH1	4:a:118:ASP:OD1	2.27	0.67
1:12:254:LYS:HD3	2:D2:364:PRO:HB2	1.76	0.67
3:A1:130:LEU:H	3:A1:162:ARG:HH12	1.43	0.67
2:A6:137:MET:HB3	2:A6:168:ASN:HA	1.76	0.67
2:E0:163:LYS:HE2	2:E0:163:LYS:HA	1.76	0.67
4:g:106:GLN:HG3	4:i:6:PHE:CZ	2.30	0.67
4:r:53:GLY:HA2	4:r:62:VAL:HG21	1.75	0.67
2:A2:222:PRO:HG2	3:A3:324:LYS:HB2	1.76	0.67
2:A8:106:GLY:HA3	2:A8:148:GLY:HA3	1.74	0.67
2:D0:174:SER:OG	2:D0:177:VAL:O	2.11	0.67
1:4:247:TYR:HE1	2:B2:81:GLY:HA2	1.59	0.67
2:A2:101:ASN:HB2	3:A3:255:VAL:HG11	1.75	0.67
2:B4:221:ARG:HH11	2:B4:221:ARG:HG3	1.60	0.67
3:D7:1:MET:N	3:D7:128:ASP:OD2	2.27	0.67
2:A0:312:TYR:HE1	2:A0:379:SER:HB3	1.59	0.67
3:A3:7:VAL:HB	3:A3:135:ILE:HG22	1.77	0.67
3:C5:293:MET:HE1	3:C5:365:VAL:HG11	1.74	0.67
3:E9:267:LEU:HD21	3:E9:374:ILE:HD11	1.77	0.67
4:t:8:SER:OG	4:t:11:ASN:ND2	2.27	0.67
4:x:63:ILE:HG22	4:y:16:ARG:HD2	1.74	0.67
2:E4:222:PRO:O	3:E5:322:SER:HB2	1.95	0.67
4:t:5:VAL:HG11	4:t:149:ARG:HD3	1.77	0.67
3:B9:200:GLN:HB2	3:B9:268:ILE:HD11	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:h:10:LEU:HD21	4:h:49:LEU:HD12	1.76	0.67
3:C9:354:CYS:SG	3:C9:355:ASP:N	2.68	0.67
2:D6:138:PHE:HZ	2:D6:235:ILE:HD12	1.59	0.67
1:21:256:LEU:CD1	2:F0:31:GLN:HG2	2.24	0.67
2:A6:403:ALA:HA	3:A7:260:PHE:CE1	2.30	0.67
2:E2:96:LYS:HZ3	3:E3:128:ASP:HB2	1.59	0.67
4:h:100:ASN:ND2	4:j:6:PHE:CZ	2.57	0.67
2:A2:26:LEU:HD22	2:A2:364:PRO:HD3	1.77	0.66
2:C4:6:SER:HA	2:C4:136:LEU:HB2	1.77	0.66
3:C9:283:ALA:CB	3:D3:54:ALA:HA	2.24	0.66
2:D6:223:THR:OG1	3:D7:245:GLN:OE1	2.12	0.66
2:B0:221:ARG:O	3:B1:322:SER:HB2	1.96	0.66
3:B5:99:ASN:ND2	3:B5:178:THR:HG23	2.09	0.66
1:21:256:LEU:HD11	2:F0:31:GLN:HG2	1.75	0.66
2:C6:10:GLY:HA2	2:C6:145:THR:HG23	1.77	0.66
2:E6:258:ASN:HB3	2:E6:352:LYS:HE3	1.76	0.66
4:x:9:PRO:HB2	4:x:143:ILE:HG23	1.77	0.66
3:C5:354:CYS:SG	3:C5:355:ASP:N	2.67	0.66
3:B1:293:MET:HE2	3:B1:365:VAL:HG11	1.76	0.66
3:D5:172:SER:HB3	3:D5:205:GLU:HG2	1.78	0.66
4:o:53:GLY:HA2	4:o:62:VAL:HG21	1.78	0.66
1:19:241:PHE:CE2	3:E7:42:LEU:HB2	2.31	0.66
1:22:251:TYR:OH	2:C6:225:THR:CB	2.43	0.66
3:B5:324:LYS:HA	3:B5:327:ASP:HB2	1.78	0.66
2:C0:210:TYR:HB3	3:C1:324:LYS:HE3	1.75	0.66
3:A7:66:MET:HE1	3:A7:147:MET:HE1	1.76	0.66
3:D1:98:GLY:H	3:D1:103:LYS:HD3	1.60	0.66
3:D9:311:LEU:HD12	3:D9:342:VAL:HG11	1.76	0.66
2:E4:176:GLN:CB	3:E5:331:LEU:HD13	2.26	0.66
2:E4:284:GLU:HG3	2:E8:88:HIS:CD2	2.30	0.66
3:C9:39:ASP:HB2	4:m:90:PRO:HG3	1.78	0.66
3:D9:102:ALA:HB2	3:D9:403:MET:HE2	1.77	0.66
2:E4:210:TYR:CE1	3:E5:324:LYS:HB2	2.31	0.66
4:t:66:SER:HB3	4:v:23:LEU:HD13	1.76	0.66
2:A8:285:GLN:HG3	2:A8:286:LEU:H	1.61	0.66
2:D2:283:HIS:HD2	2:D6:60:LYS:HE2	1.61	0.66
2:B8:250:VAL:HG21	2:B8:318:MET:HE1	1.77	0.66
2:E2:11:GLN:NE2	3:E3:246:LEU:HD12	2.11	0.66
4:e:100:ASN:HB3	4:g:6:PHE:CD1	2.31	0.66
4:g:96:TYR:HD1	4:i:159:TYR:HH	1.40	0.66
3:A9:91:VAL:HG11	3:A9:116:VAL:HG22	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D6:30:ILE:HG22	2:D6:36:MET:HB3	1.78	0.65
4:n:97:ARG:O	4:n:101:GLU:HB3	1.97	0.65
1:4:240:PRO:CB	4:g:154:TYR:CB	2.38	0.65
2:D0:229:ARG:HH11	2:D0:229:ARG:HG3	1.61	0.65
2:E4:107:HIS:HE2	2:E4:151:CYS:HG	1.40	0.65
1:2:241:PHE:CE2	3:A9:40:SER:OG	2.48	0.65
2:B8:195:LEU:HD21	2:B8:264:ARG:HE	1.61	0.65
2:D2:174:SER:HB3	2:D2:207:GLU:HG2	1.78	0.65
3:D7:219:THR:HB	2:D8:324:VAL:HG11	1.78	0.65
3:E1:248:SER:HA	3:E1:252:LYS:HG3	1.79	0.65
3:A1:117:LEU:HD13	3:A1:154:LYS:NZ	2.11	0.65
2:D4:283:HIS:CD2	2:D8:60:LYS:CE	2.79	0.65
3:E1:259:PRO:HD2	3:E1:263:LEU:HD11	1.78	0.65
4:c:9:PRO:HB2	4:c:143:ILE:HG23	1.78	0.65
4:n:59:ASN:ND2	4:p:9:PRO:HB3	2.12	0.65
4:s:67:HIS:O	4:s:71:LYS:NZ	2.29	0.65
3:A3:52:ASN:ND2	3:A3:123:GLU:OE2	2.30	0.65
2:B0:212:ILE:HG12	2:B0:275:ILE:HD11	1.78	0.65
2:B4:11:GLN:HE22	3:B5:246:LEU:CD1	2.10	0.65
2:D4:12:ALA:HB3	2:D4:140:ALA:HB2	1.78	0.65
2:D6:101:ASN:OD1	3:D7:252:LYS:HG2	1.96	0.65
2:A4:241:SER:HB2	2:A4:249:ASN:HB2	1.79	0.65
3:B3:179:VAL:HG11	2:B4:258:ASN:HA	1.77	0.65
3:C3:190:HIS:HB2	3:C3:414:ASN:HD21	1.62	0.65
4:a:78:ALA:HA	4:a:167:VAL:HG23	1.78	0.65
4:k:8:SER:OG	4:k:11:ASN:ND2	2.30	0.65
4:u:59:ASN:ND2	5:w:104:LYS:NZ	2.37	0.65
3:A5:27:GLU:HA	3:A5:359:LYS:HD2	1.78	0.65
2:C6:135:PHE:HD2	2:C6:166:LYS:HG2	1.62	0.65
3:D1:91:VAL:HG11	3:D1:116:VAL:HG22	1.78	0.65
2:E8:377:MET:HE2	2:E8:379:SER:HB3	1.79	0.65
4:g:129:MET:HE2	4:g:131:TRP:HE1	1.62	0.65
3:B5:64:ILE:HD11	3:B5:123:GLU:HG3	1.78	0.65
3:B7:212:PHE:HD1	2:B8:326:LYS:HD3	1.62	0.65
2:C2:202:VAL:HG22	2:C2:268:MET:HG3	1.78	0.65
3:C5:97:ALA:HB3	3:C5:143:THR:HB	1.79	0.65
2:A2:176:GLN:O	3:A3:347:ASN:HB2	1.96	0.64
3:A5:113:ILE:HG21	3:A5:154:LYS:HE2	1.77	0.64
3:C5:248:SER:HA	3:C5:252:LYS:HE3	1.79	0.64
2:C6:177:VAL:HG13	3:C7:327:ASP:OD2	1.97	0.64
3:C7:281:TYR:CE2	3:D1:87:PRO:HD3	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D8:262:TYR:HB3	2:D8:263:PRO:HD2	1.79	0.64
2:A0:403:ALA:HA	3:A1:260:PHE:CE1	2.32	0.64
3:E9:256:ASN:HD21	3:E9:350:LYS:HG2	1.62	0.64
2:A4:110:ILE:O	2:A4:110:ILE:HG13	1.97	0.64
3:D9:163:ILE:HD13	3:D9:250:LEU:HB3	1.78	0.64
2:E0:71:GLU:OE1	3:E1:2:ARG:NH2	2.26	0.64
4:a:191:GLU:HB2	4:a:195:ALA:HB2	1.79	0.64
4:l:130:PRO:HB3	4:n:159:TYR:CD1	2.32	0.64
4:d:96:TYR:OH	4:f:6:PHE:CE2	2.50	0.64
4:k:19:GLU:HB3	4:k:40:PRO:HD2	1.80	0.64
1:0:244:GLN:O	3:A5:320:ARG:CZ	2.44	0.64
2:E2:184:PRO:HA	2:E2:391:MET:HE1	1.78	0.64
2:E4:238:LEU:HD11	2:E4:378:ILE:HG13	1.80	0.64
2:F0:271:SER:HB2	2:F0:377:MET:HB3	1.80	0.64
1:10:248:ARG:HH21	3:C9:42:LEU:HD22	1.63	0.64
1:22:251:TYR:OH	2:C6:225:THR:HB	1.98	0.64
3:A7:27:GLU:OE2	3:A7:241:ARG:NH2	2.31	0.64
2:B4:96:LYS:NZ	3:B5:128:ASP:OD2	2.30	0.64
4:f:97:ARG:NH1	4:h:161:TYR:HA	2.13	0.64
2:A0:264:ARG:HG3	2:A0:264:ARG:HH11	1.61	0.64
3:A9:44:LEU:O	3:A9:44:LEU:HD23	1.96	0.64
2:C2:285:GLN:HB2	2:C6:56:THR:HA	1.79	0.64
2:C8:319:TYR:HB3	2:C8:323:VAL:HG11	1.78	0.64
4:c:92:LEU:HD21	4:c:110:ILE:HD13	1.79	0.64
3:A5:287:PRO:HA	3:A5:329:GLN:HE22	1.62	0.64
2:B2:11:GLN:HE22	3:B3:246:LEU:CD1	2.11	0.64
3:C9:11:GLN:NE2	2:D0:248:LEU:CD1	2.56	0.64
2:D0:285:GLN:CB	2:D4:57:GLY:H	2.09	0.64
2:D0:292:THR:HG21	2:D0:331:ALA:HB1	1.80	0.64
2:E6:217:LEU:HD21	2:E6:367:ASP:HB3	1.78	0.64
4:g:130:PRO:HB2	4:i:7:ALA:HB1	1.80	0.64
4:n:130:PRO:HB3	4:p:159:TYR:CD2	2.33	0.64
1:10:244:GLN:O	3:C9:320:ARG:NH1	2.30	0.64
3:B3:179:VAL:HG12	2:B4:258:ASN:OD1	1.98	0.64
3:B9:267:LEU:HD23	3:B9:374:ILE:HD11	1.80	0.64
1:8:257:PRO:HG3	2:C0:26:LEU:CD2	2.28	0.64
3:A5:221:THR:HG23	3:A5:223:GLY:H	1.63	0.64
3:A9:68:LEU:HB3	3:A9:96:GLY:HA2	1.80	0.64
3:B9:283:ALA:HA	3:C3:55:THR:OG1	1.98	0.64
2:D6:210:TYR:HE1	2:D6:227:LEU:HD11	1.63	0.64
2:E4:285:GLN:HG2	2:E8:60:LYS:HD3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E5:10:GLY:HA2	3:E5:143:THR:HG23	1.80	0.64
2:B0:2:ARG:HB2	2:B0:133:GLN:HE22	1.63	0.63
2:B2:179:THR:N	3:B3:347:ASN:HD21	1.95	0.63
2:C4:310:GLY:HA3	2:C4:383:ALA:HB2	1.79	0.63
2:C8:221:ARG:HB3	3:C9:322:SER:HB3	1.80	0.63
4:m:70:GLY:O	4:o:39:PRO:HD3	1.98	0.63
4:s:63:ILE:HG22	4:u:16:ARG:HG3	1.80	0.63
5:w:17:GLN:NE2	5:w:20:ASN:OD1	2.31	0.63
1:17:248:ARG:HH12	4:t:97:ARG:HG2	1.62	0.63
3:A1:396:HIS:NE2	2:A2:263:PRO:HD3	2.12	0.63
2:B2:174:SER:OG	2:B2:177:VAL:O	2.15	0.63
2:E2:259:LEU:HD21	2:E2:316:CYS:HB2	1.80	0.63
4:b:69:LYS:HB3	4:d:38:LEU:HD11	1.80	0.63
4:v:63:ILE:CD1	4:x:16:ARG:HD3	2.27	0.63
1:8:257:PRO:CB	2:C0:29:GLY:HA2	2.28	0.63
3:A9:39:ASP:CB	4:c:90:PRO:CG	2.76	0.63
2:C2:282:TYR:CZ	4:l:202:ARG:HD3	2.34	0.63
2:D0:394:LYS:HG2	3:D1:346:PRO:HG3	1.81	0.63
2:D2:98:ASP:O	2:D2:105:ARG:NH2	2.28	0.63
2:D8:238:LEU:HD11	2:D8:255:PHE:HE2	1.64	0.63
4:c:185:ILE:HG22	4:c:186:CYS:SG	2.39	0.63
4:d:14:LYS:HD3	4:d:47:LEU:HD23	1.80	0.63
4:l:8:SER:OG	4:l:11:ASN:ND2	2.31	0.63
1:2:245:SER:HB2	3:A9:42:LEU:HD21	1.81	0.63
2:C6:339:ARG:O	2:C6:342:GLN:NE2	2.31	0.63
3:C7:165:GLU:OE2	3:C7:200:GLN:NE2	2.32	0.63
4:c:7:ALA:O	4:c:161:TYR:OH	2.14	0.63
4:c:119:ARG:HH22	4:c:137:GLU:HB3	1.64	0.63
3:A5:318:ARG:HD3	3:A5:358:PRO:HD3	1.78	0.63
2:B6:50:ASN:O	2:B6:64:ARG:NH2	2.32	0.63
3:C3:293:MET:HE1	3:C3:365:VAL:HG21	1.79	0.63
4:d:105:ASN:HB3	4:f:41:ASN:HA	1.79	0.63
4:f:12:VAL:HG12	4:f:15:ARG:HH22	1.63	0.63
1:21:256:LEU:CD1	2:F0:31:GLN:CG	2.74	0.63
2:A2:195:LEU:HD21	2:A2:264:ARG:HE	1.63	0.63
3:A3:329:GLN:HA	3:A3:332:ASN:HB2	1.79	0.63
2:A6:80:THR:HA	2:A6:84:ARG:HH21	1.63	0.63
2:A8:179:THR:O	3:A9:350:LYS:HB2	1.98	0.63
3:D5:201:VAL:HG11	3:D5:377:MET:HE1	1.81	0.63
4:i:106:GLN:CD	4:k:15:ARG:CD	2.69	0.63
4:l:72:SER:HB3	4:l:108:ILE:HG22	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:s:96:TYR:HH	4:u:6:PHE:HE2	0.65	0.63
1:11:240:PRO:HG3	4:p:154:TYR:HD2	1.63	0.63
3:C3:20:PHE:HD2	3:C3:233:MET:HE3	1.64	0.63
2:C6:101:ASN:HA	2:C6:144:GLY:HA3	1.80	0.63
3:E5:175:VAL:CG1	2:E6:332:VAL:HG13	2.24	0.63
3:F1:244:GLY:HA2	3:F1:355:ASP:HB2	1.81	0.63
4:q:37:GLN:NE2	4:q:41:ASN:OD1	2.32	0.63
2:B4:174:SER:OG	2:B4:177:VAL:O	2.16	0.63
2:C2:269:LEU:HB3	2:C2:301:MET:HE2	1.80	0.63
2:C6:244:PHE:HB2	2:C6:356:ASN:HD21	1.64	0.63
3:D9:200:GLN:HB3	3:D9:268:ILE:CD1	2.29	0.63
2:E4:181:VAL:HG11	3:E5:256:ASN:O	1.97	0.63
4:s:71:LYS:HG2	4:u:39:PRO:HG3	1.81	0.63
1:18:251:TYR:OH	2:E4:19:ALA:N	2.32	0.62
1:20:256:LEU:CD1	2:E8:31:GLN:HG3	2.29	0.62
3:D1:390:ARG:HG2	3:D1:390:ARG:NH2	2.11	0.62
2:F0:151:CYS:SG	2:F0:193:SER:OG	2.50	0.62
4:b:97:ARG:NH2	4:d:7:ALA:HB2	2.13	0.62
4:m:92:LEU:HD21	4:m:110:ILE:HD13	1.81	0.62
4:a:113:VAL:HG22	4:a:134:ILE:HD12	1.80	0.62
4:j:106:GLN:CD	4:l:15:ARG:HD3	2.24	0.62
2:C4:181:VAL:HG12	3:C5:256:ASN:HB2	1.80	0.62
2:C6:407:TRP:HZ3	3:C7:255:VAL:CA	2.06	0.62
3:D9:200:GLN:HG2	3:D9:268:ILE:HD11	1.81	0.62
2:E8:292:THR:HG21	2:E8:331:ALA:HB1	1.80	0.62
2:C0:403:ALA:HA	3:C1:260:PHE:CE1	2.34	0.62
4:d:172:VAL:HG23	4:d:180:ALA:HB3	1.81	0.62
4:k:72:SER:HB3	4:k:108:ILE:HG22	1.81	0.62
4:y:72:SER:HB3	4:y:108:ILE:HG22	1.81	0.62
2:B0:403:ALA:HA	3:B1:260:PHE:CZ	2.34	0.62
3:B3:11:GLN:HE22	2:B4:248:LEU:HD12	1.65	0.62
3:B9:332:ASN:OD1	3:B9:336:LYS:NZ	2.32	0.62
3:C9:317:PHE:HB3	3:C9:321:MET:HE1	1.80	0.62
4:y:9:PRO:HB2	4:y:143:ILE:HG23	1.79	0.62
2:A2:221:ARG:O	3:A3:322:SER:HB2	2.00	0.62
2:B0:224:TYR:CE2	3:B1:246:LEU:HD13	2.31	0.62
3:C1:253:LEU:HD11	3:C1:368:VAL:HG21	1.82	0.62
2:D0:285:GLN:HB3	2:D4:57:GLY:N	2.12	0.62
2:E2:283:HIS:CD2	2:E6:60:LYS:HZ1	2.16	0.62
3:E9:10:GLY:HA2	3:E9:143:THR:HG23	1.80	0.62
4:h:106:GLN:CG	4:j:6:PHE:HZ	2.11	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:m:96:TYR:HA	4:m:108:ILE:HD11	1.82	0.62
1:18:241:PHE:CE1	3:E5:356:ILE:HG21	2.35	0.62
3:C9:1:MET:N	3:C9:128:ASP:OD2	2.30	0.62
2:E4:107:HIS:NE2	2:E4:151:CYS:SG	2.67	0.62
4:i:66:SER:HB3	4:k:23:LEU:HD22	1.81	0.62
4:y:78:ALA:HB3	4:y:112:PHE:HE1	1.63	0.62
3:B1:238:CYS:SG	3:B1:241:ARG:NH2	2.73	0.62
4:c:100:ASN:ND2	4:e:6:PHE:CE2	2.67	0.62
4:j:100:ASN:HB3	4:l:6:PHE:CE1	2.34	0.62
4:l:9:PRO:HB2	4:l:143:ILE:HG23	1.82	0.62
4:t:146:ARG:HH11	4:t:146:ARG:HG3	1.63	0.62
4:v:9:PRO:HB2	4:v:143:ILE:HG13	1.81	0.62
4:x:72:SER:HB3	4:x:108:ILE:HG22	1.81	0.62
2:A0:210:TYR:HE1	2:A0:227:LEU:HD21	1.64	0.62
2:B4:223:THR:HG23	2:B4:225:THR:HG22	1.81	0.62
2:C0:210:TYR:HB3	3:C1:324:LYS:HE2	1.82	0.62
3:C3:165:GLU:OE2	3:C3:200:GLN:NE2	2.33	0.62
2:D6:27:GLU:OE1	2:D6:243:ARG:NH1	2.33	0.62
3:D9:382:SER:HB2	3:D9:415:MET:HE3	1.82	0.62
2:E0:394:LYS:CG	3:E1:346:PRO:HG3	2.30	0.62
4:i:74:ALA:HB2	4:i:172:VAL:HG12	1.82	0.62
4:m:130:PRO:HB3	4:o:159:TYR:CD2	2.35	0.62
4:u:14:LYS:NZ	4:u:45:MET:SD	2.71	0.62
1:18:241:PHE:HE2	3:E5:42:LEU:HB2	1.63	0.62
2:A4:203:MET:HE2	2:A4:267:PHE:HB3	1.82	0.62
3:A7:303:SER:HB3	3:A7:377:MET:HE3	1.80	0.62
3:B5:16:ILE:HD11	3:B5:229:VAL:HG11	1.82	0.62
2:B6:73:THR:HG22	3:B7:46:ARG:NE	2.15	0.62
2:C6:31:GLN:NE2	2:C6:33:ASP:OD2	2.33	0.62
3:E1:283:ALA:HA	3:E5:55:THR:OG1	1.99	0.62
4:t:93:LEU:HD22	4:v:160:GLY:HA3	1.82	0.62
3:A1:42:LEU:HD21	3:A1:243:PRO:HD2	1.80	0.61
2:A6:168:ASN:HD22	2:A6:194:LEU:HD11	1.65	0.61
3:C1:283:ALA:HB2	3:C5:54:ALA:HA	1.81	0.61
4:p:70:GLY:HA3	4:r:39:PRO:HD3	1.81	0.61
4:s:130:PRO:HB3	4:u:7:ALA:HB1	1.82	0.61
4:x:78:ALA:HB3	4:x:112:PHE:HE1	1.65	0.61
2:A4:191:THR:HA	2:A4:194:LEU:HG	1.82	0.61
3:A7:107:THR:OG1	3:A7:108:GLU:OE1	2.18	0.61
2:E0:101:ASN:HB2	3:E1:255:VAL:HG21	1.81	0.61
3:E5:172:SER:HB2	3:E5:205:GLU:HG2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E6:181:VAL:HG13	3:E7:350:LYS:HZ1	1.63	0.61
2:E8:274:PRO:HB2	2:E8:276:ILE:HG12	1.82	0.61
1:13:247:TYR:HH	2:D4:81:GLY:HA3	1.61	0.61
3:C9:139:LEU:HD13	3:C9:168:SER:HB2	1.82	0.61
3:D3:49:VAL:HG21	3:D3:241:ARG:HG2	1.82	0.61
3:D7:169:VAL:HG12	3:D7:202:ILE:HB	1.82	0.61
3:D7:406:MET:HE2	3:D7:406:MET:HA	1.81	0.61
4:v:63:ILE:HD13	4:x:16:ARG:CD	2.15	0.61
1:6:247:TYR:HE2	2:B6:81:GLY:HA3	1.64	0.61
3:A3:6:HIS:NE2	3:A3:8:GLN:OE1	2.32	0.61
3:A7:132:GLY:HA3	3:A7:163:ILE:HG22	1.82	0.61
2:B0:221:ARG:C	3:B1:322:SER:HB2	2.26	0.61
2:C0:274:PRO:HG3	2:C0:286:LEU:HD13	1.83	0.61
3:C7:281:TYR:HD2	3:D1:87:PRO:HD3	1.64	0.61
3:D3:107:THR:HG21	3:D3:401:GLU:HB2	1.83	0.61
2:E4:223:THR:HA	3:E5:323:THR:H	1.66	0.61
4:k:69:LYS:HD3	4:m:23:LEU:HD21	1.81	0.61
1:19:256:LEU:CD2	2:E6:30:ILE:O	2.47	0.61
3:A1:396:HIS:CD2	2:A2:263:PRO:HD3	2.34	0.61
2:A2:259:LEU:HD21	2:A2:316:CYS:HB2	1.83	0.61
3:B3:176:SER:OG	2:B4:349:THR:HG23	1.99	0.61
3:B9:318:ARG:HD2	3:B9:358:PRO:HD3	1.82	0.61
3:C7:135:ILE:HB	3:C7:166:THR:HG22	1.81	0.61
2:D4:220:GLU:OE1	4:r:191:GLU:OE1	2.18	0.61
3:D7:177:ASP:HA	2:D8:351:PHE:O	2.00	0.61
3:E1:198:GLU:HB2	3:E1:266:PHE:HE2	1.64	0.61
4:c:22:ALA:HB1	4:c:38:LEU:CD2	2.31	0.61
4:e:106:GLN:NE2	4:g:6:PHE:HZ	1.98	0.61
4:x:5:VAL:HG11	4:x:149:ARG:HD3	1.82	0.61
4:x:8:SER:OG	4:x:11:ASN:ND2	2.32	0.61
2:A2:377:MET:HE2	2:A2:379:SER:HB2	1.83	0.61
3:B7:7:VAL:HB	3:B7:135:ILE:HG12	1.83	0.61
2:C0:399:TYR:O	2:C0:402:ARG:NH2	2.34	0.61
4:q:9:PRO:HB2	4:q:143:ILE:HG23	1.82	0.61
1:19:243:ALA:HB1	3:E7:356:ILE:CD1	2.13	0.61
2:A2:214:ARG:CD	3:A3:324:LYS:HZ1	2.10	0.61
2:B6:258:ASN:HB3	2:B6:352:LYS:HG3	1.83	0.61
3:D7:274:THR:HG21	3:D7:282:ARG:HD2	1.81	0.61
4:t:67:HIS:CE1	4:v:16:ARG:CG	2.81	0.61
1:0:247:TYR:OH	2:A4:81:GLY:HA3	1.97	0.61
2:C2:285:GLN:OE1	2:C6:57:GLY:HA2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C5:294:PHE:O	3:C5:306:ARG:NH2	2.29	0.61
2:D4:93:ILE:HG23	2:D4:117:LEU:HD23	1.83	0.61
3:E7:389:PHE:HE1	3:E7:395:LEU:HD11	1.66	0.61
4:h:96:TYR:HB3	4:j:159:TYR:HH	1.64	0.61
4:j:111:ILE:HD13	4:j:132:LEU:HB2	1.83	0.61
4:t:130:PRO:HB3	4:v:7:ALA:HB1	1.83	0.61
1:18:248:ARG:NH1	3:E5:42:LEU:HD21	2.14	0.61
3:A3:308:GLY:HA3	3:A3:373:ALA:HB2	1.82	0.61
2:A6:283:HIS:CD2	2:B0:60:LYS:NZ	2.69	0.61
2:B0:241:SER:HB2	2:B0:249:ASN:HB2	1.83	0.61
2:B4:254:GLU:OE1	2:B4:352:LYS:NZ	2.34	0.61
2:C0:33:ASP:O	2:C0:60:LYS:NZ	2.34	0.61
3:C5:257:LEU:HD11	3:C5:314:SER:HB3	1.82	0.61
2:C8:50:ASN:O	2:C8:64:ARG:NH2	2.33	0.61
2:D0:394:LYS:HG2	3:D1:346:PRO:CG	2.30	0.61
2:E2:76:ASP:HA	2:E2:79:ARG:HD2	1.81	0.61
3:F1:311:LEU:HD12	3:F1:342:VAL:HG21	1.83	0.61
1:7:256:LEU:HD11	2:B8:31:GLN:HB3	1.83	0.61
1:9:245:SER:OG	1:9:248:ARG:HG3	2.01	0.60
3:A7:27:GLU:HA	3:A7:359:LYS:HD2	1.83	0.60
3:B5:396:HIS:HA	3:B5:399:THR:HG22	1.83	0.60
2:C2:51:THR:HG23	2:C2:52:PHE:HD1	1.66	0.60
3:C5:99:ASN:HA	3:C5:142:GLY:HA3	1.81	0.60
2:F0:403:ALA:HA	3:F1:260:PHE:CE1	2.35	0.60
4:a:70:GLY:HA3	4:c:39:PRO:HD3	1.83	0.60
3:A9:107:THR:OG1	3:A9:108:GLU:OE1	2.19	0.60
2:C6:101:ASN:HA	2:C6:144:GLY:CA	2.30	0.60
4:j:66:SER:HB3	4:l:23:LEU:HD22	1.82	0.60
1:19:256:LEU:HD11	2:E6:31:GLN:HG3	1.82	0.60
1:7:256:LEU:HD21	2:B8:31:GLN:HA	1.83	0.60
3:A7:67:ASP:OD1	3:A7:73:MET:HE1	2.02	0.60
3:A7:200:GLN:HB3	3:A7:268:ILE:HD11	1.83	0.60
2:B0:210:TYR:HB3	3:B1:324:LYS:NZ	2.16	0.60
3:B5:257:LEU:HD21	3:B5:314:SER:HB2	1.83	0.60
2:C4:387:VAL:HA	2:C4:390:ARG:HH21	1.65	0.60
2:C8:292:THR:HG21	2:C8:331:ALA:HB1	1.83	0.60
4:j:9:PRO:HB2	4:j:143:ILE:HG23	1.82	0.60
4:t:66:SER:O	4:v:23:LEU:CD1	2.47	0.60
3:A9:39:ASP:CB	4:c:90:PRO:HG2	2.31	0.60
2:B0:178:SER:H	3:B1:347:ASN:ND2	1.99	0.60
1:15:257:PRO:CG	2:D8:26:LEU:O	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C1:164:MET:HB2	3:C1:197:ASP:H	1.66	0.60
3:C7:1:MET:N	3:C7:128:ASP:OD2	2.34	0.60
2:E4:12:ALA:HB3	2:E4:140:ALA:HB2	1.83	0.60
4:i:67:HIS:HA	4:k:19:GLU:OE1	2.01	0.60
4:v:96:TYR:OH	4:x:6:PHE:HE2	1.84	0.60
4:x:58:SER:OG	4:y:12:VAL:HG21	2.02	0.60
2:A0:58:ALA:HB3	4:y:84:LYS:HG2	1.81	0.60
2:A0:79:ARG:HG3	2:A0:92:LEU:HD22	1.83	0.60
3:A9:259:PRO:HG2	3:A9:311:LEU:HD21	1.83	0.60
3:B9:181:GLU:HB2	3:B9:182:PRO:HD3	1.83	0.60
3:C5:133:PHE:HB2	3:C5:164:MET:HB3	1.82	0.60
2:D0:221:ARG:HD2	3:D1:322:SER:HB3	1.83	0.60
4:f:96:TYR:HA	4:f:108:ILE:HD11	1.83	0.60
4:o:14:LYS:HB2	4:o:47:LEU:HD22	1.83	0.60
4:x:75:LEU:HD23	4:x:111:ILE:HB	1.84	0.60
2:B8:241:SER:OG	2:B8:250:VAL:O	2.16	0.60
2:C8:221:ARG:HB3	3:C9:322:SER:CB	2.32	0.60
4:f:106:GLN:CD	4:h:6:PHE:HZ	2.09	0.60
4:f:117:ARG:HH12	4:f:152:LYS:HE2	1.66	0.60
1:21:254:LYS:HD2	2:F0:364:PRO:HG2	1.84	0.60
3:A7:33:THR:O	3:A7:58:ARG:NH2	2.34	0.60
2:B0:53:PHE:HB3	2:B0:61:HIS:HB3	1.83	0.60
3:B1:135:ILE:HB	3:B1:166:THR:HG22	1.83	0.60
3:B7:293:MET:HE3	3:B7:367:PHE:HB2	1.84	0.60
3:C5:220:PRO:O	2:C6:325:PRO:HD2	2.01	0.60
2:E2:76:ASP:OD1	2:E2:79:ARG:NH2	2.33	0.60
4:b:69:LYS:HB3	4:d:38:LEU:CD1	2.32	0.60
3:A1:113:ILE:HG13	3:A1:117:LEU:HD12	1.84	0.60
3:A3:249:ASP:H	3:A3:252:LYS:HB2	1.65	0.60
2:A4:269:LEU:HB3	2:A4:301:MET:HE1	1.84	0.60
3:A5:205:GLU:OE2	2:A6:329:ASN:ND2	2.33	0.60
2:B4:223:THR:OG1	3:B5:245:GLN:OE1	2.11	0.60
3:D7:49:VAL:HG21	3:D7:241:ARG:HG2	1.84	0.60
2:E4:210:TYR:CD1	3:E5:324:LYS:CG	2.84	0.60
2:E4:221:ARG:NH2	3:E5:322:SER:O	2.35	0.60
4:a:139:PRO:O	4:a:143:ILE:HD12	2.02	0.60
3:A1:412:GLU:OE2	3:A1:416:ASN:ND2	2.35	0.60
3:A3:330:MET:HA	3:A3:330:MET:HE3	1.84	0.60
3:A9:396:HIS:HE1	2:B0:261:PRO:O	1.85	0.60
2:B6:53:PHE:HB3	2:B6:61:HIS:HB3	1.84	0.60
3:B7:55:THR:HG23	3:B7:55:THR:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C9:2:ARG:HB3	3:C9:131:GLN:HB2	1.84	0.60
2:D0:104:ALA:HB2	2:D0:413:MET:HE3	1.82	0.60
2:E2:96:LYS:HZ1	3:E3:1:MET:H2	1.48	0.60
3:E9:113:ILE:HA	3:E9:116:VAL:HG12	1.83	0.60
4:e:67:HIS:HA	4:g:19:GLU:OE2	2.01	0.60
4:i:91:PHE:HD2	4:i:193:ASP:HB3	1.66	0.60
3:A3:7:VAL:HG11	3:A3:151:LEU:HD21	1.84	0.59
2:A6:119:LEU:HD13	2:A6:122:ILE:HD11	1.82	0.59
3:B5:334:GLN:HE21	3:B5:349:MET:HG2	1.66	0.59
3:D1:67:ASP:OD2	3:D1:72:THR:OG1	2.20	0.59
3:D5:129:CYS:SG	3:D5:162:ARG:NH2	2.74	0.59
2:E4:221:ARG:NE	3:E5:322:SER:OG	2.35	0.59
3:E7:100:ASN:HB3	3:E7:103:LYS:HG2	1.84	0.59
3:F1:117:LEU:HA	3:F1:120:VAL:HG12	1.83	0.59
4:f:67:HIS:HE1	4:h:16:ARG:CG	2.15	0.59
3:A9:192:LEU:O	3:A9:192:LEU:HD23	2.02	0.59
3:B1:237:THR:HG22	3:B1:250:LEU:HD11	1.84	0.59
2:B2:53:PHE:HB3	2:B2:61:HIS:HB3	1.83	0.59
2:B8:76:ASP:HA	2:B8:79:ARG:HD2	1.83	0.59
2:C6:210:TYR:HB3	3:C7:324:LYS:HD2	1.83	0.59
4:e:67:HIS:NE2	4:g:20:GLU:CB	2.63	0.59
4:i:64:PRO:HG2	4:k:20:GLU:CD	2.27	0.59
4:t:72:SER:HB3	4:t:108:ILE:HG22	1.83	0.59
2:A0:132:LEU:HG	2:A0:164:LYS:HE2	1.84	0.59
3:C9:283:ALA:HB2	3:D3:54:ALA:CA	2.29	0.59
3:E1:317:PHE:HB3	3:E1:321:MET:SD	2.42	0.59
4:s:68:LEU:HA	4:s:71:LYS:HZ2	1.68	0.59
4:v:191:GLU:OE1	4:v:198:ARG:NH2	2.35	0.59
2:B0:73:THR:HB	3:B1:2:ARG:CZ	2.28	0.59
3:C5:117:LEU:HD11	3:C5:154:LYS:HB3	1.84	0.59
3:C7:354:CYS:SG	3:C7:355:ASP:N	2.76	0.59
3:C9:67:ASP:OD2	3:C9:72:THR:OG1	2.20	0.59
2:D2:223:THR:OG1	3:D3:245:GLN:OE1	2.15	0.59
2:D4:259:LEU:HD21	2:D4:316:CYS:HB2	1.85	0.59
3:D5:64:ILE:HD11	3:D5:123:GLU:HG3	1.84	0.59
3:D5:215:LEU:O	3:D5:216:LYS:HB2	2.01	0.59
3:D9:7:VAL:HG11	3:D9:151:LEU:CD2	2.32	0.59
2:A2:91:GLN:HA	2:A2:121:ARG:HH12	1.66	0.59
2:C6:204:LEU:HD13	2:C6:231:ILE:HD12	1.84	0.59
3:C9:219:THR:HB	2:D0:324:VAL:HG21	1.84	0.59
2:D0:309:HIS:NE2	2:D0:386:GLU:OE1	2.30	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D3:238:CYS:SG	3:D3:318:ARG:NE	2.76	0.59
2:E4:394:LYS:NZ	3:E5:347:ASN:ND2	2.51	0.59
1:10:246:CYS:SG	3:C9:355:ASP:OD2	2.60	0.59
3:A9:39:ASP:HB2	4:c:90:PRO:HG3	1.84	0.59
2:C2:399:TYR:O	2:C2:402:ARG:NH2	2.36	0.59
2:C2:404:PHE:CE1	3:C3:259:PRO:HA	2.37	0.59
2:E0:96:LYS:HZ2	3:E1:1:MET:CA	2.14	0.59
2:E2:285:GLN:HB3	2:E6:57:GLY:N	2.17	0.59
3:E3:42:LEU:HD21	3:E3:356:ILE:HD11	1.84	0.59
3:F1:239:CYS:SG	3:F1:248:SER:N	2.70	0.59
3:A1:140:GLY:O	3:A1:184:ASN:ND2	2.33	0.59
3:B3:208:TYR:CE1	3:B3:225:LEU:HD11	2.37	0.59
2:D0:230:LEU:CD2	2:D0:368:LEU:HD21	2.31	0.59
2:E4:229:ARG:HD2	2:E4:363:VAL:HG21	1.85	0.59
4:b:145:LYS:HE2	4:b:150:VAL:HG23	1.84	0.59
4:f:67:HIS:CE1	4:h:16:ARG:CG	2.85	0.59
4:l:96:TYR:HH	4:n:6:PHE:HZ	1.49	0.59
1:19:256:LEU:HD21	2:E6:31:GLN:HA	1.85	0.59
2:B6:396:ASP:OD2	2:B6:422:ARG:NH2	2.36	0.59
3:C7:178:THR:OG1	3:C7:181:GLU:OE2	2.21	0.59
3:E5:334:GLN:OE1	3:E5:348:ASN:ND2	2.35	0.59
2:E8:191:THR:HG23	2:E8:425:LEU:HD21	1.85	0.59
4:q:10:LEU:HG	4:q:143:ILE:HG22	1.85	0.59
4:x:130:PRO:CB	4:y:7:ALA:HB1	2.32	0.59
1:22:250:GLU:OE2	2:C6:225:THR:HG21	2.02	0.59
3:A5:183:TYR:HB3	3:A5:398:TYR:HE2	1.68	0.59
2:A6:254:GLU:O	2:A6:258:ASN:ND2	2.36	0.59
3:C1:249:ASP:H	3:C1:252:LYS:HB2	1.68	0.59
3:D7:139:LEU:HA	3:D7:145:SER:HB2	1.85	0.59
2:E4:71:GLU:HB2	3:E5:2:ARG:HH21	1.67	0.59
2:E4:100:ALA:HB2	3:E5:251:ARG:CG	2.29	0.59
4:f:70:GLY:O	4:h:39:PRO:HD3	2.03	0.59
4:h:101:GLU:OE2	4:j:161:TYR:OH	2.20	0.59
4:s:8:SER:OG	4:s:11:ASN:OD1	2.21	0.59
4:u:14:LYS:HD2	4:u:47:LEU:HD23	1.83	0.59
3:B5:282:ARG:O	3:B9:55:THR:CG2	2.48	0.59
3:C3:200:GLN:HB3	3:C3:266:PHE:HB2	1.85	0.59
3:C9:208:TYR:HD1	2:D0:326:LYS:HD3	1.66	0.59
2:D2:182:VAL:HG11	3:D3:255:VAL:HG12	1.83	0.59
3:E5:284:LEU:HD23	3:E5:362:LYS:HG2	1.84	0.59
3:E7:332:ASN:OD1	3:E7:336:LYS:NZ	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E9:139:LEU:HD12	3:E9:170:PHE:HE1	1.68	0.59
4:v:67:HIS:CG	4:x:19:GLU:OE2	2.54	0.59
2:A2:214:ARG:HD2	3:A3:324:LYS:CE	2.33	0.58
2:C2:250:VAL:HG23	2:C2:352:LYS:HZ3	1.68	0.58
2:D2:292:THR:HG21	2:D2:331:ALA:HB1	1.84	0.58
2:D4:326:LYS:NZ	2:D4:327:ASP:OD1	2.32	0.58
3:D5:274:THR:OG1	3:D5:279:GLN:OE1	2.21	0.58
3:D5:326:VAL:HG13	3:D5:330:MET:HE1	1.85	0.58
3:D9:97:ALA:HA	3:D9:103:LYS:HE2	1.85	0.58
2:E4:394:LYS:HZ3	3:E5:347:ASN:ND2	2.00	0.58
4:e:107:LYS:HD2	4:e:201:TRP:CD1	2.37	0.58
4:h:119:ARG:NH1	4:h:137:GLU:OE1	2.32	0.58
4:k:105:ASN:OD1	4:m:39:PRO:HG2	2.03	0.58
3:A3:91:VAL:HG21	3:A3:116:VAL:HG12	1.86	0.58
3:A9:256:ASN:HB2	3:A9:350:LYS:HE3	1.84	0.58
3:B1:171:PRO:O	3:B1:380:ARG:NH1	2.34	0.58
3:C3:68:LEU:HD12	3:C3:143:THR:HG22	1.85	0.58
2:D2:30:ILE:HG22	2:D2:36:MET:HB3	1.84	0.58
3:E3:248:SER:HA	3:E3:252:LYS:HG2	1.85	0.58
3:E7:190:HIS:HB2	3:E7:414:ASN:HD22	1.68	0.58
4:a:57:ASN:HA	4:a:132:LEU:HD23	1.85	0.58
4:f:67:HIS:HE1	4:h:16:ARG:HG2	1.68	0.58
4:j:146:ARG:NH1	4:j:156:VAL:HG11	2.18	0.58
1:18:250:GLU:HG2	2:E4:225:THR:OG1	2.04	0.58
3:A5:313:ALA:HB3	3:A5:349:MET:HG2	1.84	0.58
3:B1:135:ILE:HG13	3:B1:152:ILE:HG12	1.85	0.58
3:B9:267:LEU:CD2	3:B9:374:ILE:HD11	2.33	0.58
2:C6:130:THR:HG22	2:C6:131:GLY:H	1.67	0.58
2:C8:181:VAL:HG11	3:C9:256:ASN:O	2.03	0.58
3:E7:293:MET:HE2	3:E7:367:PHE:HB2	1.85	0.58
3:E9:208:TYR:CE1	2:F0:326:LYS:HB3	2.37	0.58
3:E9:305:PRO:HB2	3:E9:310:TYR:HE1	1.68	0.58
4:f:14:LYS:HG2	4:f:45:MET:HE3	1.84	0.58
3:A5:180:VAL:O	3:A5:184:ASN:ND2	2.37	0.58
3:A9:208:TYR:HE1	3:A9:225:LEU:HD11	1.68	0.58
3:C3:306:ARG:HA	3:C3:340:TYR:HE1	1.69	0.58
3:D9:12:CYS:SG	3:D9:13:GLY:N	2.76	0.58
2:E4:338:LYS:HZ3	2:E4:340:THR:HG22	1.69	0.58
3:F1:7:VAL:HB	3:F1:135:ILE:HG12	1.85	0.58
3:B3:16:ILE:HD11	3:B3:229:VAL:HG11	1.86	0.58
3:B7:325:GLU:HA	3:B7:328:GLU:HG3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E0:71:GLU:OE2	3:E1:2:ARG:CZ	2.52	0.58
2:E0:229:ARG:HG3	2:E0:229:ARG:NH1	2.19	0.58
4:c:171:ILE:HD11	4:c:182:PHE:HD1	1.67	0.58
4:k:20:GLU:OE2	4:k:24:MET:HE3	2.04	0.58
4:s:58:SER:OG	4:u:12:VAL:HG21	2.04	0.58
4:s:151:MET:HE2	4:s:163:SER:HB2	1.85	0.58
1:15:256:LEU:HD21	2:D8:31:GLN:CD	2.29	0.58
3:A1:289:LEU:HD21	3:A1:365:VAL:HG11	1.84	0.58
3:A3:186:THR:HG23	3:A3:415:MET:HG3	1.85	0.58
2:B0:404:PHE:CZ	3:B1:259:PRO:HA	2.38	0.58
2:D8:259:LEU:HD11	2:D8:316:CYS:HB2	1.85	0.58
2:E4:398:MET:HA	2:E4:398:MET:HE3	1.86	0.58
3:E5:12:CYS:HB3	3:E5:138:SER:HB2	1.85	0.58
4:d:97:ARG:O	4:d:101:GLU:HB3	2.03	0.58
4:t:75:LEU:HD23	4:t:111:ILE:HB	1.86	0.58
4:t:96:TYR:OH	4:v:6:PHE:CE2	2.57	0.58
1:16:240:PRO:HG3	4:u:154:TYR:HB3	1.86	0.58
2:A2:174:SER:HB3	2:A2:177:VAL:O	2.04	0.58
2:A2:221:ARG:O	3:A3:322:SER:CB	2.52	0.58
3:A3:174:LYS:NZ	3:A3:205:GLU:OE1	2.37	0.58
3:A9:320:ARG:HG3	3:A9:320:ARG:HH11	1.69	0.58
2:B0:73:THR:CG2	3:B1:2:ARG:HH22	2.15	0.58
2:C6:121:ARG:HH12	2:C6:124:LYS:HE3	1.69	0.58
2:D0:189:LEU:HD11	2:D0:418:PHE:CD1	2.38	0.58
3:D5:107:THR:HG21	3:D5:401:GLU:HB2	1.84	0.58
3:D9:66:MET:HG2	3:D9:147:MET:HE1	1.85	0.58
4:a:97:ARG:HH22	4:c:7:ALA:CB	2.14	0.58
4:x:181:GLN:HE22	4:x:200:ASP:H	1.51	0.58
2:B4:96:LYS:NZ	3:B5:1:MET:HA	2.17	0.58
3:B7:15:GLN:O	3:B7:226:ASN:ND2	2.37	0.58
2:C6:223:THR:HG21	3:C7:245:GLN:HE22	1.69	0.58
3:C7:262:ARG:NH1	3:C7:421:GLU:OE2	2.36	0.58
3:C9:100:ASN:HB3	3:C9:103:LYS:HG2	1.85	0.58
2:D0:335:ILE:HG23	2:D0:341:ILE:HD13	1.85	0.58
2:D2:328:VAL:HG21	2:D2:355:ILE:HD11	1.84	0.58
2:D8:230:LEU:HD21	2:D8:368:LEU:HD11	1.86	0.58
2:E0:259:LEU:HD21	2:E0:316:CYS:HB2	1.84	0.58
3:E5:267:LEU:HD12	3:E5:301:CYS:HB3	1.86	0.58
2:E6:280:LYS:HZ1	2:F0:89:PRO:HB2	1.68	0.58
2:E8:269:LEU:HD21	2:E8:384:ILE:HD11	1.85	0.58
2:E8:311:LYS:HE2	2:E8:344:VAL:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:b:71:LYS:HE3	4:d:39:PRO:HG3	1.86	0.58
4:g:88:LEU:HD11	4:g:185:ILE:HD13	1.85	0.58
4:u:149:ARG:HD3	4:u:161:TYR:CD1	2.37	0.58
4:v:97:ARG:HG3	4:x:161:TYR:OH	2.03	0.58
2:A0:221:ARG:NH2	4:a:189:LEU:O	2.37	0.58
2:B0:177:VAL:HA	3:B1:347:ASN:HD22	1.68	0.58
2:C6:130:THR:HG22	2:C6:131:GLY:N	2.18	0.58
2:C6:136:LEU:HD22	2:C6:167:LEU:HD23	1.85	0.58
2:C6:236:SER:O	2:C6:243:ARG:NH2	2.36	0.58
3:E9:175:VAL:HG11	2:F0:329:ASN:ND2	2.19	0.58
4:a:70:GLY:CA	4:c:39:PRO:HD3	2.33	0.58
4:s:66:SER:O	4:u:23:LEU:CD1	2.40	0.58
4:t:93:LEU:CD2	4:v:160:GLY:HA3	2.33	0.58
4:x:105:ASN:ND2	4:y:37:GLN:HE22	2.02	0.58
1:6:240:PRO:HG3	4:i:154:TYR:O	2.04	0.58
2:A4:164:LYS:NZ	2:A4:165:SER:O	2.37	0.58
2:B4:234:VAL:HG21	2:B4:302:MET:HE1	1.85	0.58
3:C3:289:LEU:HD12	3:C3:365:VAL:HG12	1.85	0.58
3:C7:97:ALA:HB3	3:C7:143:THR:HG22	1.86	0.58
2:D6:210:TYR:CE1	2:D6:227:LEU:HD11	2.38	0.58
4:g:96:TYR:HD1	4:i:159:TYR:OH	1.87	0.58
1:18:243:ALA:HB2	3:E5:357:PRO:HD2	1.86	0.57
2:A6:33:ASP:OD1	4:b:102:GLY:O	2.22	0.57
2:B2:406:HIS:HA	2:B2:409:VAL:HG12	1.86	0.57
3:B5:281:TYR:HA	3:B9:58:ARG:HD3	1.86	0.57
3:C1:221:THR:HG22	3:C1:223:GLY:H	1.69	0.57
3:C9:211:CYS:CB	2:D0:326:LYS:NZ	2.67	0.57
3:D5:7:VAL:HG11	3:D5:151:LEU:CD2	2.33	0.57
4:a:200:ASP:OD2	4:a:203:ASN:ND2	2.37	0.57
4:k:10:LEU:HG	4:k:143:ILE:HG22	1.86	0.57
4:x:10:LEU:HG	4:x:143:ILE:HG22	1.87	0.57
1:13:247:TYR:CD1	2:D4:77:GLU:HB3	2.39	0.57
2:A0:309:HIS:NE2	2:A0:386:GLU:OE2	2.35	0.57
3:A5:33:THR:O	3:A5:58:ARG:NH2	2.38	0.57
2:C2:168:ASN:HD22	2:C2:198:THR:HG21	1.68	0.57
2:C6:221:ARG:HB3	3:C7:322:SER:HB3	1.86	0.57
2:D8:178:SER:H	3:D9:347:ASN:HD22	1.51	0.57
2:E4:100:ALA:CB	3:E5:251:ARG:CG	2.67	0.57
2:E8:101:ASN:HB3	2:E8:182:VAL:HG21	1.85	0.57
4:f:107:LYS:HD2	4:f:201:TRP:CD1	2.39	0.57
4:h:187:SER:OG	4:h:188:GLY:N	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:t:130:PRO:CB	4:v:7:ALA:HB1	2.34	0.57
4:y:8:SER:OG	4:y:11:ASN:ND2	2.36	0.57
1:9:251:TYR:HH	2:C2:225:THR:HG1	1.48	0.57
2:A6:283:HIS:HD2	2:B0:60:LYS:CE	2.17	0.57
2:D0:85:HIS:NE2	4:n:98:THR:HG21	2.20	0.57
2:E0:163:LYS:HE2	2:E0:163:LYS:CA	2.34	0.57
3:E9:398:TYR:HB3	3:E9:403:MET:HG3	1.85	0.57
4:c:14:LYS:HB3	4:c:47:LEU:HD13	1.85	0.57
2:A0:88:HIS:HB3	2:A0:91:GLN:HB2	1.85	0.57
3:A1:212:PHE:CZ	2:A2:326:LYS:HB3	2.39	0.57
2:A6:174:SER:HB3	2:A6:207:GLU:HG2	1.86	0.57
2:B2:120:ASP:OD1	2:B2:123:ARG:NH2	2.37	0.57
3:B7:256:ASN:O	3:B7:256:ASN:ND2	2.37	0.57
2:C2:10:GLY:HA2	2:C2:145:THR:HG23	1.86	0.57
2:C4:70:LEU:HD13	2:C4:95:GLY:HA3	1.85	0.57
2:C4:269:LEU:HD11	2:C4:384:ILE:HD11	1.85	0.57
3:C5:107:THR:OG1	3:C5:401:GLU:OE2	2.22	0.57
3:C9:7:VAL:HB	3:C9:135:ILE:HG12	1.87	0.57
3:D1:386:THR:O	3:D1:390:ARG:HG3	2.04	0.57
3:D7:334:GLN:HE21	3:D7:349:MET:HG2	1.67	0.57
2:F0:363:VAL:HG23	2:F0:366:GLY:HA3	1.87	0.57
4:j:78:ALA:HB3	4:j:112:PHE:HE1	1.67	0.57
3:A1:52:ASN:ND2	3:A1:123:GLU:OE2	2.32	0.57
2:B8:175:PRO:HB3	2:B8:390:ARG:HH21	1.70	0.57
2:C2:255:PHE:HB3	2:C2:259:LEU:HD12	1.86	0.57
2:D6:12:ALA:CB	2:D6:140:ALA:HB2	2.33	0.57
2:D6:222:PRO:O	3:D7:324:LYS:NZ	2.37	0.57
2:E2:96:LYS:HZ1	3:E3:1:MET:N	2.02	0.57
3:F1:184:ASN:OD1	3:F1:398:TYR:OH	2.22	0.57
4:c:53:GLY:HA2	4:c:62:VAL:HG21	1.85	0.57
4:e:73:VAL:HG12	4:e:109:GLU:HB3	1.85	0.57
1:8:257:PRO:HG3	2:C0:26:LEU:HD22	1.85	0.57
2:A0:3:GLU:OE2	2:A0:64:ARG:NH1	2.38	0.57
2:A0:394:LYS:HG2	3:A1:346:PRO:HG3	1.86	0.57
3:A5:27:GLU:OE1	3:A5:241:ARG:NH2	2.38	0.57
2:B0:178:SER:H	3:B1:347:ASN:HD22	1.53	0.57
2:B2:11:GLN:HE22	3:B3:246:LEU:HD13	1.68	0.57
3:B3:179:VAL:CG1	2:B4:258:ASN:HA	2.34	0.57
2:B6:250:VAL:HG13	2:B6:318:MET:HE1	1.86	0.57
2:B8:178:SER:HB3	3:B9:347:ASN:ND2	2.20	0.57
2:C4:271:SER:HB3	2:C4:377:MET:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D3:397:TRP:NE1	2:D4:256:GLN:OE1	2.37	0.57
3:D5:23:VAL:HG11	3:D5:230:SER:HB2	1.86	0.57
4:d:23:LEU:HD11	4:d:38:LEU:CD1	2.35	0.57
2:A6:208:ALA:HB2	2:A6:304:LYS:HG2	1.85	0.57
2:B6:329:ASN:HA	2:B6:332:VAL:HG12	1.85	0.57
2:B8:11:GLN:NE2	3:B9:246:LEU:HD12	2.19	0.57
3:C9:244:GLY:HA2	3:C9:355:ASP:HB2	1.87	0.57
2:D0:107:HIS:NE2	2:D0:151:CYS:SG	2.78	0.57
3:D3:68:LEU:HB3	3:D3:96:GLY:HA2	1.86	0.57
2:F0:96:LYS:NZ	3:F1:128:ASP:OD2	2.30	0.57
4:d:7:ALA:O	4:d:161:TYR:OH	2.12	0.57
4:k:78:ALA:HB3	4:k:112:PHE:HE1	1.69	0.57
5:w:40:LYS:NZ	5:w:113:ASN:OD1	2.37	0.57
2:A2:282:TYR:CD2	2:A6:60:LYS:NZ	2.60	0.57
3:A3:207:LEU:HB3	3:A3:225:LEU:HD22	1.87	0.57
2:A6:339:ARG:HG2	2:A6:339:ARG:NH1	2.18	0.57
2:A8:138:PHE:HZ	2:A8:235:ILE:HD13	1.68	0.57
2:A8:241:SER:HB2	2:A8:249:ASN:HB2	1.86	0.57
3:C1:283:ALA:HA	3:C5:55:THR:OG1	2.05	0.57
2:D6:219:ILE:HG22	2:D6:222:PRO:HD3	1.87	0.57
2:D8:69:ASP:OD1	2:D8:70:LEU:N	2.37	0.57
3:D9:412:GLU:O	3:D9:416:ASN:ND2	2.38	0.57
3:F1:49:VAL:HG11	3:F1:241:ARG:HG2	1.87	0.57
4:e:8:SER:HB2	4:e:147:HIS:HA	1.86	0.57
4:v:106:GLN:CD	4:x:15:ARG:HD2	2.28	0.57
2:A6:241:SER:OG	2:A6:250:VAL:O	2.21	0.57
2:B4:223:THR:CG2	2:B4:225:THR:HG22	2.34	0.57
2:C2:259:LEU:HD21	2:C2:316:CYS:HB2	1.86	0.57
3:C3:105:HIS:HE1	3:C3:191:GLN:HE22	1.51	0.57
3:C5:68:LEU:HD12	3:C5:97:ALA:HB2	1.86	0.57
3:D9:135:ILE:HG22	3:D9:137:HIS:HD2	1.70	0.57
3:F1:210:ILE:HD11	3:F1:298:ASN:HA	1.87	0.57
4:f:105:ASN:ND2	4:h:37:GLN:HE22	2.03	0.57
4:k:84:LYS:HD2	4:k:186:CYS:SG	2.45	0.57
4:o:67:HIS:CE1	4:q:20:GLU:CB	2.81	0.57
3:C5:69:GLU:HG2	2:C6:2:ARG:HH22	1.70	0.57
2:C6:97:GLU:OE2	2:C6:105:ARG:NH2	2.30	0.57
2:D4:105:ARG:HH12	3:D5:251:ARG:CD	2.18	0.57
2:D6:283:HIS:CD2	2:E0:60:LYS:NZ	2.73	0.57
2:D6:286:LEU:O	2:D6:373:ARG:NH1	2.32	0.57
2:E4:319:TYR:HB3	2:E4:323:VAL:HG21	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E5:179:VAL:CG2	2:E6:350:GLY:HA2	2.35	0.57
4:g:14:LYS:HD3	4:g:47:LEU:HD12	1.85	0.57
4:i:66:SER:O	4:k:23:LEU:CD2	2.52	0.57
1:17:246:CYS:HB2	3:E3:320:ARG:NH2	2.20	0.56
3:A7:253:LEU:HD21	3:A7:316:MET:SD	2.45	0.56
2:B8:109:THR:HG22	2:B8:110:ILE:HG23	1.87	0.56
2:D6:222:PRO:HD2	3:D7:324:LYS:HZ2	1.70	0.56
2:E4:272:TYR:HB3	2:E4:275:ILE:HD11	1.87	0.56
3:E7:156:ARG:NH1	3:E7:162:ARG:O	2.37	0.56
3:F1:200:GLN:HG3	3:F1:268:ILE:HD11	1.87	0.56
3:F1:238:CYS:SG	3:F1:239:CYS:N	2.78	0.56
1:11:239:LEU:HG	1:11:240:PRO:HD2	1.86	0.56
1:21:244:GLN:O	3:F1:320:ARG:NH2	2.39	0.56
1:5:248:ARG:HH12	3:B5:42:LEU:HD21	1.70	0.56
2:A0:403:ALA:HA	3:A1:260:PHE:CZ	2.40	0.56
3:A3:7:VAL:HG11	3:A3:151:LEU:CD2	2.35	0.56
3:B3:10:GLY:HA2	3:B3:143:THR:HG23	1.86	0.56
3:B5:218:THR:HG23	3:B5:219:THR:HG23	1.88	0.56
3:C5:69:GLU:HG2	2:C6:2:ARG:NH2	2.19	0.56
3:C7:156:ARG:HG2	3:C7:195:ASN:HB2	1.87	0.56
3:D5:324:LYS:HA	3:D5:327:ASP:HB2	1.87	0.56
3:E1:172:SER:HB3	3:E1:205:GLU:HG2	1.87	0.56
3:E1:291:GLN:HB2	3:E5:122:LYS:NZ	2.20	0.56
2:E4:223:THR:HG1	3:E5:245:GLN:HE22	1.48	0.56
2:F0:403:ALA:HA	3:F1:260:PHE:HE1	1.70	0.56
4:f:105:ASN:HD21	4:h:39:PRO:HD2	1.69	0.56
4:y:75:LEU:HD23	4:y:111:ILE:HB	1.87	0.56
1:13:254:LYS:HB3	1:13:255:PRO:HD2	1.88	0.56
1:16:247:TYR:HE2	2:E0:81:GLY:HA3	1.67	0.56
1:4:240:PRO:HG3	4:g:154:TYR:N	2.21	0.56
2:A2:207:GLU:HG3	2:A2:304:LYS:HE3	1.87	0.56
2:A8:11:GLN:HE22	3:A9:246:LEU:HD12	1.70	0.56
2:B2:286:LEU:O	2:B2:373:ARG:NH1	2.33	0.56
3:B3:176:SER:CB	2:B4:349:THR:HG23	2.34	0.56
3:B7:281:TYR:CD2	3:C1:87:PRO:HD2	2.40	0.56
3:B7:283:ALA:HA	3:C1:55:THR:HG23	1.85	0.56
2:B8:240:ALA:HB1	2:B8:356:ASN:HD22	1.70	0.56
2:C6:188:VAL:HG13	2:C6:425:LEU:HD23	1.86	0.56
3:C9:323:THR:HA	3:C9:326:VAL:HG12	1.87	0.56
2:D0:223:THR:OG1	3:D1:245:GLN:NE2	2.38	0.56
2:D2:136:LEU:HD23	2:D2:235:ILE:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D6:276:ILE:HD12	2:D6:281:ALA:HA	1.86	0.56
3:D9:173:PRO:HB3	3:D9:380:ARG:CZ	2.35	0.56
2:E0:96:LYS:HD3	3:E1:128:ASP:OD2	2.06	0.56
2:E2:88:HIS:HB3	2:E2:91:GLN:HG2	1.85	0.56
3:E3:385:PHE:HE2	3:E3:412:GLU:HB3	1.70	0.56
2:E6:101:ASN:HB3	2:E6:182:VAL:HG11	1.87	0.56
4:a:105:ASN:O	4:c:42:TYR:OH	2.21	0.56
4:j:175:SER:HA	4:j:206:PHE:HE1	1.71	0.56
4:m:119:ARG:HH21	4:m:137:GLU:HB2	1.70	0.56
4:s:57:ASN:ND2	4:u:12:VAL:CG1	2.68	0.56
4:t:96:TYR:OH	4:v:6:PHE:HE2	1.88	0.56
4:u:71:LYS:HZ3	4:u:106:GLN:HG3	1.70	0.56
3:A1:210:ILE:HD11	3:A1:228:LEU:HD21	1.88	0.56
2:A2:356:ASN:OD1	2:A2:358:GLN:NE2	2.38	0.56
2:A8:262:TYR:HB3	2:A8:263:PRO:CD	2.34	0.56
2:E8:84:ARG:HH12	5:w:155:GLN:HG2	1.69	0.56
2:A4:178:SER:N	3:A5:347:ASN:HD22	1.98	0.56
3:A5:172:SER:HB3	3:A5:205:GLU:HG2	1.88	0.56
2:A6:7:ILE:HD11	2:A6:137:MET:CE	2.32	0.56
2:A8:221:ARG:HG2	3:A9:322:SER:HB3	1.88	0.56
3:C1:165:GLU:OE2	3:C1:200:GLN:NE2	2.39	0.56
2:C2:202:VAL:HA	2:C2:268:MET:HB2	1.86	0.56
2:C4:277:SER:OG	2:C4:278:ALA:N	2.38	0.56
2:D6:222:PRO:CD	3:D7:324:LYS:HZ2	2.18	0.56
2:E4:407:TRP:CH2	3:E5:197:ASP:OD2	2.58	0.56
3:E5:212:PHE:CD2	2:E6:326:LYS:HE3	2.40	0.56
3:E7:68:LEU:HD12	3:E7:143:THR:HG22	1.86	0.56
4:g:130:PRO:HG3	4:i:159:TYR:CG	2.39	0.56
2:A2:253:THR:O	2:A2:256:GLN:NE2	2.39	0.56
3:A7:117:LEU:HA	3:A7:120:VAL:HG12	1.88	0.56
2:B2:107:HIS:NE2	2:B2:151:CYS:SG	2.78	0.56
2:B6:271:SER:HB2	2:B6:301:MET:HE2	1.88	0.56
3:D1:375:GLN:HG3	3:D1:419:VAL:HG13	1.87	0.56
3:D9:68:LEU:HD23	3:D9:112:LEU:HD13	1.85	0.56
2:E2:96:LYS:NZ	3:E3:128:ASP:HB2	2.20	0.56
3:E3:180:VAL:O	3:E3:184:ASN:ND2	2.38	0.56
3:E3:283:ALA:HA	3:E7:55:THR:HB	1.87	0.56
2:E6:76:ASP:OD1	2:E6:79:ARG:NH2	2.39	0.56
2:E6:339:ARG:NH2	2:E6:342:GLN:OE1	2.38	0.56
4:o:115:LEU:HD21	4:o:145:LYS:HD3	1.87	0.56
4:y:181:GLN:HE22	4:y:200:ASP:H	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B6:88:HIS:HB3	2:B6:91:GLN:HG3	1.88	0.56
2:C2:7:ILE:HG22	2:C2:9:VAL:HG23	1.86	0.56
2:D8:2:ARG:HG3	2:D8:51:THR:HG22	1.88	0.56
3:E5:172:SER:OG	3:E5:175:VAL:O	2.22	0.56
4:o:164:ARG:HG2	4:o:164:ARG:HH11	1.71	0.56
4:s:70:GLY:O	4:u:39:PRO:CD	2.49	0.56
4:x:63:ILE:CG2	4:y:16:ARG:HG3	2.36	0.56
2:B4:56:THR:O	2:B4:60:LYS:HB3	2.04	0.56
2:C0:202:VAL:HA	2:C0:268:MET:HB2	1.88	0.56
3:C5:207:LEU:HB3	3:C5:225:LEU:HD12	1.87	0.56
3:D5:95:THR:OG1	3:D5:108:GLU:OE2	2.24	0.56
3:E1:311:LEU:HD12	3:E1:342:VAL:HG11	1.87	0.56
4:c:112:PHE:CG	4:c:129:MET:HE1	2.41	0.56
4:m:171:ILE:HD11	4:m:179:GLU:HB2	1.87	0.56
4:s:57:ASN:ND2	4:u:12:VAL:HG13	2.21	0.56
4:y:146:ARG:HD3	4:y:156:VAL:HG21	1.87	0.56
2:A8:282:TYR:O	2:B2:60:LYS:NZ	2.39	0.56
2:B6:221:ARG:HB3	3:B7:322:SER:CB	2.36	0.56
2:B8:88:HIS:HB3	2:B8:91:GLN:HG3	1.88	0.56
2:D2:221:ARG:NH2	4:q:190:GLU:O	2.39	0.56
4:c:119:ARG:NH2	4:c:137:GLU:HB3	2.21	0.56
4:f:15:ARG:HA	4:f:45:MET:HE1	1.87	0.56
2:B0:115:VAL:HG21	2:B0:152:LEU:HD22	1.87	0.56
3:B1:260:PHE:HB3	3:B1:261:PRO:HD2	1.88	0.56
3:B5:132:GLY:HA3	3:B5:163:ILE:HG22	1.88	0.56
3:C3:249:ASP:H	3:C3:252:LYS:HB2	1.71	0.56
2:C4:287:SER:OG	2:C4:290:GLU:OE1	2.21	0.56
2:E4:394:LYS:HG2	3:E5:346:PRO:CG	2.36	0.56
2:E6:71:GLU:HB2	2:E6:98:ASP:HB3	1.88	0.56
3:F1:358:PRO:HG2	3:F1:361:LEU:HB3	1.88	0.56
4:b:67:HIS:ND1	4:d:19:GLU:OE1	2.38	0.56
4:t:65:GLN:HE21	4:t:206:PHE:HZ	1.54	0.56
4:y:9:PRO:HA	4:y:12:VAL:HG22	1.86	0.56
3:A5:219:THR:CB	2:A6:324:VAL:HG21	2.33	0.55
2:B8:175:PRO:HB3	2:B8:390:ARG:NH2	2.20	0.55
2:C2:404:PHE:CD1	3:C3:259:PRO:HA	2.41	0.55
2:C4:236:SER:O	2:C4:243:ARG:NH2	2.39	0.55
2:C6:309:HIS:NE2	2:C6:386:GLU:OE1	2.39	0.55
2:D4:309:HIS:NE2	2:D4:386:GLU:OE1	2.38	0.55
4:f:97:ARG:HH12	4:h:161:TYR:HA	1.70	0.55
4:i:63:ILE:HD13	4:k:16:ARG:HD3	1.83	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:142:GLU:OE2	4:j:146:ARG:NH2	2.39	0.55
4:m:64:PRO:HD2	4:m:67:HIS:CE1	2.40	0.55
4:m:117:ARG:NH1	4:m:118:ASP:OD1	2.38	0.55
4:x:15:ARG:O	4:x:19:GLU:HG3	2.05	0.55
2:D6:222:PRO:HD2	3:D7:324:LYS:NZ	2.20	0.55
3:E7:211:CYS:SG	3:E7:220:PRO:HG3	2.46	0.55
4:b:106:GLN:NE2	4:b:108:ILE:O	2.39	0.55
4:f:67:HIS:CE1	4:h:16:ARG:HG2	2.41	0.55
1:3:251:TYR:HE1	2:B0:22:GLU:OE2	1.89	0.55
3:B5:27:GLU:OE1	3:B5:318:ARG:NH2	2.35	0.55
3:C3:68:LEU:HA	3:C3:93:GLY:HA3	1.88	0.55
2:C4:71:GLU:HG2	2:C4:73:THR:HG22	1.87	0.55
3:C9:66:MET:CE	3:C9:151:LEU:HD22	2.35	0.55
2:D0:90:GLU:HG3	2:D0:121:ARG:HD3	1.88	0.55
3:D9:283:ALA:HA	3:E3:55:THR:CG2	2.37	0.55
2:E4:97:GLU:HG3	3:E5:129:CYS:SG	2.46	0.55
3:E5:113:ILE:HA	3:E5:116:VAL:HG12	1.87	0.55
2:E6:230:LEU:HD22	2:E6:275:ILE:HD12	1.88	0.55
4:i:175:SER:HA	4:i:206:PHE:HE1	1.70	0.55
4:j:106:GLN:HE22	4:l:42:TYR:HE1	1.46	0.55
4:j:187:SER:OG	4:j:188:GLY:N	2.40	0.55
4:q:111:ILE:HD13	4:q:132:LEU:HB2	1.88	0.55
4:t:8:SER:HB2	4:t:147:HIS:HA	1.89	0.55
4:x:67:HIS:NE2	4:y:20:GLU:OE1	2.39	0.55
3:A1:130:LEU:O	3:A1:162:ARG:NH1	2.37	0.55
3:A5:77:ARG:HG3	3:A5:90:PHE:HE2	1.71	0.55
2:B0:71:GLU:HG2	2:B0:73:THR:HG22	1.88	0.55
3:B1:68:LEU:HB3	3:B1:96:GLY:HA2	1.88	0.55
3:B9:11:GLN:HA	3:B9:72:THR:HG21	1.87	0.55
3:C1:263:LEU:HB2	3:C1:422:TYR:CZ	2.41	0.55
2:C2:306:ASP:OD1	2:C2:308:ARG:NH1	2.40	0.55
2:C8:12:ALA:CB	2:C8:140:ALA:HB2	2.35	0.55
2:D0:283:HIS:HA	2:D4:60:LYS:NZ	2.21	0.55
2:D2:203:MET:HE2	2:D2:267:PHE:HB3	1.88	0.55
3:D3:172:SER:HB3	3:D3:205:GLU:HG2	1.87	0.55
3:D7:117:LEU:HA	3:D7:120:VAL:HG12	1.87	0.55
3:D9:313:ALA:HB3	3:D9:349:MET:HG2	1.87	0.55
2:E8:2:ARG:HE	2:E8:133:GLN:HE21	1.55	0.55
4:d:71:LYS:CG	4:f:39:PRO:HG3	2.36	0.55
4:e:53:GLY:HA2	4:e:62:VAL:HG21	1.87	0.55
4:k:69:LYS:CD	4:m:23:LEU:HD21	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:23:255:PRO:HD2	2:C4:364:PRO:HB2	1.88	0.55
2:A0:242:LEU:HD21	2:A0:251:ASP:CB	2.37	0.55
3:A7:180:VAL:O	3:A7:184:ASN:ND2	2.39	0.55
2:B6:221:ARG:HB3	3:B7:322:SER:HB2	1.88	0.55
3:C3:100:ASN:HB3	3:C3:103:LYS:HG2	1.88	0.55
3:C3:259:PRO:HG2	3:C3:311:LEU:CD2	2.35	0.55
3:C5:6:HIS:CD2	3:C5:134:GLN:HG3	2.41	0.55
2:E0:222:PRO:HG2	3:E1:324:LYS:HB2	1.88	0.55
3:E7:49:VAL:HG11	3:E7:241:ARG:HG2	1.88	0.55
4:l:67:HIS:CE1	4:n:16:ARG:HG3	2.41	0.55
4:t:146:ARG:HG3	4:t:146:ARG:NH1	2.20	0.55
2:A0:37:PRO:C	4:y:86:ALA:HB1	2.23	0.55
2:A0:268:MET:N	2:A0:268:MET:SD	2.80	0.55
2:A6:30:ILE:HG22	2:A6:36:MET:HB3	1.88	0.55
3:B5:14:ASN:HD21	3:B5:73:MET:HE3	1.72	0.55
2:C0:269:LEU:HB3	2:C0:301:MET:HE2	1.88	0.55
2:C4:97:GLU:OE2	2:C4:105:ARG:NH2	2.31	0.55
2:C4:288:VAL:HA	2:C4:291:ILE:HG12	1.88	0.55
2:D2:69:ASP:OD1	2:D2:70:LEU:N	2.38	0.55
4:d:18:ASN:HB2	4:d:45:MET:HG2	1.87	0.55
4:h:64:PRO:HD2	4:h:67:HIS:CE1	2.42	0.55
4:o:202:ARG:HH11	4:o:202:ARG:HG2	1.72	0.55
3:A3:117:LEU:HA	3:A3:120:VAL:HG12	1.89	0.55
2:A8:221:ARG:NH2	4:e:190:GLU:O	2.40	0.55
3:C3:192:LEU:HD11	3:C3:199:VAL:HG21	1.89	0.55
3:C3:380:ARG:HH11	3:C3:381:VAL:HG23	1.72	0.55
3:D5:238:CYS:SG	3:D5:318:ARG:NE	2.79	0.55
2:D6:33:ASP:O	2:D6:60:LYS:NZ	2.38	0.55
3:D9:11:GLN:O	3:D9:15:GLN:HG3	2.06	0.55
2:E4:68:LEU:HD11	2:E4:118:SER:HB2	1.87	0.55
4:m:10:LEU:HG	4:m:143:ILE:HG22	1.89	0.55
1:6:247:TYR:HE2	2:B6:81:GLY:CA	2.20	0.55
2:A2:102:ASN:HB2	2:A2:105:ARG:HB2	1.89	0.55
2:A6:403:ALA:HA	3:A7:260:PHE:HE1	1.69	0.55
2:B6:178:SER:HB3	3:B7:347:ASN:ND2	2.21	0.55
2:B6:394:LYS:HG2	3:B7:346:PRO:HG3	1.89	0.55
3:B9:55:THR:HG23	3:B9:55:THR:O	2.07	0.55
2:D4:214:ARG:CB	3:D5:324:LYS:NZ	2.62	0.55
3:E9:121:ARG:NH2	3:E9:158:GLU:OE2	2.40	0.55
3:F1:248:SER:OG	3:F1:350:LYS:NZ	2.39	0.55
4:i:106:GLN:HG2	4:k:6:PHE:CE1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:y:5:VAL:HG11	4:y:149:ARG:HD3	1.88	0.55
4:y:15:ARG:O	4:y:19:GLU:HG3	2.07	0.55
2:A0:339:ARG:O	2:A0:342:GLN:NE2	2.40	0.55
3:A3:207:LEU:HD11	3:A3:300:MET:HE2	1.88	0.55
2:B2:269:LEU:HD11	2:B2:384:ILE:HD11	1.89	0.55
3:B3:220:PRO:O	2:B4:325:PRO:HD2	2.07	0.55
2:B8:11:GLN:HE22	3:B9:246:LEU:CD1	2.20	0.55
3:D3:101:TRP:NE1	3:D3:145:SER:O	2.40	0.55
3:D3:129:CYS:SG	3:D3:162:ARG:NH2	2.80	0.55
3:D7:322:SER:OG	3:D7:325:GLU:OE2	2.24	0.55
2:E4:210:TYR:CD1	3:E5:324:LYS:HG3	2.42	0.55
4:c:66:SER:O	4:e:23:LEU:HD21	2.06	0.55
4:e:128:HIS:O	4:g:159:TYR:HD1	1.90	0.55
4:v:140:LEU:HA	4:v:143:ILE:HG22	1.88	0.55
2:A8:285:GLN:HG3	2:A8:286:LEU:N	2.21	0.55
2:B0:138:PHE:HZ	2:B0:235:ILE:HD12	1.72	0.55
2:C0:207:GLU:HA	2:C0:210:TYR:HB2	1.89	0.55
2:C0:306:ASP:N	2:C0:386:GLU:OE2	2.40	0.55
2:C2:406:HIS:CE1	3:C3:261:PRO:HB3	2.42	0.55
3:E1:49:VAL:HG21	3:E1:241:ARG:HG2	1.89	0.55
3:E3:215:LEU:HD21	3:E3:273:LEU:HD22	1.87	0.55
4:f:142:GLU:OE2	4:f:146:ARG:NE	2.40	0.55
4:h:75:LEU:O	4:h:170:VAL:HA	2.07	0.55
4:q:8:SER:OG	4:q:11:ASN:OD1	2.24	0.55
4:q:96:TYR:OH	4:s:6:PHE:HE2	1.89	0.55
4:v:100:ASN:HB3	4:x:6:PHE:CD1	2.42	0.55
4:x:198:ARG:HH11	4:x:198:ARG:CG	2.20	0.55
3:A3:77:ARG:HH22	3:A3:92:PHE:HZ	1.54	0.54
2:A6:323:VAL:HG13	2:A6:355:ILE:HG23	1.88	0.54
3:A7:259:PRO:HG2	3:A7:311:LEU:HD21	1.89	0.54
2:A8:71:GLU:HB2	2:A8:98:ASP:OD1	2.06	0.54
2:B0:73:THR:HG21	3:B1:2:ARG:HH22	1.72	0.54
3:C5:12:CYS:HB3	3:C5:138:SER:HB3	1.88	0.54
3:C9:220:PRO:HG2	2:D0:326:LYS:CE	2.36	0.54
2:D2:269:LEU:HD11	2:D2:384:ILE:HD11	1.88	0.54
3:D3:91:VAL:HG21	3:D3:116:VAL:HG22	1.89	0.54
3:E1:291:GLN:HB2	3:E5:122:LYS:HZ1	1.72	0.54
2:E8:298:PRO:HA	2:E8:301:MET:HE3	1.89	0.54
4:r:106:GLN:NE2	4:r:109:GLU:OE1	2.40	0.54
4:t:63:ILE:HG22	4:v:16:ARG:HG3	1.89	0.54
2:A6:109:THR:HG21	2:A6:411:GLU:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B8:406:HIS:HA	2:B8:409:VAL:HG12	1.89	0.54
2:C4:339:ARG:O	2:C4:342:GLN:NE2	2.40	0.54
2:C6:262:TYR:HB3	2:C6:263:PRO:HD2	1.89	0.54
2:C8:386:GLU:OE1	2:C8:390:ARG:NH1	2.41	0.54
2:D6:283:HIS:CD2	2:E0:60:LYS:HZ1	2.25	0.54
2:E4:241:SER:HB2	2:E4:249:ASN:HB2	1.89	0.54
2:F0:80:THR:HA	2:F0:84:ARG:HE	1.72	0.54
4:a:96:TYR:HH	4:c:6:PHE:HE2	1.54	0.54
4:k:15:ARG:O	4:k:19:GLU:HG3	2.07	0.54
4:l:181:GLN:HE22	4:l:200:ASP:H	1.53	0.54
4:p:18:ASN:HD22	4:p:45:MET:HG2	1.71	0.54
2:A0:356:ASN:OD1	2:A0:358:GLN:NE2	2.40	0.54
3:A5:176:SER:CB	2:A6:349:THR:HB	2.38	0.54
2:A6:221:ARG:C	3:A7:322:SER:HB2	2.33	0.54
2:B2:163:LYS:H	2:B2:163:LYS:HD3	1.73	0.54
2:D0:377:MET:HE2	2:D0:379:SER:HB3	1.90	0.54
2:D2:182:VAL:HG11	3:D3:255:VAL:CG1	2.37	0.54
2:D4:214:ARG:HB2	3:D5:324:LYS:HZ1	1.67	0.54
3:D5:100:ASN:ND2	3:D5:397:TRP:O	2.41	0.54
2:D8:123:ARG:NH1	2:D8:160:ASP:OD2	2.37	0.54
2:D8:238:LEU:HD11	2:D8:255:PHE:CE2	2.42	0.54
3:E1:10:GLY:O	3:E1:14:ASN:ND2	2.40	0.54
2:E8:236:SER:O	2:E8:243:ARG:NH2	2.38	0.54
4:j:57:ASN:OD1	4:j:61:THR:OG1	2.22	0.54
2:A0:406:HIS:HE1	3:A1:259:PRO:O	1.91	0.54
2:A6:178:SER:H	3:A7:347:ASN:ND2	2.04	0.54
3:A7:318:ARG:HH11	3:A7:358:PRO:HD3	1.72	0.54
3:C3:10:GLY:O	3:C3:14:ASN:ND2	2.41	0.54
2:C6:304:LYS:O	2:C6:304:LYS:HD3	2.08	0.54
3:C9:281:TYR:CE1	3:D3:58:ARG:CZ	2.89	0.54
3:D3:179:VAL:HG12	2:D4:258:ASN:OD1	2.07	0.54
3:D9:200:GLN:HB3	3:D9:268:ILE:HD12	1.88	0.54
3:E3:64:ILE:HD12	3:E3:119:VAL:HG12	1.89	0.54
3:E5:113:ILE:HD11	3:E5:147:MET:HG3	1.89	0.54
4:b:97:ARG:NH2	4:d:7:ALA:H	2.04	0.54
4:i:91:PHE:CD2	4:i:193:ASP:HB3	2.43	0.54
4:j:93:LEU:HD22	4:l:160:GLY:HA3	1.88	0.54
4:l:67:HIS:HE1	4:n:16:ARG:CG	2.20	0.54
4:v:67:HIS:CD2	4:x:19:GLU:OE1	2.60	0.54
3:A9:66:MET:HE2	3:A9:147:MET:HE3	1.88	0.54
3:B7:100:ASN:HB3	3:B7:103:LYS:HD3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C5:68:LEU:HA	3:C5:93:GLY:HA3	1.89	0.54
3:C5:135:ILE:HG12	3:C5:166:THR:HG22	1.89	0.54
2:C6:26:LEU:HD21	2:C6:363:VAL:HG12	1.89	0.54
2:C6:276:ILE:HD12	2:C6:281:ALA:HA	1.90	0.54
2:C8:259:LEU:HD21	2:C8:316:CYS:HB2	1.90	0.54
4:b:78:ALA:HB3	4:b:112:PHE:HE1	1.72	0.54
4:c:97:ARG:HG2	4:e:161:TYR:OH	2.08	0.54
4:f:18:ASN:HD21	4:f:46:ASP:H	1.54	0.54
4:i:37:GLN:NE2	4:i:41:ASN:OD1	2.41	0.54
2:A6:22:GLU:OE2	2:A6:229:ARG:NH1	2.41	0.54
2:A8:288:VAL:HG21	2:A8:323:VAL:HG13	1.88	0.54
2:B4:404:PHE:CE1	3:B5:259:PRO:HA	2.42	0.54
3:C1:248:SER:HA	3:C1:252:LYS:HG3	1.90	0.54
3:C7:139:LEU:HD13	3:C7:168:SER:HB2	1.88	0.54
3:D5:49:VAL:HG21	3:D5:241:ARG:HG2	1.89	0.54
2:D8:12:ALA:HB3	2:D8:140:ALA:HB2	1.89	0.54
2:E0:76:ASP:HA	2:E0:79:ARG:HD2	1.89	0.54
2:E0:223:THR:CG2	2:E0:225:THR:HG22	2.38	0.54
2:E4:178:SER:HB3	3:E5:347:ASN:CB	2.37	0.54
3:E5:318:ARG:HG2	3:E5:354:CYS:HB3	1.89	0.54
3:F1:113:ILE:HA	3:F1:116:VAL:HG12	1.88	0.54
4:e:93:LEU:HD13	4:g:160:GLY:N	2.23	0.54
4:i:93:LEU:HD21	4:k:159:TYR:C	2.30	0.54
1:22:251:TYR:OH	2:C6:225:THR:OG1	2.24	0.54
3:A9:292:GLN:O	3:A9:298:ASN:ND2	2.41	0.54
3:B9:290:THR:HA	3:B9:293:MET:HE3	1.88	0.54
3:B9:311:LEU:HD12	3:B9:342:VAL:HG11	1.87	0.54
3:C1:317:PHE:HB3	3:C1:321:MET:HE1	1.89	0.54
3:C3:54:ALA:HB3	3:C3:58:ARG:HG2	1.89	0.54
2:C4:401:LYS:NZ	3:C5:425:TYR:CE1	2.76	0.54
2:E0:71:GLU:CD	3:E1:2:ARG:HH22	2.14	0.54
2:E4:210:TYR:CD1	3:E5:324:LYS:CB	2.90	0.54
2:F0:208:ALA:HB2	2:F0:304:LYS:HB2	1.89	0.54
4:k:5:VAL:HG11	4:k:149:ARG:HD3	1.89	0.54
4:k:9:PRO:HB2	4:k:143:ILE:HG23	1.88	0.54
4:x:198:ARG:HH11	4:x:198:ARG:HG3	1.73	0.54
1:15:244:GLN:NE2	4:t:162:GLY:HA3	2.22	0.54
1:18:251:TYR:CE1	2:E4:22:GLU:HB2	2.43	0.54
2:A6:279:GLU:OE2	4:d:198:ARG:HD3	2.07	0.54
2:A8:33:ASP:O	2:A8:60:LYS:NZ	2.41	0.54
3:A9:163:ILE:HD13	3:A9:250:LEU:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B4:377:MET:HE3	2:B4:379:SER:HB3	1.90	0.54
2:C0:241:SER:OG	2:C0:250:VAL:O	2.25	0.54
2:C4:181:VAL:HG12	3:C5:256:ASN:CB	2.38	0.54
2:C6:186:ASN:OD1	2:C6:408:TYR:OH	2.25	0.54
2:D2:229:ARG:HG3	2:D2:229:ARG:HH11	1.73	0.54
2:D6:69:ASP:OD1	2:D6:70:LEU:N	2.40	0.54
3:D7:135:ILE:HB	3:D7:166:THR:HG22	1.90	0.54
2:E4:223:THR:CG2	2:E4:225:THR:HG22	2.36	0.54
2:E4:422:ARG:HH12	2:E4:426:ALA:HB2	1.72	0.54
3:F1:43:GLN:HA	3:F1:242:PHE:HE1	1.72	0.54
4:c:8:SER:OG	4:c:11:ASN:OD1	2.25	0.54
4:e:106:GLN:NE2	4:g:6:PHE:CZ	2.76	0.54
4:f:198:ARG:HG3	4:f:198:ARG:NH1	2.22	0.54
4:g:78:ALA:HB3	4:g:112:PHE:HE1	1.73	0.54
4:j:128:HIS:O	4:l:159:TYR:CD1	2.61	0.54
4:m:9:PRO:HB2	4:m:143:ILE:HG23	1.89	0.54
3:A1:193:VAL:HG12	3:A1:265:PHE:CE2	2.43	0.54
3:A1:341:PHE:HB3	3:A1:348:ASN:HD22	1.72	0.54
2:A6:285:GLN:HB2	2:B0:57:GLY:H	1.72	0.54
3:A7:73:MET:HG3	3:A7:90:PHE:HD2	1.73	0.54
3:A9:192:LEU:CD2	3:A9:199:VAL:HG21	2.38	0.54
3:C1:192:LEU:HD11	3:C1:199:VAL:HG11	1.89	0.54
2:D4:283:HIS:HD2	2:D8:60:LYS:CE	2.20	0.54
2:D6:11:GLN:NE2	2:D6:15:GLN:OE1	2.39	0.54
3:D7:128:ASP:OD1	3:D7:129:CYS:N	2.36	0.54
2:E2:242:LEU:HD11	2:E2:252:VAL:HG23	1.90	0.54
2:E4:285:GLN:HG3	2:E8:56:THR:C	2.33	0.54
2:F0:269:LEU:HD11	2:F0:384:ILE:HD11	1.89	0.54
4:c:97:ARG:HE	4:e:161:TYR:HE1	1.53	0.54
4:l:5:VAL:HG11	4:l:149:ARG:HD3	1.89	0.54
1:10:241:PHE:HB2	3:C9:359:LYS:HG2	1.89	0.54
1:18:248:ARG:HH12	3:E5:42:LEU:CD2	2.15	0.54
2:A4:220:GLU:HG2	2:A4:221:ARG:HG3	1.88	0.54
3:B1:292:GLN:NE2	3:B1:298:ASN:OD1	2.40	0.54
2:D0:8:HIS:CD2	2:D0:17:GLY:HA3	2.42	0.54
2:E0:244:PHE:HB2	2:E0:356:ASN:HD21	1.70	0.54
3:E1:281:TYR:O	3:E5:54:ALA:HB1	2.07	0.54
2:E2:96:LYS:NZ	3:E3:1:MET:N	2.55	0.54
3:E7:257:LEU:HD21	3:E7:314:SER:HB3	1.89	0.54
3:E9:220:PRO:HD2	2:F0:326:LYS:CE	2.38	0.54
4:l:66:SER:O	4:n:23:LEU:HD11	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:m:55:LEU:HD22	4:m:111:ILE:HD12	1.90	0.54
4:r:69:LYS:O	4:t:39:PRO:HD3	2.08	0.54
4:s:14:LYS:HD3	4:s:47:LEU:HD22	1.90	0.54
4:x:67:HIS:CD2	4:y:20:GLU:OE1	2.60	0.54
3:A3:311:LEU:HD12	3:A3:342:VAL:HG11	1.89	0.53
2:B6:262:TYR:HB2	2:B6:265:ILE:HD12	1.90	0.53
2:C0:2:ARG:NH2	2:C0:133:GLN:OE1	2.38	0.53
2:C2:267:PHE:O	2:C2:380:ASN:ND2	2.42	0.53
3:D5:330:MET:HE3	3:D5:351:SER:HB3	1.89	0.53
2:E8:252:VAL:HA	2:E8:255:PHE:HD2	1.72	0.53
3:F1:139:LEU:HA	3:F1:145:SER:HB2	1.89	0.53
4:e:7:ALA:HB3	4:e:161:TYR:HE2	1.73	0.53
4:g:9:PRO:HB2	4:g:143:ILE:HG23	1.90	0.53
4:k:181:GLN:HE22	4:k:200:ASP:H	1.55	0.53
4:v:66:SER:HB2	4:x:23:LEU:HD22	1.91	0.53
3:A1:139:LEU:HD13	3:A1:168:SER:HB2	1.90	0.53
3:A5:113:ILE:HG22	3:A5:154:LYS:HE2	1.90	0.53
3:B9:12:CYS:HB3	3:B9:138:SER:HB2	1.90	0.53
3:D5:192:LEU:HD21	3:D5:199:VAL:HG11	1.90	0.53
2:E6:180:ALA:HB3	2:E6:183:GLU:HB3	1.90	0.53
2:E8:178:SER:HB3	2:E8:183:GLU:HG3	1.90	0.53
4:l:146:ARG:HH11	4:l:146:ARG:HG3	1.74	0.53
4:o:53:GLY:HA2	4:o:62:VAL:CG2	2.38	0.53
1:23:257:PRO:HG2	2:C4:26:LEU:CD1	2.38	0.53
2:B4:188:VAL:HG23	2:B4:425:LEU:HD22	1.90	0.53
2:C0:217:LEU:HD21	2:C0:275:ILE:HG13	1.91	0.53
2:C6:298:PRO:HA	2:C6:301:MET:HE1	1.91	0.53
2:C8:276:ILE:HG23	2:C8:280:LYS:HB2	1.91	0.53
2:D0:224:TYR:HB2	3:D1:245:GLN:OE1	2.09	0.53
3:D7:396:HIS:HA	3:D7:399:THR:HG22	1.89	0.53
2:E2:185:TYR:HE2	2:E2:404:PHE:HB2	1.73	0.53
2:E6:176:GLN:HB3	3:E7:331:LEU:HD11	1.91	0.53
3:E7:284:LEU:HB3	3:E7:362:LYS:HE3	1.90	0.53
4:a:169:SER:HA	4:a:185:ILE:HD11	1.90	0.53
4:b:97:ARG:NH2	4:d:7:ALA:N	2.57	0.53
4:u:146:ARG:HH12	4:u:156:VAL:HG11	1.73	0.53
2:A0:382:THR:HG22	2:A0:382:THR:O	2.07	0.53
2:A2:126:ALA:HB1	2:A2:132:LEU:HD22	1.90	0.53
2:A2:324:VAL:HG12	2:A2:326:LYS:H	1.74	0.53
2:A4:119:LEU:HD13	2:A4:122:ILE:HD11	1.90	0.53
2:A6:79:ARG:NH1	2:A6:94:SER:OG	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A6:283:HIS:CD2	2:B0:60:LYS:HE2	2.42	0.53
3:B3:176:SER:HB2	2:B4:349:THR:HG23	1.90	0.53
2:B8:53:PHE:HB3	2:B8:61:HIS:HB3	1.91	0.53
3:B9:49:VAL:HG11	3:B9:241:ARG:HG2	1.90	0.53
3:B9:128:ASP:OD1	3:B9:129:CYS:N	2.37	0.53
3:C5:167:PHE:CD2	3:C5:233:MET:HG2	2.43	0.53
2:C6:352:LYS:NZ	2:C6:353:CYS:O	2.41	0.53
3:C9:334:GLN:HE22	3:C9:348:ASN:H	1.56	0.53
2:D4:407:TRP:CH2	3:D5:258:ILE:HB	2.39	0.53
3:D9:238:CYS:SG	3:D9:318:ARG:NE	2.82	0.53
2:E4:10:GLY:HA2	2:E4:145:THR:HG23	1.90	0.53
3:E5:175:VAL:HG11	2:E6:332:VAL:CG1	2.26	0.53
3:E7:186:THR:HG22	3:E7:415:MET:SD	2.49	0.53
4:h:8:SER:OG	4:h:11:ASN:OD1	2.26	0.53
4:l:15:ARG:O	4:l:19:GLU:HG3	2.08	0.53
4:q:181:GLN:NE2	4:q:200:ASP:OD1	2.41	0.53
5:w:34:VAL:HA	5:w:70:GLU:O	2.08	0.53
1:19:250:GLU:HG3	2:E6:225:THR:HG21	1.90	0.53
1:23:250:GLU:OE2	2:C4:225:THR:HG21	2.08	0.53
2:A4:48:ALA:HB1	2:A4:243:ARG:O	2.09	0.53
3:B1:2:ARG:NH1	3:B1:249:ASP:OD2	2.42	0.53
3:B9:11:GLN:HG3	3:B9:12:CYS:N	2.23	0.53
2:C4:290:GLU:HA	2:C4:293:ASN:HB2	1.89	0.53
2:C6:277:SER:OG	2:C6:278:ALA:N	2.40	0.53
2:D0:85:HIS:NE2	4:n:98:THR:HG22	2.22	0.53
2:D0:283:HIS:HA	2:D4:60:LYS:HZ3	1.73	0.53
2:E0:176:GLN:CB	3:E1:331:LEU:HD13	2.23	0.53
2:E6:277:SER:OG	2:E6:278:ALA:N	2.42	0.53
3:E7:311:LEU:HD12	3:E7:342:VAL:HG11	1.90	0.53
4:i:96:TYR:HA	4:i:108:ILE:HD11	1.91	0.53
2:A0:18:ASN:HD21	2:A0:78:VAL:HG22	1.74	0.53
3:A9:345:ILE:O	3:A9:348:ASN:ND2	2.41	0.53
2:B2:230:LEU:HD21	2:B2:368:LEU:HD11	1.91	0.53
3:B3:372:THR:HG21	3:B3:426:GLN:HB3	1.91	0.53
2:D2:11:GLN:HE22	3:D3:246:LEU:CD1	2.21	0.53
2:D2:207:GLU:HA	2:D2:210:TYR:HB2	1.90	0.53
2:D4:262:TYR:HB3	2:D4:263:PRO:HD2	1.89	0.53
3:D5:321:MET:HE2	3:D5:353:VAL:HG13	1.90	0.53
3:E7:139:LEU:HA	3:E7:145:SER:HB2	1.90	0.53
2:E8:296:PHE:CE2	2:E8:335:ILE:HG21	2.43	0.53
2:B0:394:LYS:CD	3:B1:346:PRO:HG3	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B3:336:LYS:HA	3:B3:336:LYS:CE	2.39	0.53
2:B4:404:PHE:CZ	3:B5:259:PRO:HA	2.44	0.53
2:C4:287:SER:HA	2:C4:373:ARG:HH21	1.73	0.53
3:D1:282:ARG:NH1	3:D1:288:GLU:OE2	2.41	0.53
3:F1:330:MET:HG2	3:F1:349:MET:HG2	1.91	0.53
4:e:12:VAL:HG12	4:e:15:ARG:NH1	2.23	0.53
4:m:119:ARG:NH2	4:m:137:GLU:HB2	2.23	0.53
4:q:9:PRO:HA	4:q:12:VAL:HG22	1.90	0.53
4:q:170:VAL:HG23	4:q:183:LEU:HB2	1.91	0.53
4:y:20:GLU:OE2	4:y:24:MET:HE3	2.09	0.53
1:16:246:CYS:CB	3:E1:320:ARG:NH2	2.72	0.53
3:A5:128:ASP:OD1	3:A5:129:CYS:N	2.38	0.53
2:B6:132:LEU:HB3	2:B6:164:LYS:HE2	1.91	0.53
2:C0:279:GLU:HG2	4:k:197:LEU:O	2.09	0.53
2:C0:286:LEU:O	2:C0:373:ARG:NH1	2.42	0.53
3:C3:35:THR:OG1	3:C3:36:TYR:N	2.41	0.53
3:C3:73:MET:HB3	3:C3:77:ARG:HH22	1.73	0.53
3:C7:320:ARG:CD	4:n:188:GLY:HA2	2.39	0.53
3:C9:281:TYR:CE1	3:D3:58:ARG:NH1	2.77	0.53
2:E4:224:TYR:HE2	3:E5:246:LEU:HD13	1.74	0.53
2:E6:223:THR:HG23	2:E6:225:THR:HG22	1.90	0.53
4:d:38:LEU:HD23	4:d:38:LEU:H	1.74	0.53
4:f:106:GLN:NE2	4:h:6:PHE:HZ	2.07	0.53
4:h:106:GLN:NE2	4:j:6:PHE:HZ	2.06	0.53
4:i:106:GLN:HG3	4:k:42:TYR:OH	2.08	0.53
4:s:25:GLN:HE22	4:s:36:ILE:HG21	1.72	0.53
3:B3:3:GLU:HA	3:B3:49:VAL:HA	1.90	0.53
2:B4:178:SER:HG	2:B4:180:ALA:H	1.55	0.53
3:B7:175:VAL:HG21	2:B8:332:VAL:HG13	1.90	0.53
3:C5:213:ARG:HH22	3:C5:297:LYS:HG3	1.72	0.53
2:C6:240:ALA:HB1	2:C6:356:ASN:HD22	1.74	0.53
3:C7:83:GLN:OE1	3:C7:83:GLN:N	2.42	0.53
3:C7:320:ARG:NE	4:n:188:GLY:HA2	2.24	0.53
3:C9:293:MET:SD	3:C9:365:VAL:HG11	2.49	0.53
3:D1:173:PRO:HD3	3:D1:380:ARG:CZ	2.38	0.53
2:D4:279:GLU:OE2	4:r:198:ARG:HD3	2.09	0.53
2:E0:73:THR:HB	3:E1:46:ARG:HH22	1.74	0.53
2:E4:71:GLU:HB3	2:E4:98:ASP:HB2	1.90	0.53
2:F0:265:ILE:HG23	2:F0:432:TYR:HE1	1.74	0.53
4:a:97:ARG:NH2	4:c:7:ALA:CB	2.68	0.53
4:e:100:ASN:HB3	4:g:6:PHE:CG	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:h:97:ARG:N	4:j:159:TYR:OH	2.42	0.53
4:i:100:ASN:HB3	4:k:6:PHE:CE1	2.44	0.53
4:t:15:ARG:O	4:t:19:GLU:HG3	2.09	0.53
1:22:254:LYS:HB3	1:22:255:PRO:HD2	1.91	0.53
2:A2:101:ASN:HB2	3:A3:255:VAL:CG1	2.39	0.53
2:A8:102:ASN:HB2	2:A8:105:ARG:HB2	1.91	0.53
3:B3:15:GLN:O	3:B3:226:ASN:ND2	2.42	0.53
3:B5:3:GLU:HA	3:B5:49:VAL:HA	1.90	0.53
2:B6:234:VAL:HG21	2:B6:302:MET:HE1	1.91	0.53
3:B9:293:MET:HE2	3:B9:365:VAL:HG11	1.89	0.53
3:D1:316:MET:HG3	3:D1:352:SER:OG	2.09	0.53
3:D5:213:ARG:HH12	3:D5:297:LYS:HB2	1.73	0.53
3:E7:176:SER:OG	3:E7:181:GLU:OE1	2.27	0.53
3:E9:68:LEU:HG	3:E9:147:MET:HE2	1.91	0.53
4:r:111:ILE:HD13	4:r:132:LEU:HB2	1.91	0.53
4:r:129:MET:SD	4:r:131:TRP:NE1	2.81	0.53
4:x:71:LYS:HG3	4:y:39:PRO:HG3	1.91	0.53
1:21:238:THR:HG21	3:F1:359:LYS:NZ	2.24	0.52
2:A0:120:ASP:O	2:A0:124:LYS:HG2	2.09	0.52
3:A1:205:GLU:HA	3:A1:208:TYR:HD2	1.73	0.52
3:A1:259:PRO:HB2	3:A1:260:PHE:CD2	2.44	0.52
2:A6:313:MET:HE3	2:A6:435:VAL:HG11	1.91	0.52
3:B7:212:PHE:CD1	2:B8:326:LYS:HD3	2.44	0.52
2:C0:11:GLN:NE2	2:C0:15:GLN:OE1	2.42	0.52
2:C6:271:SER:HB3	2:C6:377:MET:HB3	1.91	0.52
2:C8:141:VAL:HG23	2:C8:170:CYS:HB3	1.90	0.52
2:D4:66:VAL:HG21	2:D4:122:ILE:HD11	1.91	0.52
2:E6:4:VAL:HG12	2:E6:133:GLN:HB3	1.92	0.52
2:E6:64:ARG:HB3	2:E6:125:LEU:HD21	1.90	0.52
3:E9:239:CYS:SG	3:E9:248:SER:N	2.78	0.52
2:F0:322:ASP:O	2:F0:373:ARG:NH2	2.42	0.52
2:F0:329:ASN:HA	2:F0:332:VAL:HG12	1.91	0.52
3:F1:285:SER:N	3:F1:288:GLU:OE2	2.37	0.52
4:b:115:LEU:HD21	4:b:145:LYS:HE3	1.90	0.52
4:d:84:LYS:HE3	4:d:168:PRO:HD2	1.89	0.52
4:g:106:GLN:HG3	4:i:6:PHE:HZ	1.70	0.52
4:q:112:PHE:HB2	4:q:131:TRP:HE1	1.75	0.52
1:6:256:LEU:HD22	2:B6:31:GLN:HG2	1.91	0.52
2:A0:88:HIS:CE1	2:A0:90:GLU:HG3	2.45	0.52
2:A0:174:SER:OG	2:A0:177:VAL:O	2.27	0.52
3:A9:27:GLU:OE2	3:A9:241:ARG:NH1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B0:209:ILE:HA	2:B0:212:ILE:HG22	1.91	0.52
3:B1:57:GLY:HA3	4:d:83:PRO:HB2	1.91	0.52
3:C1:135:ILE:HG22	3:C1:137:HIS:HD2	1.74	0.52
2:C6:250:VAL:HG22	2:C6:352:LYS:HE3	1.91	0.52
3:D1:192:LEU:HD21	3:D1:199:VAL:HG11	1.91	0.52
2:D2:199:ASP:OD2	2:D2:256:GLN:NE2	2.41	0.52
3:E1:70:PRO:HD2	2:E2:2:ARG:HH21	1.74	0.52
2:E2:319:TYR:HB3	2:E2:323:VAL:HG21	1.92	0.52
4:a:112:PHE:HB2	4:a:131:TRP:HE1	1.73	0.52
4:l:78:ALA:HB3	4:l:112:PHE:HE1	1.74	0.52
3:A5:105:HIS:CD2	3:A5:150:LEU:HB2	2.45	0.52
3:A9:10:GLY:HA2	3:A9:143:THR:HG23	1.90	0.52
2:B4:282:TYR:HD2	2:B4:283:HIS:CE1	2.26	0.52
3:C1:317:PHE:CB	3:C1:321:MET:HE1	2.39	0.52
3:C9:309:ARG:H	3:C9:372:THR:HG22	1.74	0.52
3:D1:7:VAL:HB	3:D1:135:ILE:HG12	1.91	0.52
2:D4:210:TYR:HB3	3:D5:324:LYS:HE2	1.90	0.52
2:D8:319:TYR:CD2	2:D8:375:VAL:HG22	2.44	0.52
3:D9:248:SER:HA	3:D9:252:LYS:HD2	1.91	0.52
2:E2:259:LEU:HB3	2:E2:268:MET:HE1	1.90	0.52
2:E4:108:TYR:O	2:E4:112:LYS:NZ	2.29	0.52
4:g:96:TYR:CD1	4:i:159:TYR:OH	2.57	0.52
4:n:182:PHE:HE2	4:n:187:SER:HB3	1.75	0.52
4:x:130:PRO:HB3	4:y:7:ALA:HB1	1.90	0.52
1:10:248:ARG:NH2	3:C9:42:LEU:HD13	2.24	0.52
1:8:257:PRO:HB2	2:C0:29:GLY:CA	2.35	0.52
2:A0:58:ALA:CB	4:y:84:LYS:HG2	2.39	0.52
2:B0:397:LEU:HD21	3:B1:344:TRP:CB	2.39	0.52
3:B1:16:ILE:HG22	3:B1:226:ASN:CG	2.34	0.52
2:B2:107:HIS:HE2	2:B2:151:CYS:HG	1.56	0.52
2:B4:401:LYS:HE3	3:B5:344:TRP:CD1	2.45	0.52
3:C3:230:SER:HA	3:C3:233:MET:HE2	1.91	0.52
2:C4:370:LYS:O	2:C4:370:LYS:HD3	2.09	0.52
2:D6:226:ASN:O	2:D6:230:LEU:HD23	2.09	0.52
3:E1:318:ARG:HG2	3:E1:354:CYS:HB3	1.92	0.52
3:E5:169:VAL:HG12	3:E5:202:ILE:HB	1.91	0.52
2:E8:306:ASP:HB3	2:E8:309:HIS:CE1	2.45	0.52
2:E8:396:ASP:OD1	2:E8:422:ARG:NH1	2.42	0.52
4:h:151:MET:HE1	4:h:158:THR:HG21	1.91	0.52
2:B4:219:ILE:HG22	2:B4:222:PRO:HD3	1.91	0.52
2:B8:306:ASP:OD2	2:B8:308:ARG:NH2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C3:309:ARG:NH1	3:C3:339:SER:O	2.43	0.52
2:D8:395:PHE:HD2	2:D8:422:ARG:HD3	1.73	0.52
2:E4:239:THR:OG1	2:E4:243:ARG:NH1	2.43	0.52
3:E7:105:HIS:CD2	3:E7:150:LEU:HB2	2.45	0.52
4:b:126:ARG:NH2	4:b:131:TRP:O	2.42	0.52
4:h:96:TYR:CB	4:j:159:TYR:OH	2.58	0.52
4:m:75:LEU:HD23	4:m:173:ILE:HG13	1.90	0.52
4:y:15:ARG:HG2	4:y:45:MET:HE1	1.91	0.52
1:17:247:TYR:CE2	2:E2:81:GLY:HA3	2.44	0.52
2:A8:309:HIS:NE2	2:A8:386:GLU:OE1	2.39	0.52
2:B2:259:LEU:HB3	2:B2:268:MET:HE2	1.92	0.52
3:B7:128:ASP:OD1	3:B7:129:CYS:N	2.37	0.52
3:C1:7:VAL:HB	3:C1:135:ILE:HD13	1.91	0.52
2:C2:215:ARG:NH2	2:C2:297:GLU:OE2	2.42	0.52
2:C6:319:TYR:CD1	2:C6:375:VAL:HG22	2.45	0.52
2:D2:259:LEU:HD13	2:D2:268:MET:HE2	1.90	0.52
3:E1:99:ASN:HD21	2:E2:258:ASN:HD21	1.55	0.52
2:E4:176:GLN:O	3:E5:347:ASN:HB3	2.09	0.52
2:F0:103:PHE:CD2	2:F0:189:LEU:HB3	2.45	0.52
4:i:10:LEU:HD22	4:i:47:LEU:HD21	1.91	0.52
4:k:15:ARG:HG2	4:k:45:MET:HE1	1.91	0.52
4:m:111:ILE:HD13	4:m:132:LEU:HB2	1.91	0.52
4:q:75:LEU:HD23	4:q:111:ILE:HB	1.92	0.52
4:u:2:SER:O	4:u:2:SER:OG	2.24	0.52
4:u:181:GLN:NE2	4:u:200:ASP:OD1	2.43	0.52
3:A1:70:PRO:CD	2:A2:2:ARG:NH2	2.70	0.52
2:A6:155:GLU:OE1	2:A6:197:HIS:NE2	2.33	0.52
3:B5:12:CYS:SG	3:B5:138:SER:OG	2.63	0.52
2:B6:241:SER:HB2	2:B6:249:ASN:HB2	1.91	0.52
3:B9:167:PHE:CZ	3:B9:233:MET:HG2	2.45	0.52
2:C2:217:LEU:HB3	2:C2:219:ILE:HG13	1.92	0.52
2:C4:313:MET:HE3	2:C4:380:ASN:HB3	1.92	0.52
2:C6:241:SER:HB2	2:C6:249:ASN:HB2	1.91	0.52
2:C8:177:VAL:HG22	3:C9:327:ASP:OD2	2.10	0.52
3:C9:179:VAL:HG11	2:D0:258:ASN:O	2.10	0.52
3:D3:100:ASN:HB3	3:D3:103:LYS:HB2	1.90	0.52
3:E5:304:ASP:OD2	3:E5:306:ARG:NH1	2.43	0.52
2:E6:222:PRO:HG2	3:E7:324:LYS:HB2	1.91	0.52
2:E8:12:ALA:HB3	2:E8:140:ALA:HB2	1.92	0.52
2:F0:50:ASN:O	2:F0:64:ARG:NH2	2.41	0.52
3:F1:207:LEU:HD21	3:F1:225:LEU:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:105:ASN:HD22	4:g:37:GLN:NE2	2.07	0.52
4:g:130:PRO:HB2	4:i:7:ALA:CB	2.40	0.52
4:h:15:ARG:O	4:h:19:GLU:HG3	2.10	0.52
1:19:241:PHE:CZ	3:E7:356:ILE:HD12	2.45	0.52
3:A7:139:LEU:HA	3:A7:145:SER:HB2	1.92	0.52
2:A8:338:LYS:HG2	2:A8:340:THR:HG22	1.90	0.52
3:A9:187:LEU:HA	3:A9:190:HIS:CE1	2.45	0.52
2:B6:306:ASP:OD2	2:B6:308:ARG:NH2	2.38	0.52
2:B8:50:ASN:O	2:B8:64:ARG:NH2	2.43	0.52
2:C4:309:HIS:NE2	2:C4:386:GLU:OE1	2.39	0.52
3:C5:7:VAL:HB	3:C5:135:ILE:HG22	1.92	0.52
3:D3:397:TRP:CD1	2:D4:256:GLN:OE1	2.63	0.52
3:D7:153:SER:HB2	3:D7:191:GLN:HE22	1.75	0.52
2:D8:205:ASP:OD1	2:D8:206:ASN:N	2.43	0.52
3:E9:177:ASP:HA	2:F0:351:PHE:O	2.10	0.52
4:d:23:LEU:HD11	4:d:38:LEU:HD13	1.91	0.52
4:e:93:LEU:HD22	4:g:159:TYR:HB3	1.92	0.52
4:f:105:ASN:OD1	4:f:106:GLN:N	2.43	0.52
4:f:106:GLN:HG3	4:h:6:PHE:HZ	1.72	0.52
4:p:154:TYR:HE1	4:p:158:THR:HG22	1.75	0.52
1:2:241:PHE:CD2	3:A9:40:SER:HB2	2.45	0.52
2:A4:30:ILE:HG22	2:A4:36:MET:HB3	1.92	0.52
2:A4:104:ALA:HB2	2:A4:413:MET:HE3	1.92	0.52
3:A7:203:ASP:HB2	3:A7:301:CYS:HA	1.92	0.52
3:B7:404:ASP:OD1	3:B7:405:GLU:N	2.42	0.52
2:B8:27:GLU:OE2	2:B8:243:ARG:NH1	2.43	0.52
3:C1:68:LEU:HA	3:C1:93:GLY:HA3	1.92	0.52
3:C3:183:TYR:HB3	3:C3:398:TYR:HE2	1.73	0.52
2:D0:137:MET:HE1	2:D0:154:LEU:HD11	1.92	0.52
2:E4:277:SER:OG	2:E4:278:ALA:N	2.43	0.52
3:F1:321:MET:HE3	3:F1:363:MET:SD	2.49	0.52
4:d:9:PRO:HA	4:d:12:VAL:HG22	1.92	0.52
4:f:14:LYS:HB2	4:f:47:LEU:HD12	1.91	0.52
4:m:18:ASN:CB	4:m:45:MET:HG3	2.40	0.52
4:n:10:LEU:HB2	4:n:147:HIS:CE1	2.44	0.52
4:p:18:ASN:HD22	4:p:45:MET:HA	1.75	0.52
4:s:96:TYR:OH	4:u:6:PHE:CE2	2.26	0.52
4:x:15:ARG:HG2	4:x:45:MET:HE1	1.91	0.52
2:A0:208:ALA:HB2	2:A0:304:LYS:HB2	1.91	0.52
3:B1:10:GLY:HA2	3:B1:143:THR:HG23	1.91	0.52
2:B2:177:VAL:HG13	3:B3:331:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C1:117:LEU:O	3:C1:117:LEU:HD23	2.10	0.52
2:C2:254:GLU:HG2	2:C2:352:LYS:HZ3	1.75	0.52
3:C3:163:ILE:HD13	3:C3:250:LEU:HB3	1.92	0.52
3:C7:286:VAL:HB	3:C7:287:PRO:HD3	1.92	0.52
3:E5:207:LEU:HB3	3:E5:225:LEU:HD22	1.92	0.52
3:E7:64:ILE:HD13	3:E7:119:VAL:HG13	1.92	0.52
3:E9:184:ASN:OD1	3:E9:398:TYR:OH	2.26	0.52
3:F1:180:VAL:O	3:F1:184:ASN:ND2	2.43	0.52
4:c:78:ALA:HB3	4:c:112:PHE:HE1	1.74	0.52
4:j:130:PRO:CD	4:l:159:TYR:CD1	2.91	0.52
2:A2:402:ARG:O	3:A3:260:PHE:HE1	1.94	0.51
2:A8:282:TYR:O	2:B2:60:LYS:CE	2.58	0.51
2:A8:336:LYS:O	2:A8:339:ARG:NH2	2.43	0.51
3:A9:190:HIS:HB2	3:A9:414:ASN:HB3	1.92	0.51
2:B2:240:ALA:HB1	2:B2:356:ASN:HD22	1.74	0.51
3:C1:334:GLN:OE1	3:C1:348:ASN:N	2.42	0.51
3:C7:283:ALA:HB2	3:D1:54:ALA:HA	1.93	0.51
3:C9:128:ASP:OD1	3:C9:129:CYS:N	2.40	0.51
3:D1:10:GLY:O	3:D1:14:ASN:ND2	2.40	0.51
2:D8:404:PHE:CE1	3:D9:259:PRO:HA	2.45	0.51
3:D9:87:PRO:HA	3:D9:90:PHE:CD1	2.45	0.51
3:D9:178:THR:O	3:D9:181:GLU:HG2	2.10	0.51
4:i:106:GLN:HG2	4:k:6:PHE:HE1	1.73	0.51
4:j:151:MET:HE2	4:j:154:TYR:HA	1.92	0.51
4:m:7:ALA:HB1	4:m:159:TYR:CD1	2.45	0.51
4:t:57:ASN:HB2	4:v:12:VAL:HG11	1.91	0.51
3:A1:77:ARG:HH22	3:A1:92:PHE:HZ	1.59	0.51
3:A1:341:PHE:HB3	3:A1:348:ASN:ND2	2.25	0.51
2:A6:276:ILE:HB	2:A6:280:LYS:HB2	1.92	0.51
3:A7:139:LEU:HD12	3:A7:170:PHE:HE1	1.75	0.51
2:B0:12:ALA:HB3	2:B0:140:ALA:HB2	1.92	0.51
2:B0:65:CYS:O	2:B0:91:GLN:NE2	2.42	0.51
2:B6:178:SER:HB3	3:B7:347:ASN:CG	2.34	0.51
2:C6:71:GLU:HB3	2:C6:98:ASP:HB3	1.92	0.51
2:E0:102:ASN:HB3	2:E0:105:ARG:HB3	1.92	0.51
2:F0:176:GLN:CG	3:F1:331:LEU:HD21	2.40	0.51
4:e:70:GLY:O	4:g:39:PRO:HD3	2.10	0.51
4:n:184:PRO:HB3	4:n:189:LEU:HB2	1.91	0.51
4:s:106:GLN:NE2	4:s:108:ILE:O	2.43	0.51
4:v:40:PRO:HG2	4:v:45:MET:HE2	1.91	0.51
1:18:254:LYS:HB3	2:E4:26:LEU:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:242:ASN:ND2	4:h:153:GLU:OE1	2.44	0.51
3:B1:102:ALA:HB2	3:B1:403:MET:HE3	1.91	0.51
3:C1:200:GLN:HG3	3:C1:268:ILE:HD11	1.91	0.51
2:D4:298:PRO:HB3	2:D4:307:PRO:HD2	1.92	0.51
3:D5:307:HIS:ND1	3:D5:376:GLU:OE2	2.40	0.51
2:D6:181:VAL:H	3:D7:256:ASN:HD22	1.57	0.51
2:E2:176:GLN:HB3	3:E3:331:LEU:HD13	1.92	0.51
3:E5:163:ILE:HD13	3:E5:250:LEU:HB3	1.92	0.51
2:E6:107:HIS:NE2	2:E6:151:CYS:SG	2.75	0.51
3:E9:105:HIS:HD2	3:E9:150:LEU:HD12	1.76	0.51
3:A1:219:THR:HG22	3:A1:219:THR:O	2.10	0.51
3:A5:16:ILE:HG22	3:A5:226:ASN:CG	2.35	0.51
3:C1:220:PRO:HD2	2:C2:326:LYS:HB2	1.92	0.51
3:C7:140:GLY:O	3:C7:184:ASN:ND2	2.42	0.51
3:C9:101:TRP:HB3	3:C9:398:TYR:HE1	1.76	0.51
3:D1:1:MET:N	3:D1:128:ASP:OD2	2.32	0.51
3:D3:291:GLN:HB3	3:D7:122:LYS:HZ3	1.76	0.51
2:E8:274:PRO:HG3	2:E8:286:LEU:HD13	1.92	0.51
3:E9:66:MET:HG3	3:E9:116:VAL:HG21	1.92	0.51
3:F1:183:TYR:OH	3:F1:388:MET:O	2.24	0.51
4:l:9:PRO:HA	4:l:12:VAL:HG22	1.92	0.51
4:r:97:ARG:NH2	4:t:161:TYR:HA	2.09	0.51
4:v:59:ASN:HD22	4:x:143:ILE:HD11	1.75	0.51
1:12:244:GLN:O	3:D3:320:ARG:NH2	2.43	0.51
3:A1:128:ASP:OD1	3:A1:129:CYS:N	2.42	0.51
2:B4:9:VAL:HG12	2:B4:68:LEU:HB2	1.92	0.51
3:B9:216:LYS:HE2	3:B9:275:SER:HB3	1.93	0.51
3:F1:100:ASN:HB3	3:F1:103:LYS:HG2	1.92	0.51
4:a:53:GLY:HA2	4:a:62:VAL:HG21	1.91	0.51
4:f:67:HIS:CE1	4:h:16:ARG:HG3	2.45	0.51
4:h:78:ALA:HB3	4:h:112:PHE:HE1	1.75	0.51
4:j:51:PRO:HD2	4:j:54:SER:HB3	1.91	0.51
2:A0:133:GLN:O	2:A0:165:SER:OG	2.29	0.51
2:A0:180:ALA:HB3	2:A0:183:GLU:HG2	1.91	0.51
2:A4:27:GLU:HG3	2:A4:361:THR:HG21	1.93	0.51
2:A8:214:ARG:HG3	3:A9:324:LYS:NZ	2.26	0.51
2:C0:106:GLY:HA3	2:C0:148:GLY:HA3	1.91	0.51
3:C7:100:ASN:HB3	3:C7:103:LYS:HG2	1.93	0.51
2:C8:168:ASN:ND2	2:C8:170:CYS:SG	2.84	0.51
2:C8:420:GLU:O	2:C8:420:GLU:HG3	2.09	0.51
3:D3:117:LEU:HD11	3:D3:154:LYS:HD3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E0:167:LEU:HD13	2:E0:252:VAL:HG13	1.93	0.51
2:E8:137:MET:HE3	2:E8:154:LEU:HD12	1.92	0.51
3:E9:169:VAL:HG12	3:E9:202:ILE:HB	1.92	0.51
4:d:78:ALA:HB3	4:d:112:PHE:HE1	1.74	0.51
4:h:158:THR:HB	4:h:161:TYR:HB2	1.92	0.51
3:A1:107:THR:HG21	3:A1:401:GLU:HG2	1.93	0.51
2:A2:292:THR:HG21	2:A2:331:ALA:HB1	1.92	0.51
2:A8:280:LYS:O	2:A8:284:GLU:HG2	2.11	0.51
3:A9:283:ALA:HA	3:B3:55:THR:HG22	1.92	0.51
2:B6:76:ASP:HA	2:B6:79:ARG:HD2	1.93	0.51
3:B9:10:GLY:HA2	3:B9:143:THR:HG23	1.93	0.51
3:C3:149:THR:O	3:C3:191:GLN:NE2	2.44	0.51
2:C4:274:PRO:HG2	2:C4:371:VAL:HG11	1.92	0.51
3:D1:14:ASN:ND2	3:D1:67:ASP:OD1	2.43	0.51
3:D9:107:THR:OG1	3:D9:108:GLU:OE1	2.29	0.51
3:E1:208:TYR:CE2	2:E2:329:ASN:ND2	2.78	0.51
2:E2:397:LEU:O	2:E2:397:LEU:HD23	2.10	0.51
2:E4:261:PRO:HG3	2:E4:313:MET:HE2	1.92	0.51
3:E5:68:LEU:HA	3:E5:93:GLY:HA3	1.91	0.51
4:f:10:LEU:HG	4:f:143:ILE:HG22	1.93	0.51
4:n:106:GLN:HG3	4:p:6:PHE:CZ	2.46	0.51
2:A0:245:ASP:O	2:A0:358:GLN:NE2	2.30	0.51
2:A6:221:ARG:HG2	3:A7:322:SER:OG	2.11	0.51
2:A8:306:ASP:HB3	2:A8:309:HIS:CE1	2.46	0.51
3:B9:334:GLN:HE21	3:B9:349:MET:HG2	1.74	0.51
2:C6:195:LEU:HD21	2:C6:264:ARG:HD3	1.92	0.51
3:D1:281:TYR:CE1	3:D5:58:ARG:CZ	2.93	0.51
2:D2:134:GLY:HA2	2:D2:164:LYS:HE2	1.93	0.51
3:D3:15:GLN:O	3:D3:226:ASN:ND2	2.44	0.51
2:D6:298:PRO:HB3	2:D6:307:PRO:HD2	1.93	0.51
2:E2:79:ARG:NH1	2:E2:92:LEU:O	2.43	0.51
2:E8:395:PHE:HZ	2:E8:418:PHE:HB3	1.75	0.51
4:f:9:PRO:HA	4:f:12:VAL:HG22	1.92	0.51
4:k:130:PRO:HB3	4:m:159:TYR:CD2	2.46	0.51
4:s:64:PRO:HD2	4:s:67:HIS:CD2	2.46	0.51
1:9:241:PHE:CD2	3:C3:43:GLN:NE2	2.78	0.51
2:C6:79:ARG:NH1	2:C6:92:LEU:O	2.43	0.51
2:C6:399:TYR:OH	2:C6:415:GLU:OE2	2.29	0.51
3:C7:407:GLU:HA	3:C7:410:GLU:HB3	1.93	0.51
3:D3:293:MET:SD	3:D3:365:VAL:HG11	2.51	0.51
3:E7:389:PHE:CE1	3:E7:395:LEU:HD11	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F0:137:MET:O	2:F0:168:ASN:ND2	2.42	0.51
2:F0:152:LEU:HD11	2:F0:156:ARG:HH11	1.76	0.51
2:F0:223:THR:CG2	2:F0:225:THR:HG22	2.40	0.51
4:h:111:ILE:HD13	4:h:132:LEU:HB2	1.92	0.51
4:s:130:PRO:CB	4:u:7:ALA:HB1	2.41	0.51
4:t:79:ASP:OD2	4:t:152:LYS:NZ	2.37	0.51
4:x:130:PRO:HB2	4:y:7:ALA:HB1	1.92	0.51
1:10:257:PRO:CD	2:C8:26:LEU:HD22	2.34	0.51
3:B3:210:ILE:O	3:B3:214:THR:OG1	2.27	0.51
3:C3:172:SER:OG	3:C3:205:GLU:OE2	2.29	0.51
3:D1:130:LEU:O	3:D1:162:ARG:HD2	2.11	0.51
3:D3:21:TRP:HA	3:D3:24:ILE:HG22	1.93	0.51
3:E1:12:CYS:HB3	3:E1:138:SER:HB2	1.92	0.51
2:E2:223:THR:HG23	2:E2:225:THR:HG22	1.92	0.51
2:E4:105:ARG:NH1	3:E5:251:ARG:HD3	2.26	0.51
3:F1:19:LYS:NZ	3:F1:223:GLY:O	2.44	0.51
3:A1:117:LEU:HD13	3:A1:154:LYS:HZ2	1.76	0.50
2:B4:50:ASN:O	2:B4:64:ARG:NH2	2.45	0.50
3:B9:7:VAL:HB	3:B9:135:ILE:HG13	1.94	0.50
3:D7:324:LYS:O	3:D7:328:GLU:N	2.31	0.50
2:D8:265:ILE:HG22	2:D8:380:ASN:HD21	1.75	0.50
3:E1:176:SER:CB	2:E2:351:PHE:H	2.23	0.50
3:E3:316:MET:HE1	3:E3:368:VAL:HG22	1.93	0.50
3:E5:394:PHE:CE1	2:E6:261:PRO:HB3	2.46	0.50
2:E8:84:ARG:NH1	5:w:155:GLN:HG2	2.26	0.50
3:E9:329:GLN:HA	3:E9:332:ASN:HB3	1.93	0.50
4:a:77:PHE:HE2	4:a:171:ILE:HD11	1.76	0.50
4:m:100:ASN:ND2	4:o:6:PHE:CZ	2.79	0.50
4:q:106:GLN:NE2	4:q:109:GLU:OE1	2.44	0.50
4:v:5:VAL:O	4:v:11:ASN:ND2	2.44	0.50
4:x:146:ARG:HH11	4:x:146:ARG:HG3	1.76	0.50
3:A7:282:ARG:O	3:B1:55:THR:HG22	2.08	0.50
3:A9:207:LEU:HB3	3:A9:225:LEU:HD22	1.92	0.50
3:B1:16:ILE:HG22	3:B1:226:ASN:OD1	2.11	0.50
3:B9:313:ALA:HB3	3:B9:349:MET:HE1	1.92	0.50
2:C0:356:ASN:OD1	2:C0:357:TYR:N	2.44	0.50
2:D0:229:ARG:HG3	2:D0:229:ARG:NH1	2.24	0.50
3:D3:139:LEU:HG	3:D3:168:SER:HB2	1.93	0.50
2:D4:97:GLU:OE2	3:D5:131:GLN:HG2	2.11	0.50
3:D5:128:ASP:OD1	3:D5:129:CYS:N	2.44	0.50
3:D5:200:GLN:HB3	3:D5:268:ILE:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D6:265:ILE:HG22	2:D6:380:ASN:HD21	1.74	0.50
3:D7:249:ASP:OD1	3:D7:250:LEU:N	2.43	0.50
2:D8:53:PHE:O	2:D8:64:ARG:NH2	2.44	0.50
3:D9:283:ALA:HA	3:E3:55:THR:CB	2.41	0.50
2:E4:210:TYR:CE1	2:E4:227:LEU:HD21	2.46	0.50
4:c:18:ASN:ND2	4:c:46:ASP:OD1	2.35	0.50
4:e:105:ASN:ND2	4:g:37:GLN:NE2	2.60	0.50
4:m:9:PRO:HA	4:m:12:VAL:HG22	1.94	0.50
4:o:78:ALA:HB3	4:o:112:PHE:HE1	1.76	0.50
4:y:65:GLN:HE21	4:y:206:PHE:HZ	1.58	0.50
1:6:257:PRO:HD3	2:B6:26:LEU:CD1	2.41	0.50
3:B7:313:ALA:HB3	3:B7:349:MET:HE2	1.92	0.50
2:B8:256:GLN:O	2:B8:260:VAL:HG22	2.12	0.50
2:C8:174:SER:OG	2:C8:177:VAL:O	2.25	0.50
4:i:105:ASN:HB2	4:k:39:PRO:HG2	1.92	0.50
4:p:18:ASN:ND2	4:p:46:ASP:H	2.08	0.50
3:A3:8:GLN:HE22	3:A3:17:GLY:HA3	1.76	0.50
3:A9:313:ALA:HB3	3:A9:349:MET:HG2	1.94	0.50
3:B7:178:THR:HA	2:B8:258:ASN:HD21	1.76	0.50
3:C1:274:THR:OG1	3:C1:282:ARG:NE	2.41	0.50
2:C2:103:PHE:H	2:C2:408:TYR:HE1	1.59	0.50
3:C3:337:ASN:HB3	3:C3:340:TYR:HB2	1.94	0.50
2:D8:174:SER:HB2	2:D8:177:VAL:O	2.11	0.50
3:E1:208:TYR:HE2	2:E2:329:ASN:ND2	2.09	0.50
2:E2:73:THR:HA	3:E3:46:ARG:HH12	1.75	0.50
3:E3:49:VAL:HG21	3:E3:241:ARG:HG2	1.94	0.50
3:E3:100:ASN:HB3	3:E3:103:LYS:HG2	1.93	0.50
2:E4:276:ILE:HG23	2:E4:281:ALA:HB2	1.93	0.50
3:E5:261:PRO:O	3:E5:264:HIS:ND1	2.42	0.50
2:E8:107:HIS:NE2	2:E8:151:CYS:SG	2.81	0.50
2:E8:268:MET:N	2:E8:268:MET:SD	2.85	0.50
2:F0:239:THR:OG1	2:F0:243:ARG:NH1	2.43	0.50
3:F1:320:ARG:NH1	3:F1:320:ARG:HB2	2.26	0.50
3:F1:375:GLN:HE21	3:F1:379:LYS:HD3	1.75	0.50
4:c:14:LYS:HD2	4:c:47:LEU:HD22	1.93	0.50
4:r:142:GLU:O	4:r:146:ARG:HG2	2.12	0.50
1:20:251:TYR:O	2:E8:82:THR:HG21	2.12	0.50
1:9:246:CYS:HB3	3:C3:245:GLN:HE21	1.76	0.50
2:A2:210:TYR:HB3	3:A3:324:LYS:HE2	1.93	0.50
3:A3:383:ASP:HA	3:A3:386:THR:HG22	1.93	0.50
3:A3:398:TYR:HB3	3:A3:403:MET:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B2:8:HIS:CE1	2:B2:17:GLY:HA3	2.47	0.50
2:B4:156:ARG:HA	2:B4:159:VAL:HG12	1.93	0.50
3:C1:215:LEU:HD21	3:C1:273:LEU:HD22	1.93	0.50
3:C1:267:LEU:HD23	3:C1:299:MET:HE3	1.94	0.50
3:C5:140:GLY:O	3:C5:184:ASN:ND2	2.41	0.50
3:D1:140:GLY:O	3:D1:184:ASN:ND2	2.43	0.50
3:D1:238:CYS:SG	3:D1:318:ARG:NE	2.84	0.50
3:E7:289:LEU:HD12	3:E7:365:VAL:HG12	1.93	0.50
2:F0:8:HIS:CD2	2:F0:17:GLY:HA3	2.45	0.50
4:k:65:GLN:HE21	4:k:206:PHE:HZ	1.60	0.50
4:t:96:TYR:CE2	4:v:6:PHE:CE2	2.99	0.50
4:v:94:ASN:C	4:v:94:ASN:HD22	2.20	0.50
1:6:241:PHE:HE2	3:B7:42:LEU:HD12	1.76	0.50
3:A3:297:LYS:NZ	3:A3:306:ARG:HH22	2.10	0.50
3:A5:117:LEU:HA	3:A5:120:VAL:HG12	1.93	0.50
2:A6:191:THR:HA	2:A6:194:LEU:HB3	1.94	0.50
2:B6:195:LEU:HD21	2:B6:264:ARG:HE	1.77	0.50
3:B7:281:TYR:HD2	3:C1:87:PRO:HD2	1.77	0.50
2:C4:206:ASN:HA	2:C4:209:ILE:HG22	1.92	0.50
2:D4:107:HIS:NE2	2:D4:151:CYS:SG	2.78	0.50
3:D5:239:CYS:SG	3:D5:247:ASN:HB3	2.52	0.50
3:F1:65:LEU:CD2	3:F1:76:VAL:HG21	2.41	0.50
4:d:71:LYS:HG2	4:f:39:PRO:HG3	1.92	0.50
4:d:126:ARG:NH1	4:d:133:SER:OG	2.45	0.50
4:f:14:LYS:HD3	4:f:47:LEU:HB2	1.94	0.50
4:j:128:HIS:O	4:l:159:TYR:HD1	1.94	0.50
4:v:78:ALA:HB3	4:v:112:PHE:HE1	1.76	0.50
1:8:257:PRO:HG2	2:C0:29:GLY:HA2	1.93	0.50
3:A3:205:GLU:HA	3:A3:208:TYR:HD2	1.77	0.50
2:C2:76:ASP:HA	2:C2:79:ARG:HD2	1.94	0.50
2:C2:186:ASN:OD1	2:C2:408:TYR:OH	2.29	0.50
2:C2:338:LYS:NZ	2:C2:340:THR:OG1	2.41	0.50
3:C5:207:LEU:HG	3:C5:228:LEU:HD11	1.92	0.50
3:C9:86:ARG:HG2	3:C9:88:ASP:HB3	1.92	0.50
2:E2:262:TYR:HD2	2:E2:265:ILE:HD12	1.77	0.50
2:E4:73:THR:HB	3:E5:2:ARG:HH12	1.76	0.50
3:E9:244:GLY:HA2	3:E9:355:ASP:HB2	1.94	0.50
4:s:15:ARG:O	4:s:19:GLU:HG3	2.12	0.50
3:A1:172:SER:OG	3:A1:175:VAL:O	2.29	0.50
3:A7:173:PRO:HB3	3:A7:380:ARG:HD2	1.93	0.50
2:B0:102:ASN:HB3	2:B0:105:ARG:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B0:115:VAL:HG12	2:B0:119:LEU:HD23	1.93	0.50
3:B1:153:SER:HA	3:B1:195:ASN:HD22	1.75	0.50
2:C2:107:HIS:NE2	2:C2:151:CYS:SG	2.59	0.50
3:C3:69:GLU:HG2	3:C3:71:GLY:H	1.76	0.50
3:C7:239:CYS:HB3	3:C7:248:SER:O	2.11	0.50
2:D4:178:SER:H	3:D5:347:ASN:ND2	2.08	0.50
3:D9:132:GLY:HA3	3:D9:163:ILE:HG22	1.93	0.50
3:D9:200:GLN:HB3	3:D9:268:ILE:HD11	1.93	0.50
2:E0:98:ASP:OD1	2:E0:99:ALA:N	2.45	0.50
2:E0:178:SER:HB3	2:E0:183:GLU:HG2	1.92	0.50
2:E0:181:VAL:HG12	3:E1:256:ASN:HA	1.93	0.50
2:E0:192:HIS:NE2	2:E0:420:GLU:OE2	2.44	0.50
3:E7:128:ASP:OD1	3:E7:129:CYS:N	2.41	0.50
3:E7:234:SER:O	3:E7:241:ARG:NH2	2.44	0.50
3:E7:256:ASN:HB3	3:E7:350:LYS:HE2	1.94	0.50
2:E8:214:ARG:HH22	2:E8:220:GLU:HG2	1.77	0.50
2:F0:60:LYS:O	2:F0:61:HIS:ND1	2.45	0.50
2:F0:213:CYS:HA	2:F0:217:LEU:HB2	1.93	0.50
2:F0:254:GLU:OE1	2:F0:352:LYS:NZ	2.41	0.50
4:e:117:ARG:HH11	4:e:117:ARG:HG2	1.75	0.50
4:h:72:SER:HG	4:h:199:TRP:HE1	1.60	0.50
4:l:15:ARG:HG2	4:l:45:MET:HE1	1.93	0.50
4:o:18:ASN:ND2	4:o:46:ASP:OD1	2.44	0.50
4:t:185:ILE:HD13	4:t:195:ALA:HB3	1.93	0.50
2:A8:36:MET:SD	2:A8:61:HIS:NE2	2.75	0.50
3:B5:330:MET:HE1	3:B5:349:MET:HE3	1.93	0.50
3:C5:91:VAL:HB	3:C5:112:LEU:HD11	1.93	0.50
3:C7:257:LEU:HD21	3:C7:314:SER:HB2	1.94	0.50
2:D2:298:PRO:HB3	2:D2:307:PRO:HD2	1.94	0.50
2:D2:302:MET:O	2:D2:302:MET:HG2	2.11	0.50
3:D3:128:ASP:N	3:D3:128:ASP:OD1	2.42	0.50
2:D6:172:TRP:HZ2	2:D6:391:MET:HE1	1.77	0.50
2:D6:221:ARG:HB3	3:D7:322:SER:HB3	1.94	0.50
3:D7:282:ARG:NH1	3:D7:288:GLU:OE2	2.45	0.50
2:E8:151:CYS:SG	2:E8:193:SER:OG	2.55	0.50
4:g:149:ARG:HD3	4:g:161:TYR:HD2	1.77	0.50
4:i:104:ALA:O	4:k:42:TYR:CD2	2.65	0.50
4:t:71:LYS:HD2	4:v:39:PRO:HB3	1.93	0.50
4:t:106:GLN:NE2	4:v:6:PHE:CZ	2.66	0.50
4:v:130:PRO:CB	4:x:7:ALA:CB	2.90	0.50
4:y:71:LYS:HE3	4:y:106:GLN:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A6:214:ARG:HD3	3:A7:324:LYS:NZ	2.27	0.49
2:B0:76:ASP:HA	2:B0:79:ARG:HG2	1.94	0.49
3:B3:187:LEU:HD21	3:B3:403:MET:HE1	1.94	0.49
3:B7:139:LEU:HA	3:B7:145:SER:HB3	1.94	0.49
3:B7:175:VAL:HG11	2:B8:332:VAL:HG13	1.94	0.49
2:C4:427:ALA:HA	2:C4:430:LYS:HE3	1.94	0.49
3:C5:350:LYS:NZ	3:C5:352:SER:OG	2.42	0.49
2:C6:198:THR:O	2:C6:266:HIS:NE2	2.45	0.49
3:E3:238:CYS:SG	3:E3:318:ARG:NE	2.85	0.49
3:E7:173:PRO:HB2	3:E7:174:LYS:HG2	1.94	0.49
4:s:10:LEU:HD12	4:s:147:HIS:CD2	2.47	0.49
4:s:78:ALA:HB3	4:s:112:PHE:HE1	1.75	0.49
4:t:78:ALA:HB3	4:t:112:PHE:HE1	1.76	0.49
1:0:247:TYR:CZ	2:A4:81:GLY:HA2	2.44	0.49
2:A8:30:ILE:HG22	2:A8:36:MET:HB3	1.93	0.49
2:A8:151:CYS:SG	2:A8:193:SER:OG	2.61	0.49
3:A9:406:MET:HE3	3:A9:406:MET:HA	1.92	0.49
3:B3:68:LEU:HD23	3:B3:112:LEU:HD22	1.94	0.49
2:B4:392:ASP:OD1	2:B4:422:ARG:NE	2.45	0.49
2:B6:217:LEU:HD11	2:B6:275:ILE:HG22	1.93	0.49
3:C1:113:ILE:HA	3:C1:116:VAL:HG12	1.93	0.49
2:C4:12:ALA:CB	2:C4:140:ALA:HB2	2.39	0.49
2:C6:251:ASP:N	2:C6:254:GLU:OE2	2.42	0.49
2:D4:182:VAL:HG11	3:D5:255:VAL:HG12	1.94	0.49
2:E0:5:ILE:HD12	2:E0:132:LEU:HD11	1.94	0.49
3:E1:249:ASP:OD1	3:E1:252:LYS:HG2	2.12	0.49
2:E2:274:PRO:HB2	2:E2:276:ILE:HG12	1.94	0.49
3:E3:2:ARG:HB2	3:E3:131:GLN:HB2	1.93	0.49
2:E8:301:MET:HE1	2:E8:307:PRO:HG3	1.95	0.49
2:F0:65:CYS:SG	2:F0:66:VAL:N	2.85	0.49
2:F0:209:ILE:HB	2:F0:227:LEU:HD13	1.94	0.49
3:F1:293:MET:HE3	3:F1:367:PHE:HB2	1.94	0.49
2:A2:96:LYS:HG3	3:A3:129:CYS:SG	2.52	0.49
2:B4:158:SER:OG	2:B4:166:LYS:NZ	2.45	0.49
3:B5:10:GLY:HA2	3:B5:143:THR:HG23	1.95	0.49
3:B7:311:LEU:HD12	3:B7:342:VAL:HG11	1.93	0.49
2:C0:53:PHE:O	2:C0:64:ARG:NH2	2.45	0.49
3:D5:107:THR:OG1	3:D5:108:GLU:N	2.44	0.49
3:D9:6:HIS:CE1	3:D9:8:GLN:HG2	2.47	0.49
2:E4:174:SER:OG	2:E4:177:VAL:O	2.24	0.49
2:E6:65:CYS:SG	2:E6:66:VAL:N	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E9:267:LEU:HB3	3:E9:299:MET:SD	2.53	0.49
2:F0:28:HIS:NE2	2:F0:243:ARG:HD2	2.28	0.49
3:F1:117:LEU:HB3	3:F1:121:ARG:HH22	1.77	0.49
4:s:66:SER:HB3	4:u:23:LEU:HD13	1.93	0.49
4:x:63:ILE:HG21	4:y:16:ARG:HG3	1.95	0.49
1:16:254:LYS:HB2	2:E0:26:LEU:HD11	1.94	0.49
1:21:254:LYS:CD	2:F0:364:PRO:HD2	2.37	0.49
1:21:256:LEU:CD1	2:F0:31:GLN:HG3	2.36	0.49
1:8:257:PRO:HG3	2:C0:26:LEU:HD23	1.94	0.49
2:B6:73:THR:CG2	3:B7:46:ARG:NH1	2.74	0.49
2:B8:208:ALA:HB2	2:B8:304:LYS:HB2	1.93	0.49
3:D7:324:LYS:O	3:D7:327:ASP:N	2.38	0.49
3:E9:221:THR:HA	2:F0:325:PRO:HD3	1.94	0.49
4:e:170:VAL:HG23	4:e:183:LEU:HB2	1.94	0.49
3:A5:205:GLU:CD	2:A6:329:ASN:HD21	2.20	0.49
3:A9:281:TYR:O	3:B3:54:ALA:HB1	2.13	0.49
2:B2:174:SER:HB2	2:B2:207:GLU:HG2	1.92	0.49
3:B3:12:CYS:HB3	3:B3:138:SER:OG	2.11	0.49
3:B5:282:ARG:NH2	3:B5:292:GLN:OE1	2.46	0.49
2:B6:213:CYS:HA	2:B6:217:LEU:HD13	1.93	0.49
3:B9:280:GLN:HG3	3:B9:280:GLN:O	2.11	0.49
3:C1:20:PHE:HD2	3:C1:233:MET:HE3	1.78	0.49
2:C4:401:LYS:NZ	3:C5:425:TYR:HE1	2.10	0.49
2:D6:50:ASN:O	2:D6:64:ARG:NH2	2.43	0.49
2:D8:298:PRO:HB3	2:D8:307:PRO:HD2	1.94	0.49
3:E1:174:LYS:O	2:E2:336:LYS:HE3	2.13	0.49
3:E3:290:THR:HA	3:E3:293:MET:HE2	1.94	0.49
4:i:69:LYS:HB2	4:k:23:LEU:HD21	1.93	0.49
4:i:78:ALA:HB3	4:i:112:PHE:HE1	1.78	0.49
4:i:176:ASP:OD2	4:i:178:ARG:NH1	2.45	0.49
4:p:74:ALA:HB2	4:p:172:VAL:HG12	1.94	0.49
4:p:170:VAL:HG22	4:p:185:ILE:HD11	1.94	0.49
4:s:9:PRO:HA	4:s:12:VAL:HG22	1.93	0.49
4:x:59:ASN:OD1	4:y:9:PRO:HB3	2.13	0.49
4:y:57:ASN:HB3	4:y:132:LEU:CD2	2.43	0.49
1:6:239:LEU:HD13	1:6:240:PRO:HD2	1.94	0.49
2:A0:103:PHE:HD2	2:A0:189:LEU:HD23	1.77	0.49
3:A1:391:ARG:O	2:A2:262:TYR:OH	2.24	0.49
2:A4:250:VAL:HG23	2:A4:255:PHE:HE1	1.78	0.49
2:B4:286:LEU:O	2:B4:373:ARG:NH1	2.40	0.49
3:B5:181:GLU:HB2	3:B5:182:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C3:306:ARG:HG2	3:C3:340:TYR:CE1	2.48	0.49
3:C7:295:ASP:HB3	3:C7:298:ASN:HB2	1.95	0.49
2:D2:33:ASP:OD1	2:D2:34:GLY:N	2.46	0.49
3:D3:64:ILE:HD11	3:D3:123:GLU:HG3	1.93	0.49
3:D7:91:VAL:HG11	3:D7:116:VAL:HB	1.94	0.49
2:E0:71:GLU:CD	3:E1:2:ARG:NH2	2.70	0.49
2:E0:276:ILE:HG23	2:E0:280:LYS:HB2	1.92	0.49
2:E2:251:ASP:OD1	2:E2:254:GLU:HG2	2.13	0.49
3:E5:260:PHE:HB3	3:E5:261:PRO:HD2	1.95	0.49
3:E9:209:ASP:OD1	3:E9:213:ARG:NH1	2.46	0.49
4:e:106:GLN:O	4:e:39:PRO:HG3	2.13	0.49
4:d:53:GLY:HA2	4:d:62:VAL:HG21	1.95	0.49
4:i:71:LYS:NZ	4:i:106:GLN:HB2	2.26	0.49
4:k:146:ARG:HH11	4:k:146:ARG:HG3	1.78	0.49
4:m:78:ALA:HB3	4:m:112:PHE:HE1	1.78	0.49
4:o:9:PRO:HA	4:o:12:VAL:HG12	1.95	0.49
3:B5:156:ARG:HD3	3:B5:164:MET:HG2	1.94	0.49
3:B9:170:PHE:HE2	3:B9:378:PHE:HE1	1.61	0.49
2:C6:177:VAL:HB	2:C6:207:GLU:HB3	1.94	0.49
2:C6:282:TYR:HE2	4:n:201:TRP:HZ2	1.59	0.49
2:C8:98:ASP:O	2:C8:105:ARG:NH2	2.45	0.49
2:D0:50:ASN:O	2:D0:64:ARG:NH2	2.35	0.49
3:D1:206:ALA:HB2	3:D1:302:ALA:HB2	1.94	0.49
3:D3:165:GLU:OE2	3:D3:200:GLN:NE2	2.45	0.49
2:D4:8:HIS:HD2	2:D4:67:PHE:CE1	2.31	0.49
2:E4:271:SER:HB2	2:E4:377:MET:HB3	1.95	0.49
4:f:106:GLN:CG	4:h:6:PHE:HZ	2.25	0.49
4:j:71:LYS:NZ	4:j:106:GLN:HB2	2.27	0.49
4:r:154:TYR:CE1	4:r:158:THR:HG22	2.31	0.49
4:t:71:LYS:HG3	4:v:39:PRO:HG3	1.93	0.49
4:t:181:GLN:HE22	4:t:200:ASP:H	1.58	0.49
5:w:38:PHE:HE1	5:w:106:ILE:HD13	1.77	0.49
3:A3:309:ARG:NE	3:A3:339:SER:O	2.46	0.49
2:A6:112:LYS:HA	2:A6:115:VAL:HG12	1.95	0.49
2:A6:306:ASP:HB3	2:A6:309:HIS:CE1	2.47	0.49
3:B5:63:ALA:O	3:B5:89:ASN:ND2	2.45	0.49
2:B6:213:CYS:SG	2:B6:222:PRO:HG3	2.53	0.49
2:C6:51:THR:HG23	2:C6:52:PHE:HD1	1.76	0.49
2:C6:181:VAL:HG23	3:C7:256:ASN:OD1	2.12	0.49
3:C9:334:GLN:HE22	3:C9:348:ASN:N	2.10	0.49
3:D5:54:ALA:HB3	3:D5:58:ARG:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D7:176:SER:HB3	3:D7:181:GLU:OE1	2.13	0.49
3:E1:3:GLU:HA	3:E1:49:VAL:HA	1.94	0.49
2:E2:406:HIS:HA	2:E2:409:VAL:HG12	1.94	0.49
2:E4:403:ALA:HA	3:E5:260:PHE:CD1	2.40	0.49
4:e:75:LEU:O	4:e:170:VAL:HA	2.13	0.49
4:e:139:PRO:O	4:e:143:ILE:HG12	2.13	0.49
4:f:73:VAL:HG12	4:f:109:GLU:HB3	1.95	0.49
4:g:89:LEU:HB3	4:g:90:PRO:HD3	1.94	0.49
4:h:103:GLY:HA3	4:h:107:LYS:HZ1	1.78	0.49
4:k:75:LEU:HG	4:k:173:ILE:HD13	1.95	0.49
4:o:170:VAL:HG23	4:o:183:LEU:HB2	1.95	0.49
2:A2:284:GLU:HG2	2:A2:286:LEU:HD22	1.94	0.49
2:A6:77:GLU:OE2	3:A7:243:PRO:HB3	2.12	0.49
3:C7:66:MET:HB3	3:C7:91:VAL:HG23	1.95	0.49
2:E2:319:TYR:CD1	2:E2:375:VAL:HG22	2.48	0.49
4:g:72:SER:HB3	4:g:108:ILE:HG22	1.94	0.49
4:n:106:GLN:HG3	4:p:6:PHE:HZ	1.77	0.49
4:n:130:PRO:HG3	4:p:159:TYR:HB3	1.95	0.49
4:t:66:SER:HB3	4:v:23:LEU:CD1	2.42	0.49
1:16:247:TYR:HE2	2:E0:81:GLY:CA	2.26	0.49
1:3:254:LYS:HB3	1:3:255:PRO:HD2	1.95	0.49
1:6:257:PRO:HD3	2:B6:26:LEU:HD12	1.95	0.49
3:B9:274:THR:HG21	3:B9:279:GLN:HA	1.94	0.49
2:C2:105:ARG:HH21	2:C2:110:ILE:HG21	1.77	0.49
3:C3:113:ILE:HA	3:C3:116:VAL:HG12	1.95	0.49
3:C5:329:GLN:OE1	3:C5:332:ASN:ND2	2.38	0.49
3:D3:44:LEU:O	3:D3:44:LEU:HD23	2.13	0.49
2:D8:50:ASN:O	2:D8:64:ARG:NH2	2.46	0.49
2:E2:65:CYS:SG	2:E2:66:VAL:N	2.85	0.49
3:E3:213:ARG:NH2	3:E3:216:LYS:HE3	2.28	0.49
4:c:97:ARG:HG3	4:e:161:TYR:CE1	2.48	0.49
4:k:66:SER:O	4:m:23:LEU:HD11	2.13	0.49
4:l:25:GLN:HE22	4:l:36:ILE:HG21	1.78	0.49
4:m:14:LYS:HE2	4:m:45:MET:HB3	1.95	0.49
4:m:18:ASN:HB2	4:m:45:MET:HG3	1.93	0.49
4:v:158:THR:OG1	4:v:161:TYR:HB2	2.13	0.49
4:x:100:ASN:HD21	4:y:6:PHE:HE1	1.56	0.49
1:21:256:LEU:HD12	2:F0:37:PRO:HD3	1.95	0.48
2:A2:103:PHE:H	2:A2:408:TYR:HE1	1.61	0.48
3:A3:304:ASP:CG	3:A3:307:HIS:HD1	2.21	0.48
3:A7:139:LEU:HG	3:A7:168:SER:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A8:88:HIS:NE2	2:A8:90:GLU:OE1	2.46	0.48
2:B0:2:ARG:HB2	2:B0:133:GLN:NE2	2.28	0.48
2:B0:254:GLU:O	2:B0:258:ASN:ND2	2.43	0.48
2:B6:33:ASP:O	2:B6:60:LYS:NZ	2.46	0.48
3:B7:276:ARG:NE	3:B7:276:ARG:HA	2.28	0.48
3:B7:396:HIS:CE1	2:B8:263:PRO:HD3	2.48	0.48
2:B8:288:VAL:HA	2:B8:291:ILE:HG12	1.94	0.48
2:D2:98:ASP:OD1	2:D2:99:ALA:N	2.45	0.48
3:D5:114:ASP:OD1	3:D5:114:ASP:N	2.45	0.48
2:E0:5:ILE:CD1	2:E0:132:LEU:HD11	2.43	0.48
2:E0:176:GLN:CD	3:E1:331:LEU:HD11	2.38	0.48
2:E4:69:ASP:OD1	2:E4:70:LEU:N	2.45	0.48
2:E4:132:LEU:HG	2:E4:164:LYS:NZ	2.28	0.48
3:E5:182:PRO:O	3:E5:186:THR:OG1	2.28	0.48
4:j:106:GLN:CD	4:l:42:TYR:CE1	2.84	0.48
4:l:10:LEU:HG	4:l:143:ILE:HG22	1.95	0.48
4:t:100:ASN:ND2	4:v:6:PHE:CE1	2.81	0.48
2:A8:259:LEU:HD11	2:A8:316:CYS:HB2	1.95	0.48
3:B3:257:LEU:HD21	3:B3:314:SER:HB2	1.95	0.48
3:B9:354:CYS:SG	3:B9:355:ASP:N	2.86	0.48
3:B9:358:PRO:HG2	3:B9:361:LEU:HD12	1.94	0.48
3:C1:220:PRO:HD2	2:C2:326:LYS:CB	2.43	0.48
2:D4:12:ALA:CB	2:D4:140:ALA:HB2	2.43	0.48
3:E1:163:ILE:HD12	3:E1:250:LEU:HB2	1.95	0.48
3:E1:164:MET:HB3	3:E1:197:ASP:H	1.77	0.48
2:E4:217:LEU:HD21	2:E4:367:ASP:OD2	2.13	0.48
3:E5:100:ASN:HB3	3:E5:103:LYS:HG2	1.94	0.48
2:E6:276:ILE:HG13	2:E6:280:LYS:HB2	1.94	0.48
3:F1:128:ASP:OD1	3:F1:129:CYS:N	2.45	0.48
4:f:105:ASN:OD1	4:h:39:PRO:HG2	2.13	0.48
3:A1:398:TYR:HB3	3:A1:403:MET:HG3	1.95	0.48
2:A6:394:LYS:HG2	3:A7:346:PRO:HG3	1.94	0.48
2:A8:183:GLU:HB2	2:A8:184:PRO:HD3	1.95	0.48
3:B1:107:THR:OG1	3:B1:108:GLU:OE1	2.31	0.48
3:B3:117:LEU:HA	3:B3:120:VAL:HG12	1.95	0.48
3:B5:57:GLY:CA	4:f:83:PRO:CB	2.70	0.48
3:D1:99:ASN:ND2	3:D1:141:GLY:HA2	2.27	0.48
3:D7:66:MET:HE2	3:D7:116:VAL:HG21	1.94	0.48
3:D9:139:LEU:HD12	3:D9:170:PHE:CE1	2.48	0.48
3:E5:94:GLN:HA	2:E6:2:ARG:HH22	1.77	0.48
2:E6:221:ARG:HB3	3:E7:322:SER:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:l:96:TYR:CE2	4:n:6:PHE:CZ	3.00	0.48
4:l:99:MET:HE2	4:l:108:ILE:HG23	1.96	0.48
3:A1:141:GLY:O	3:A1:184:ASN:ND2	2.39	0.48
2:A2:96:LYS:HB3	3:A3:129:CYS:SG	2.53	0.48
2:A4:221:ARG:CZ	4:c:189:LEU:O	2.57	0.48
2:A4:285:GLN:HB2	2:A8:57:GLY:N	2.28	0.48
3:A7:11:GLN:HA	3:A7:72:THR:HG21	1.96	0.48
2:A8:298:PRO:HG2	2:A8:308:ARG:HH21	1.79	0.48
2:B0:135:PHE:HD2	2:B0:166:LYS:HG2	1.78	0.48
3:B5:73:MET:HA	3:B5:76:VAL:HG12	1.96	0.48
2:C4:417:GLU:HA	2:C4:420:GLU:HG3	1.95	0.48
3:C5:220:PRO:HB2	3:C5:225:LEU:CD2	2.43	0.48
3:C5:262:ARG:O	3:C5:264:HIS:ND1	2.46	0.48
2:D0:204:LEU:HD13	2:D0:231:ILE:HD12	1.95	0.48
3:E1:380:ARG:O	3:E1:384:GLN:HG3	2.13	0.48
4:o:8:SER:HB2	4:o:147:HIS:HA	1.95	0.48
4:o:165:THR:OG1	4:o:166:GLY:N	2.47	0.48
4:s:96:TYR:CE1	4:u:6:PHE:CD2	3.01	0.48
4:x:63:ILE:HG22	4:y:16:ARG:CD	2.42	0.48
3:A1:105:HIS:CD2	3:A1:150:LEU:HB2	2.49	0.48
3:A3:230:SER:HA	3:A3:233:MET:HB3	1.95	0.48
2:B0:172:TRP:HB3	2:B0:205:ASP:OD1	2.13	0.48
3:B5:313:ALA:HB3	3:B5:349:MET:SD	2.54	0.48
2:B6:27:GLU:OE2	2:B6:320:ARG:NH2	2.47	0.48
3:C1:20:PHE:CD2	3:C1:233:MET:HE3	2.48	0.48
3:C9:286:VAL:N	3:C9:287:PRO:CD	2.77	0.48
3:D5:272:PRO:HG3	3:D5:284:LEU:HD11	1.95	0.48
3:D7:2:ARG:HB2	3:D7:131:GLN:HB2	1.96	0.48
3:D9:6:HIS:HD2	3:D9:134:GLN:HE21	1.60	0.48
3:E3:267:LEU:HD21	3:E3:374:ILE:HG12	1.96	0.48
2:E4:176:GLN:CB	3:E5:331:LEU:CD1	2.90	0.48
2:E8:271:SER:HB3	2:E8:377:MET:HB3	1.95	0.48
4:o:70:GLY:HA3	4:q:39:PRO:HD3	1.95	0.48
4:r:63:ILE:O	4:r:63:ILE:HG13	2.12	0.48
4:s:146:ARG:HG3	4:s:146:ARG:NH1	2.28	0.48
4:t:175:SER:HA	4:t:206:PHE:CE1	2.49	0.48
1:11:244:GLN:H	3:D1:320:ARG:HH22	1.60	0.48
1:18:243:ALA:HB3	3:E5:356:ILE:HD12	1.96	0.48
3:A9:39:ASP:CB	4:c:90:PRO:HG3	2.42	0.48
2:B2:80:THR:HA	2:B2:84:ARG:HE	1.79	0.48
3:B3:239:CYS:SG	3:B3:248:SER:N	2.80	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B4:183:GLU:HG2	2:B4:184:PRO:HD3	1.94	0.48
3:D5:289:LEU:HD13	3:D5:365:VAL:HG23	1.96	0.48
3:D7:77:ARG:HH22	3:D7:92:PHE:HZ	1.60	0.48
2:E2:392:ASP:OD1	2:E2:422:ARG:NH1	2.46	0.48
3:E5:105:HIS:HD2	3:E5:150:LEU:HD22	1.79	0.48
2:F0:122:ILE:HG21	2:F0:157:LEU:HD21	1.94	0.48
4:c:176:ASP:OD1	4:c:176:ASP:N	2.45	0.48
4:d:96:TYR:HA	4:d:108:ILE:HD11	1.95	0.48
4:f:174:GLY:HA3	4:f:178:ARG:NH2	2.28	0.48
4:k:57:ASN:HA	4:k:132:LEU:HD23	1.95	0.48
4:n:56:LYS:NZ	4:n:62:VAL:HG13	2.28	0.48
4:y:10:LEU:HG	4:y:143:ILE:HG22	1.95	0.48
1:2:247:TYR:CE1	2:A8:81:GLY:HA3	2.49	0.48
3:A5:98:GLY:H	3:A5:103:LYS:HD3	1.79	0.48
2:B0:108:TYR:HE2	2:B0:413:MET:HB3	1.78	0.48
3:B5:105:HIS:CE1	3:B5:150:LEU:HD12	2.48	0.48
3:B9:43:GLN:HA	3:B9:242:PHE:HE1	1.79	0.48
3:C1:200:GLN:HB3	3:C1:266:PHE:HB2	1.94	0.48
2:D0:34:GLY:O	2:D0:61:HIS:N	2.42	0.48
2:D2:170:CYS:SG	2:D2:194:LEU:HD11	2.53	0.48
2:D2:174:SER:HB2	2:D2:177:VAL:O	2.13	0.48
2:E0:96:LYS:NZ	3:E1:1:MET:N	2.61	0.48
2:E2:185:TYR:CZ	2:E2:398:MET:HE3	2.49	0.48
2:E8:10:GLY:HA2	2:E8:145:THR:HG23	1.95	0.48
2:E8:70:LEU:HD12	2:E8:99:ALA:HB2	1.94	0.48
2:F0:278:ALA:HA	2:F0:369:ALA:HB2	1.96	0.48
4:i:69:LYS:HD3	4:k:23:LEU:CD2	2.43	0.48
2:A0:73:THR:HB	3:A1:2:ARG:NH2	2.29	0.48
3:B5:128:ASP:N	3:B5:128:ASP:OD1	2.45	0.48
3:B7:287:PRO:HA	3:B7:290:THR:HG22	1.96	0.48
2:B8:265:ILE:HG23	2:B8:432:TYR:HE1	1.79	0.48
3:C5:238:CYS:SG	3:C5:239:CYS:N	2.87	0.48
3:D1:385:PHE:CE2	3:D1:412:GLU:HB3	2.49	0.48
3:D7:324:LYS:HE2	3:D7:324:LYS:HB2	1.53	0.48
2:E2:276:ILE:HG23	2:E2:280:LYS:HB2	1.95	0.48
3:E5:128:ASP:OD1	3:E5:129:CYS:N	2.45	0.48
3:E5:309:ARG:NH1	3:E5:341:PHE:O	2.46	0.48
3:E5:326:VAL:O	3:E5:330:MET:HG2	2.13	0.48
4:k:9:PRO:HA	4:k:12:VAL:HG22	1.96	0.48
4:y:185:ILE:HD13	4:y:195:ALA:HB3	1.96	0.48
1:19:244:GLN:HB2	3:E7:320:ARG:NH1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:240:PRO:CB	4:e:154:TYR:HB3	2.43	0.48
3:A1:207:LEU:HB3	3:A1:225:LEU:HD22	1.95	0.48
2:A4:76:ASP:HA	2:A4:79:ARG:HG2	1.94	0.48
2:A8:179:THR:O	3:A9:350:LYS:CB	2.62	0.48
3:B3:324:LYS:O	3:B3:328:GLU:N	2.46	0.48
3:B5:66:MET:HG3	3:B5:116:VAL:HG21	1.96	0.48
3:B5:97:ALA:HA	3:B5:103:LYS:HE2	1.95	0.48
3:B7:267:LEU:HD13	3:B7:371:SER:HB3	1.96	0.48
2:C0:276:ILE:HG23	2:C0:281:ALA:HB2	1.95	0.48
2:C6:135:PHE:CD2	2:C6:166:LYS:HG2	2.46	0.48
2:C6:158:SER:OG	2:C6:166:LYS:NZ	2.47	0.48
3:D1:180:VAL:O	3:D1:184:ASN:ND2	2.47	0.48
3:D1:293:MET:HE2	3:D1:293:MET:HB3	1.75	0.48
3:D3:289:LEU:HD21	3:D3:365:VAL:HG23	1.95	0.48
2:E6:254:GLU:O	2:E6:258:ASN:ND2	2.47	0.48
3:E7:184:ASN:OD1	3:E7:398:TYR:OH	2.30	0.48
3:E9:176:SER:OG	2:F0:349:THR:OG1	2.10	0.48
4:e:176:ASP:OD1	4:e:176:ASP:N	2.46	0.48
4:q:97:ARG:NH2	4:s:5:VAL:HG12	2.29	0.48
1:9:241:PHE:HZ	3:C3:356:ILE:HG23	1.79	0.48
2:A2:221:ARG:NE	3:A3:325:GLU:OE1	2.47	0.48
3:A5:105:HIS:CE1	3:A5:150:LEU:HD12	2.49	0.48
2:C0:172:TRP:HB2	2:C0:203:MET:HB3	1.95	0.48
2:C8:274:PRO:HB2	2:C8:276:ILE:HG12	1.95	0.48
2:C8:392:ASP:OD1	2:C8:422:ARG:NE	2.43	0.48
2:D4:230:LEU:HD21	2:D4:368:LEU:HD11	1.96	0.48
2:D8:285:GLN:HB2	2:E2:56:THR:HA	1.96	0.48
3:D9:139:LEU:HD12	3:D9:170:PHE:HE1	1.79	0.48
2:F0:367:ASP:OD1	2:F0:367:ASP:N	2.47	0.48
4:d:21:ARG:HH21	4:d:21:ARG:HG2	1.79	0.48
4:l:65:GLN:HE21	4:l:206:PHE:HZ	1.60	0.48
4:s:185:ILE:HD13	4:s:195:ALA:HB3	1.96	0.48
4:t:146:ARG:HD3	4:t:156:VAL:HG21	1.96	0.48
1:19:256:LEU:HA	2:E6:26:LEU:HD23	1.96	0.47
1:19:257:PRO:HD2	2:E6:26:LEU:C	2.37	0.47
2:A2:283:HIS:HA	2:A6:60:LYS:HE2	1.96	0.47
3:A3:130:LEU:H	3:A3:162:ARG:HH21	1.62	0.47
2:A4:210:TYR:HB3	3:A5:324:LYS:HE2	1.96	0.47
2:A4:310:GLY:HA3	2:A4:383:ALA:HB2	1.94	0.47
3:A9:192:LEU:HD21	3:A9:199:VAL:CG2	2.41	0.47
2:B0:82:THR:HG21	4:d:101:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B1:383:ASP:HA	3:B1:386:THR:HG22	1.95	0.47
2:B4:6:SER:OG	2:B4:8:HIS:NE2	2.46	0.47
3:B7:49:VAL:HG11	3:B7:241:ARG:HG2	1.96	0.47
2:C0:36:MET:HB2	2:C0:37:PRO:HD2	1.95	0.47
3:C3:215:LEU:HD21	3:C3:273:LEU:HD22	1.96	0.47
2:C4:174:SER:HB3	2:C4:177:VAL:O	2.14	0.47
3:C7:281:TYR:CD2	3:D1:87:PRO:CD	2.95	0.47
3:C9:117:LEU:HA	3:C9:120:VAL:HG12	1.95	0.47
3:D1:99:ASN:HD21	3:D1:141:GLY:HA2	1.79	0.47
2:D2:180:ALA:HB1	3:D3:256:ASN:ND2	2.26	0.47
3:D5:16:ILE:HD11	3:D5:229:VAL:HG11	1.96	0.47
2:D6:309:HIS:NE2	2:D6:386:GLU:OE1	2.46	0.47
2:D8:241:SER:OG	2:D8:250:VAL:O	2.23	0.47
3:D9:7:VAL:HG11	3:D9:151:LEU:HD21	1.96	0.47
3:E3:317:PHE:HB3	3:E3:321:MET:SD	2.54	0.47
2:E4:256:GLN:HE21	2:E4:256:GLN:H	1.60	0.47
2:E6:176:GLN:HB3	3:E7:331:LEU:CD1	2.44	0.47
2:E8:9:VAL:HG22	2:E8:68:LEU:HB3	1.96	0.47
2:E8:319:TYR:HB3	2:E8:323:VAL:HG11	1.95	0.47
4:r:94:ASN:O	4:r:97:ARG:HB3	2.14	0.47
4:y:79:ASP:OD2	4:y:152:LYS:NZ	2.40	0.47
2:A2:181:VAL:HG13	3:A3:345:ILE:HG21	1.96	0.47
2:A2:204:LEU:CD2	2:A2:231:ILE:HD12	2.44	0.47
2:B4:311:LYS:H	2:B4:382:THR:HG22	1.79	0.47
2:C0:209:ILE:HG22	2:C0:227:LEU:HD22	1.96	0.47
3:C5:196:ALA:O	3:C5:264:HIS:NE2	2.47	0.47
3:C7:192:LEU:HG	3:C7:199:VAL:HG21	1.95	0.47
2:D4:161:TYR:HB3	2:D4:164:LYS:HG3	1.96	0.47
2:D8:324:VAL:HG23	2:D8:327:ASP:H	1.77	0.47
3:E1:64:ILE:HD12	3:E1:119:VAL:HG12	1.95	0.47
3:E3:321:MET:HG2	3:E3:363:MET:SD	2.54	0.47
2:E4:338:LYS:HZ1	2:E4:341:ILE:HG12	1.79	0.47
3:E5:286:VAL:HG13	3:E5:363:MET:SD	2.55	0.47
2:F0:25:CYS:SG	2:F0:86:LEU:HD11	2.53	0.47
4:l:146:ARG:HG3	4:l:146:ARG:NH1	2.29	0.47
4:n:149:ARG:HE	4:n:164:ARG:HB2	1.79	0.47
4:p:70:GLY:HA3	4:r:38:LEU:O	2.15	0.47
2:A0:91:GLN:HA	2:A0:121:ARG:HH12	1.79	0.47
2:A0:179:THR:H	3:A1:347:ASN:ND2	2.12	0.47
2:A2:244:PHE:HD2	2:A2:358:GLN:HG2	1.79	0.47
3:A3:274:THR:HG21	3:A3:282:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5:139:LEU:HG	3:A5:168:SER:HB3	1.96	0.47
2:A8:97:GLU:OE2	3:A9:251:ARG:NE	2.48	0.47
3:A9:391:ARG:CZ	3:A9:391:ARG:HB2	2.44	0.47
2:B2:10:GLY:HA2	2:B2:145:THR:HG23	1.96	0.47
2:B6:339:ARG:NH1	2:B6:342:GLN:OE1	2.46	0.47
2:C0:4:VAL:HG21	2:C0:136:LEU:CD1	2.44	0.47
3:C1:1:MET:N	3:C1:128:ASP:OD2	2.45	0.47
2:C4:79:ARG:NH1	2:C4:92:LEU:O	2.48	0.47
3:C5:133:PHE:HB2	3:C5:164:MET:CB	2.44	0.47
2:C6:216:ASN:HB3	2:C6:275:ILE:O	2.14	0.47
3:D1:203:ASP:OD2	3:D1:302:ALA:N	2.40	0.47
2:D4:397:LEU:HD23	3:D5:346:PRO:HD3	1.96	0.47
3:D9:289:LEU:HD11	3:D9:363:MET:HG2	1.94	0.47
2:E2:1:MET:N	2:E2:3:GLU:OE2	2.44	0.47
2:F0:207:GLU:HA	2:F0:210:TYR:HB2	1.95	0.47
4:g:70:GLY:O	4:i:39:PRO:HD3	2.15	0.47
4:o:106:GLN:HA	4:q:42:TYR:OH	2.14	0.47
4:p:37:GLN:NE2	4:p:41:ASN:OD1	2.47	0.47
4:q:97:ARG:CZ	4:s:5:VAL:HG12	2.44	0.47
4:x:9:PRO:HA	4:x:12:VAL:HG22	1.96	0.47
2:A2:320:ARG:NH1	2:A2:360:PRO:HA	2.30	0.47
3:A7:321:MET:HE2	3:A7:326:VAL:CG2	2.36	0.47
3:B1:27:GLU:OE1	3:B1:318:ARG:NH2	2.48	0.47
3:B9:272:PRO:HG3	3:B9:284:LEU:HD11	1.96	0.47
3:C1:101:TRP:NE1	3:C1:145:SER:O	2.40	0.47
3:D1:173:PRO:HD2	3:D1:205:GLU:OE2	2.14	0.47
2:D6:269:LEU:HD23	2:D6:301:MET:HG2	1.97	0.47
3:D7:117:LEU:HD23	3:D7:121:ARG:HH22	1.80	0.47
3:E3:213:ARG:NE	3:E3:213:ARG:HA	2.30	0.47
3:E9:149:THR:HA	3:E9:152:ILE:HD12	1.96	0.47
4:e:95:TYR:CZ	4:e:99:MET:HE1	2.50	0.47
1:21:252:VAL:HG22	1:21:253:ALA:H	1.79	0.47
3:A9:272:PRO:HB2	3:A9:282:ARG:HH12	1.80	0.47
2:B2:183:GLU:OE2	2:B2:187:SER:OG	2.32	0.47
2:B2:252:VAL:HA	2:B2:255:PHE:HD2	1.78	0.47
3:B3:396:HIS:HA	3:B3:399:THR:HG22	1.97	0.47
2:C0:121:ARG:HD2	2:C0:121:ARG:HA	1.67	0.47
2:C2:251:ASP:OD1	2:C2:254:GLU:N	2.48	0.47
3:C7:91:VAL:HG21	3:C7:116:VAL:HG12	1.96	0.47
2:D2:85:HIS:HE1	4:o:99:MET:SD	2.38	0.47
3:D3:77:ARG:HH22	3:D3:92:PHE:HZ	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D4:292:THR:HG21	2:D4:331:ALA:HB1	1.96	0.47
3:E3:121:ARG:NE	3:E3:158:GLU:OE2	2.47	0.47
2:E4:403:ALA:N	3:E5:260:PHE:HE1	2.12	0.47
4:m:90:PRO:HA	4:m:93:LEU:HD12	1.96	0.47
4:r:78:ALA:HB3	4:r:112:PHE:HE1	1.79	0.47
4:r:110:ILE:O	4:r:131:TRP:HB2	2.15	0.47
4:x:65:GLN:HE21	4:x:206:PHE:HZ	1.61	0.47
4:y:146:ARG:HH11	4:y:146:ARG:HG3	1.79	0.47
1:20:241:PHE:HE1	3:E9:356:ILE:CG2	2.27	0.47
3:A5:94:GLN:O	2:A6:2:ARG:NH2	2.48	0.47
3:A7:293:MET:SD	3:A7:365:VAL:HG11	2.54	0.47
3:B7:2:ARG:HB2	3:B7:131:GLN:HB2	1.96	0.47
3:B7:219:THR:HB	2:B8:324:VAL:HG11	1.96	0.47
2:C2:285:GLN:OE1	2:C6:57:GLY:CA	2.62	0.47
2:C6:34:GLY:O	2:C6:61:HIS:N	2.38	0.47
2:D2:241:SER:OG	2:D2:250:VAL:O	2.28	0.47
3:D3:101:TRP:CE3	3:D3:403:MET:HE1	2.49	0.47
3:D3:205:GLU:CD	2:D4:329:ASN:HD21	2.21	0.47
2:D6:222:PRO:HD2	3:D7:324:LYS:CE	2.44	0.47
2:D6:241:SER:OG	2:D6:250:VAL:O	2.23	0.47
3:D7:70:PRO:HD2	2:D8:2:ARG:NH2	2.29	0.47
3:D7:374:ILE:HD11	3:D7:422:TYR:CZ	2.50	0.47
3:D9:139:LEU:HA	3:D9:145:SER:HB2	1.97	0.47
2:E2:311:LYS:NZ	2:E2:342:GLN:OE1	2.47	0.47
2:E4:236:SER:OG	2:E4:243:ARG:NH2	2.48	0.47
3:E9:69:GLU:HG2	2:F0:2:ARG:HH12	1.79	0.47
2:F0:9:VAL:HG13	2:F0:149:LEU:HD23	1.97	0.47
4:m:50:PHE:HD2	4:m:55:LEU:HD11	1.79	0.47
4:p:172:VAL:HG23	4:p:180:ALA:HB3	1.97	0.47
4:u:72:SER:HB3	4:u:108:ILE:HG22	1.97	0.47
4:y:25:GLN:HE22	4:y:36:ILE:HG21	1.79	0.47
1:19:241:PHE:HE1	3:E7:356:ILE:HG21	1.79	0.47
1:20:256:LEU:HD13	2:E8:29:GLY:O	2.14	0.47
1:3:245:SER:HB2	3:B1:42:LEU:HD21	1.97	0.47
2:A0:168:ASN:ND2	2:A0:170:CYS:SG	2.87	0.47
2:A0:285:GLN:OE1	2:A4:57:GLY:CA	2.62	0.47
3:A1:392:LYS:HE2	3:A1:395:LEU:HD22	1.97	0.47
2:A2:345:ASP:OD1	2:A2:346:TRP:N	2.48	0.47
2:A8:221:ARG:HG2	3:A9:322:SER:CB	2.44	0.47
2:A8:282:TYR:O	2:B2:60:LYS:HE2	2.15	0.47
2:A8:309:HIS:HE2	2:A8:386:GLU:CD	2.23	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B1:100:ASN:HB3	3:B1:103:LYS:HG2	1.96	0.47
3:B1:212:PHE:HE1	3:B1:220:PRO:HG3	1.80	0.47
2:B4:406:HIS:HA	2:B4:409:VAL:HG12	1.96	0.47
3:B7:259:PRO:HD2	3:B7:263:LEU:HD11	1.95	0.47
3:B9:13:GLY:HA2	3:B9:136:THR:HG22	1.97	0.47
2:C2:168:ASN:OD1	2:C2:169:PHE:N	2.47	0.47
2:C2:306:ASP:N	2:C2:386:GLU:OE2	2.48	0.47
3:C3:42:LEU:HD21	3:C3:356:ILE:HG13	1.97	0.47
3:C3:275:SER:OG	3:C3:276:ARG:N	2.47	0.47
2:C4:121:ARG:HH22	2:C4:124:LYS:HE3	1.79	0.47
3:C7:97:ALA:HA	3:C7:103:LYS:HZ2	1.79	0.47
2:C8:245:ASP:OD1	2:C8:245:ASP:N	2.48	0.47
3:C9:137:HIS:HE1	3:C9:166:THR:HB	1.79	0.47
2:D2:279:GLU:OE2	4:q:198:ARG:HD3	2.14	0.47
2:D4:65:CYS:O	2:D4:91:GLN:NE2	2.47	0.47
2:D4:221:ARG:HG2	3:D5:322:SER:CB	2.37	0.47
2:D6:119:LEU:HA	2:D6:122:ILE:HG22	1.96	0.47
2:D6:209:ILE:CG2	2:D6:227:LEU:HG	2.44	0.47
3:D9:27:GLU:OE2	3:D9:241:ARG:NH1	2.43	0.47
2:E0:189:LEU:HD13	2:E0:413:MET:HE1	1.97	0.47
3:E1:7:VAL:HB	3:E1:135:ILE:HG13	1.97	0.47
3:E3:247:ASN:C	3:E3:247:ASN:HD22	2.23	0.47
2:E4:176:GLN:O	3:E5:347:ASN:CB	2.63	0.47
3:E9:293:MET:HE3	3:E9:365:VAL:HG13	1.97	0.47
4:b:106:GLN:HB2	4:d:42:TYR:OH	2.15	0.47
4:c:22:ALA:HB1	4:c:38:LEU:HD21	1.96	0.47
4:k:25:GLN:HE22	4:k:36:ILE:HG21	1.80	0.47
4:s:96:TYR:CE1	4:u:6:PHE:CE2	3.02	0.47
4:t:9:PRO:HA	4:t:12:VAL:HG22	1.95	0.47
4:v:12:VAL:HG22	4:v:15:ARG:HH12	1.79	0.47
1:1:246:CYS:SG	1:1:247:TYR:N	2.88	0.47
1:10:241:PHE:CZ	3:C9:356:ILE:HG23	2.50	0.47
3:A9:284:LEU:H	3:B3:55:THR:HG21	1.80	0.47
3:B5:260:PHE:HB3	3:B5:261:PRO:HD2	1.96	0.47
2:B6:33:ASP:OD2	2:B6:35:GLN:NE2	2.48	0.47
2:C0:103:PHE:H	2:C0:408:TYR:HE1	1.63	0.47
2:C2:399:TYR:OH	2:C2:415:GLU:OE2	2.33	0.47
2:C4:285:GLN:CG	2:C8:56:THR:HA	2.44	0.47
2:C4:285:GLN:HG2	2:C8:56:THR:HA	1.97	0.47
3:C5:6:HIS:HE2	3:C5:136:THR:HG23	1.79	0.47
2:C6:218:ASP:O	4:n:194:ARG:NH2	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D0:132:LEU:HB3	2:D0:164:LYS:HZ2	1.80	0.47
2:D0:132:LEU:HB3	2:D0:164:LYS:NZ	2.29	0.47
2:D2:181:VAL:H	3:D3:256:ASN:HD22	1.63	0.47
2:D2:229:ARG:HG3	2:D2:229:ARG:NH1	2.29	0.47
2:D4:214:ARG:CG	3:D5:324:LYS:HZ3	2.28	0.47
3:D5:334:GLN:HE22	3:D5:347:ASN:HA	1.80	0.47
3:D7:135:ILE:HD11	3:D7:164:MET:HE3	1.97	0.47
2:E2:316:CYS:HA	2:E2:352:LYS:HB2	1.97	0.47
2:F0:306:ASP:HB3	2:F0:309:HIS:CE1	2.50	0.47
4:a:181:GLN:HG3	4:a:183:LEU:HD22	1.97	0.47
4:l:67:HIS:HE1	4:n:16:ARG:HG2	1.80	0.47
1:18:241:PHE:HE2	3:E5:42:LEU:CB	2.28	0.47
2:A2:156:ARG:HD3	2:A2:156:ARG:HA	1.77	0.47
2:A2:191:THR:HA	2:A2:194:LEU:HB3	1.97	0.47
2:A2:384:ILE:HA	2:A2:387:VAL:HG12	1.97	0.47
2:A8:174:SER:HB2	2:A8:177:VAL:O	2.15	0.47
2:B0:286:LEU:HD13	2:B0:371:VAL:HG23	1.96	0.47
3:B5:65:LEU:HB3	3:B5:73:MET:HE2	1.96	0.47
2:B6:217:LEU:HD11	2:B6:275:ILE:CG2	2.45	0.47
3:B7:281:TYR:CD2	3:C1:87:PRO:CD	2.97	0.47
2:C2:319:TYR:CD1	2:C2:375:VAL:HG22	2.50	0.47
3:C5:329:GLN:HA	3:C5:332:ASN:HB3	1.97	0.47
3:C7:164:MET:N	3:C7:197:ASP:OD2	2.41	0.47
3:C9:68:LEU:HD22	3:C9:108:GLU:HG3	1.97	0.47
3:C9:172:SER:HB3	3:C9:205:GLU:OE1	2.14	0.47
3:D3:289:LEU:CD2	3:D3:365:VAL:HG23	2.45	0.47
2:D6:3:GLU:HA	2:D6:51:THR:HA	1.96	0.47
2:D6:116:ASP:OD1	2:D6:117:LEU:N	2.48	0.47
3:D9:171:PRO:HG2	3:D9:185:ALA:HB2	1.96	0.47
2:E4:98:ASP:OD1	2:E4:100:ALA:N	2.40	0.47
2:E8:234:VAL:HG21	2:E8:302:MET:HE1	1.97	0.47
4:e:68:LEU:HB3	4:e:206:PHE:HD2	1.80	0.47
4:j:70:GLY:O	4:l:39:PRO:HD3	2.14	0.47
4:j:181:GLN:NE2	4:j:198:ARG:O	2.44	0.47
4:o:194:ARG:HG3	4:o:194:ARG:O	2.14	0.47
4:u:181:GLN:HE22	4:u:200:ASP:H	1.62	0.47
4:x:185:ILE:HD13	4:x:195:ALA:HB3	1.97	0.47
3:A1:289:LEU:HD21	3:A1:365:VAL:CG1	2.45	0.47
2:A2:6:SER:OG	2:A2:8:HIS:NE2	2.48	0.47
2:A2:214:ARG:HD2	3:A3:324:LYS:HZ1	1.61	0.47
2:A4:306:ASP:HB3	2:A4:309:HIS:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5:10:GLY:HA2	3:A5:143:THR:HG23	1.95	0.47
3:A5:238:CYS:SG	3:A5:318:ARG:NE	2.87	0.47
2:A6:283:HIS:CD2	2:B0:60:LYS:CE	2.97	0.47
3:B5:171:PRO:HB3	3:B5:181:GLU:OE1	2.15	0.47
3:B5:279:GLN:HG2	3:B5:279:GLN:O	2.13	0.47
3:C1:103:LYS:HA	3:C1:107:THR:HB	1.96	0.47
2:C2:209:ILE:HA	2:C2:212:ILE:HG22	1.97	0.47
3:C3:20:PHE:CD2	3:C3:233:MET:HE3	2.47	0.47
3:C3:262:ARG:HA	3:C3:262:ARG:HD2	1.73	0.47
2:C6:172:TRP:HB3	2:C6:205:ASP:OD1	2.15	0.47
2:C6:212:ILE:HD13	2:C6:215:ARG:HH22	1.80	0.47
3:C7:68:LEU:HA	3:C7:93:GLY:HA3	1.96	0.47
2:D0:265:ILE:HG23	2:D0:432:TYR:CZ	2.50	0.47
2:E4:404:PHE:N	3:E5:259:PRO:O	2.38	0.47
3:E5:257:LEU:HD21	3:E5:314:SER:HB2	1.97	0.47
2:E8:329:ASN:HA	2:E8:332:VAL:HG12	1.95	0.47
3:E9:289:LEU:HD23	3:E9:365:VAL:HG12	1.97	0.47
3:E9:330:MET:SD	3:E9:349:MET:HG3	2.55	0.47
4:h:41:ASN:O	4:h:45:MET:HG3	2.15	0.47
4:o:100:ASN:ND2	4:q:6:PHE:CE2	2.83	0.47
4:v:59:ASN:ND2	4:x:143:ILE:HD11	2.30	0.47
1:21:238:THR:CG2	3:F1:359:LYS:NZ	2.78	0.46
2:A0:221:ARG:CG	3:A1:322:SER:OG	2.63	0.46
2:B0:204:LEU:HD12	2:B0:209:ILE:HD11	1.96	0.46
2:B0:210:TYR:HE2	3:B1:327:ASP:OD2	1.98	0.46
3:B3:6:HIS:CE1	3:B3:20:PHE:CD2	3.03	0.46
2:B4:154:LEU:HB3	2:B4:197:HIS:HB3	1.97	0.46
3:B9:396:HIS:HA	3:B9:399:THR:HG22	1.95	0.46
2:C4:405:VAL:HG13	2:C4:418:PHE:HE2	1.80	0.46
3:D1:290:THR:HA	3:D1:293:MET:HE2	1.97	0.46
2:D8:119:LEU:HD13	2:D8:156:ARG:HD2	1.97	0.46
3:E1:215:LEU:HB3	3:E1:217:LEU:HD13	1.97	0.46
3:E1:238:CYS:SG	3:E1:239:CYS:N	2.88	0.46
2:E2:154:LEU:HD13	2:E2:166:LYS:HE3	1.97	0.46
2:E2:224:TYR:HD1	2:E2:227:LEU:HD12	1.80	0.46
3:E9:221:THR:HA	2:F0:325:PRO:CD	2.44	0.46
2:F0:339:ARG:O	2:F0:342:GLN:NE2	2.48	0.46
4:b:141:THR:O	4:b:145:LYS:HG2	2.15	0.46
4:c:9:PRO:HA	4:c:12:VAL:HG22	1.98	0.46
4:g:106:GLN:CD	4:i:6:PHE:HZ	2.23	0.46
4:r:106:GLN:CD	4:t:6:PHE:HZ	2.22	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:244:GLN:O	3:A5:320:ARG:NH2	2.48	0.46
1:11:245:SER:HG	3:D1:42:LEU:HD22	1.80	0.46
1:15:247:TYR:OH	2:D8:81:GLY:HA2	2.01	0.46
1:20:256:LEU:HD11	2:E8:31:GLN:CG	2.37	0.46
3:A3:192:LEU:HG	3:A3:199:VAL:HG21	1.97	0.46
2:A6:174:SER:HB2	2:A6:177:VAL:O	2.14	0.46
3:A7:318:ARG:HD3	3:A7:358:PRO:HD3	1.96	0.46
3:A9:167:PHE:CE2	3:A9:233:MET:HG2	2.50	0.46
2:B0:285:GLN:O	2:B0:285:GLN:HG3	2.15	0.46
2:B4:250:VAL:HG23	2:B4:254:GLU:HG3	1.95	0.46
2:B6:215:ARG:NH2	2:B6:299:ALA:O	2.47	0.46
3:B7:318:ARG:HD3	3:B7:358:PRO:HD3	1.97	0.46
3:B9:252:LYS:HG3	3:B9:350:LYS:HE3	1.98	0.46
3:C1:275:SER:OG	3:C1:276:ARG:N	2.48	0.46
3:C3:173:PRO:HA	3:C3:380:ARG:HH21	1.80	0.46
2:C4:135:PHE:HB2	2:C4:166:LYS:HA	1.97	0.46
3:D9:139:LEU:HD11	3:D9:192:LEU:HD13	1.97	0.46
3:E3:153:SER:HB2	3:E3:191:GLN:NE2	2.30	0.46
3:E9:179:VAL:HG11	2:F0:258:ASN:O	2.15	0.46
3:E9:403:MET:HA	3:E9:403:MET:HE2	1.96	0.46
4:e:101:GLU:OE2	4:g:5:VAL:HA	2.15	0.46
4:o:57:ASN:HA	4:o:132:LEU:HD23	1.96	0.46
4:p:78:ALA:HB3	4:p:112:PHE:HE1	1.80	0.46
4:s:146:ARG:HG3	4:s:146:ARG:HH11	1.80	0.46
4:v:118:ASP:N	4:v:118:ASP:OD1	2.48	0.46
2:A0:152:LEU:HD21	2:A0:156:ARG:NH1	2.29	0.46
3:A1:91:VAL:HG21	3:A1:116:VAL:CG2	2.46	0.46
3:A3:349:MET:HE3	3:A3:349:MET:HB2	1.64	0.46
2:B4:285:GLN:HG3	2:B4:285:GLN:O	2.15	0.46
3:B7:66:MET:HE3	3:B7:116:VAL:HG21	1.97	0.46
3:B7:107:THR:HG21	3:B7:401:GLU:OE2	2.14	0.46
3:B7:220:PRO:HG2	2:B8:326:LYS:HB2	1.97	0.46
2:B8:141:VAL:HA	2:B8:147:SER:HB2	1.98	0.46
2:C4:18:ASN:O	2:C4:22:GLU:HG2	2.15	0.46
2:C8:217:LEU:CD2	2:C8:275:ILE:HG22	2.45	0.46
3:C9:161:ASP:OD1	3:C9:161:ASP:N	2.44	0.46
3:D3:140:GLY:O	3:D3:184:ASN:ND2	2.44	0.46
3:D3:239:CYS:SG	3:D3:248:SER:N	2.87	0.46
3:D5:248:SER:HA	3:D5:252:LYS:HG2	1.96	0.46
3:D9:39:ASP:CB	4:r:90:PRO:HG3	2.44	0.46
3:E1:1:MET:N	3:E1:128:ASP:OD2	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E6:60:LYS:NZ	2:E6:85:HIS:O	2.48	0.46
3:E9:5:VAL:HB	3:E9:133:PHE:HD1	1.81	0.46
4:i:71:LYS:HZ2	4:i:106:GLN:HB2	1.80	0.46
4:j:98:THR:HA	4:j:101:GLU:HG3	1.97	0.46
4:m:105:ASN:HB3	4:o:39:PRO:HG2	1.97	0.46
4:q:95:TYR:HA	4:q:98:THR:HG22	1.97	0.46
4:v:63:ILE:HD11	4:x:16:ARG:HD3	1.97	0.46
4:x:146:ARG:HG3	4:x:146:ARG:NH1	2.31	0.46
2:A0:56:THR:HA	3:F1:283:ALA:HB2	1.97	0.46
3:A1:10:GLY:O	3:A1:14:ASN:ND2	2.40	0.46
2:A2:222:PRO:CG	3:A3:324:LYS:HB2	2.45	0.46
3:A3:64:ILE:HD12	3:A3:119:VAL:HG12	1.97	0.46
3:A7:128:ASP:OD1	3:A7:128:ASP:N	2.47	0.46
2:A8:395:PHE:HD2	2:A8:422:ARG:HD3	1.81	0.46
2:C0:298:PRO:HG3	2:C0:308:ARG:HH12	1.80	0.46
3:C1:73:MET:HB3	3:C1:77:ARG:HH22	1.79	0.46
3:C1:382:SER:O	3:C1:386:THR:N	2.45	0.46
3:C3:200:GLN:HG3	3:C3:268:ILE:HD11	1.96	0.46
2:C4:88:HIS:O	2:C4:90:GLU:N	2.48	0.46
2:C4:178:SER:HB3	3:C5:347:ASN:ND2	2.31	0.46
3:F1:320:ARG:HB2	3:F1:320:ARG:HH11	1.79	0.46
4:b:97:ARG:HH22	4:d:7:ALA:N	2.14	0.46
4:f:56:LYS:HD3	4:f:60:ASN:OD1	2.15	0.46
4:f:75:LEU:O	4:f:170:VAL:HA	2.14	0.46
4:h:106:GLN:NE2	4:j:6:PHE:CZ	2.83	0.46
4:q:78:ALA:HB3	4:q:112:PHE:HE1	1.81	0.46
4:s:63:ILE:CG2	4:u:16:ARG:HG3	2.45	0.46
4:y:57:ASN:HA	4:y:132:LEU:HD23	1.97	0.46
1:11:240:PRO:HG3	4:p:154:TYR:CD2	2.49	0.46
2:A2:241:SER:HB3	2:A2:249:ASN:HB3	1.97	0.46
2:A2:336:LYS:HD2	2:A2:336:LYS:HA	1.81	0.46
2:A4:285:GLN:HB2	2:A8:57:GLY:HA2	1.95	0.46
3:A9:219:THR:HA	2:B0:324:VAL:HG11	1.97	0.46
2:B0:27:GLU:OE1	2:B0:243:ARG:NH2	2.49	0.46
3:B1:63:ALA:O	3:B1:89:ASN:ND2	2.48	0.46
3:B3:248:SER:HA	3:B3:252:LYS:HE2	1.98	0.46
2:B4:204:LEU:HD22	2:B4:302:MET:HE3	1.98	0.46
2:B6:108:TYR:O	2:B6:112:LYS:NZ	2.39	0.46
2:C6:189:LEU:HD11	2:C6:413:MET:HE2	1.96	0.46
3:C7:311:LEU:HD12	3:C7:342:VAL:HG11	1.98	0.46
2:C8:238:LEU:HD11	2:C8:255:PHE:HE2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D4:88:HIS:HB3	2:D4:91:GLN:HG2	1.98	0.46
2:D8:156:ARG:CZ	2:D8:156:ARG:HB2	2.46	0.46
2:E0:100:ALA:CB	3:E1:251:ARG:HD2	2.45	0.46
2:E4:132:LEU:HG	2:E4:164:LYS:HZ3	1.80	0.46
2:E4:422:ARG:NH1	2:E4:426:ALA:HB2	2.29	0.46
2:E8:296:PHE:CZ	2:E8:317:LEU:HD21	2.50	0.46
4:g:106:GLN:CG	4:i:6:PHE:HZ	2.27	0.46
4:s:67:HIS:CA	4:u:19:GLU:OE1	2.54	0.46
3:A3:8:GLN:HG3	3:A3:65:LEU:HD13	1.97	0.46
3:A3:163:ILE:HG12	3:A3:250:LEU:HB3	1.96	0.46
2:C2:105:ARG:HG2	2:C2:411:GLU:HG2	1.98	0.46
2:C6:282:TYR:HB2	4:n:202:ARG:NH1	2.30	0.46
3:D1:274:THR:OG1	3:D1:279:GLN:OE1	2.34	0.46
2:D2:194:LEU:O	2:D2:198:THR:HG22	2.16	0.46
3:D7:163:ILE:HD11	3:D7:251:ARG:HG3	1.97	0.46
2:D8:119:LEU:CD1	2:D8:156:ARG:HD2	2.46	0.46
3:D9:321:MET:HE2	3:D9:363:MET:HG3	1.98	0.46
3:E5:248:SER:HA	3:E5:252:LYS:HG2	1.98	0.46
2:F0:176:GLN:OE1	3:F1:331:LEU:HD11	2.15	0.46
4:d:96:TYR:OH	4:f:6:PHE:HE2	1.96	0.46
4:h:106:GLN:HE21	4:j:6:PHE:HZ	1.63	0.46
4:n:142:GLU:HA	4:n:145:LYS:HG2	1.96	0.46
4:x:14:LYS:HD3	4:x:47:LEU:HD22	1.98	0.46
1:7:244:GLN:HE22	1:7:249:SER:N	2.14	0.46
2:A0:269:LEU:HD23	2:A0:303:ALA:HB3	1.98	0.46
3:A1:91:VAL:HG21	3:A1:116:VAL:HG23	1.97	0.46
3:A1:179:VAL:HG11	2:A2:258:ASN:O	2.15	0.46
2:A2:3:GLU:OE1	2:A2:64:ARG:NH1	2.49	0.46
2:B8:1:MET:N	2:B8:129:CYS:SG	2.86	0.46
2:B8:26:LEU:HD21	2:B8:364:PRO:HD3	1.98	0.46
3:C3:49:VAL:HG11	3:C3:241:ARG:HG2	1.98	0.46
2:C6:274:PRO:HG2	2:C6:371:VAL:HG11	1.97	0.46
2:C8:34:GLY:O	2:C8:61:HIS:N	2.43	0.46
2:C8:88:HIS:HB3	2:C8:91:GLN:HB2	1.96	0.46
3:D3:294:PHE:CD2	3:D3:333:VAL:HG21	2.51	0.46
2:D8:203:MET:HE2	2:D8:267:PHE:HB3	1.97	0.46
3:D9:10:GLY:HA2	3:D9:143:THR:HG23	1.98	0.46
2:E0:96:LYS:HD3	3:E1:128:ASP:CG	2.41	0.46
3:E7:382:SER:OG	3:E7:412:GLU:OE1	2.32	0.46
4:b:67:HIS:O	4:b:71:LYS:NZ	2.47	0.46
4:h:15:ARG:HG3	4:h:45:MET:HE1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:n:138:ASN:O	4:n:141:THR:HG22	2.16	0.46
4:p:18:ASN:ND2	4:p:45:MET:HA	2.30	0.46
4:s:59:ASN:OD1	4:u:9:PRO:HB3	2.16	0.46
4:s:184:PRO:HB2	4:s:189:LEU:HB2	1.96	0.46
5:w:73:TYR:CG	5:w:90:MET:HE1	2.50	0.46
1:8:251:TYR:OH	2:C0:225:THR:OG1	2.34	0.46
2:A6:331:ALA:O	2:A6:334:THR:OG1	2.32	0.46
3:A9:173:PRO:HG2	3:A9:205:GLU:OE2	2.15	0.46
2:B6:265:ILE:HG23	2:B6:432:TYR:CZ	2.51	0.46
3:C1:208:TYR:HA	2:C2:326:LYS:NZ	2.31	0.46
2:C8:206:ASN:HD22	2:C8:227:LEU:HD23	1.80	0.46
2:C8:241:SER:HB2	2:C8:249:ASN:HB2	1.97	0.46
2:C8:304:LYS:O	2:C8:304:LYS:HD3	2.16	0.46
3:C9:66:MET:HE2	3:C9:116:VAL:HG21	1.98	0.46
3:D1:117:LEU:HA	3:D1:120:VAL:HG12	1.97	0.46
2:D2:221:ARG:NE	4:q:189:LEU:O	2.49	0.46
2:D2:250:VAL:HG11	2:D2:318:MET:HE1	1.97	0.46
2:E6:180:ALA:HA	3:E7:350:LYS:HE3	1.97	0.46
4:c:111:ILE:CD1	4:c:132:LEU:HB2	2.44	0.46
4:c:129:MET:HE3	4:c:131:TRP:HE1	1.80	0.46
4:k:97:ARG:HD3	4:m:161:TYR:CE1	2.51	0.46
4:s:159:TYR:HB2	4:s:161:TYR:CE2	2.51	0.46
1:2:247:TYR:HE1	2:A8:81:GLY:HA3	1.81	0.46
2:A4:407:TRP:CZ3	3:A5:255:VAL:HA	2.50	0.46
2:B2:145:THR:O	2:B2:149:LEU:HB2	2.16	0.46
3:B3:63:ALA:O	3:B3:89:ASN:ND2	2.49	0.46
2:B4:167:LEU:HD22	2:B4:200:VAL:HB	1.98	0.46
2:C4:296:PHE:CD1	2:C4:377:MET:HE2	2.51	0.46
3:D3:218:THR:O	2:D4:326:LYS:HE2	2.16	0.46
3:D5:68:LEU:HB3	3:D5:96:GLY:HA2	1.98	0.46
2:D8:12:ALA:CB	2:D8:140:ALA:HB2	2.46	0.46
2:E2:220:GLU:HG3	2:E2:220:GLU:O	2.15	0.46
2:F0:28:HIS:CE1	2:F0:243:ARG:HD2	2.51	0.46
4:e:149:ARG:HG3	4:e:164:ARG:HB2	1.98	0.46
4:o:166:GLY:O	4:o:169:SER:OG	2.34	0.46
4:r:15:ARG:HG2	4:r:45:MET:CE	2.43	0.46
5:w:68:VAL:HB	5:w:159:TYR:CE2	2.51	0.46
1:23:240:PRO:HG3	4:m:154:TYR:O	2.15	0.46
3:A5:267:LEU:HB3	3:A5:299:MET:HE2	1.98	0.46
2:A6:204:LEU:HD13	2:A6:231:ILE:HD12	1.97	0.46
3:C1:392:LYS:HA	3:C1:395:LEU:HD23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C5:187:LEU:HD11	3:C5:408:PHE:CZ	2.50	0.46
3:C9:39:ASP:CB	4:m:90:PRO:HG3	2.44	0.46
2:D0:203:MET:HE2	2:D0:267:PHE:CD1	2.50	0.46
3:D3:67:ASP:OD1	3:D3:68:LEU:N	2.49	0.46
3:D3:117:LEU:HA	3:D3:120:VAL:HG12	1.98	0.46
2:D4:30:ILE:HG22	2:D4:36:MET:HB3	1.97	0.46
3:D5:323:THR:O	3:D5:327:ASP:N	2.47	0.46
2:E4:223:THR:HA	3:E5:323:THR:OG1	2.15	0.46
3:E5:221:THR:HA	2:E6:325:PRO:HD2	1.98	0.46
2:E8:79:ARG:NH1	2:E8:92:LEU:O	2.48	0.46
4:a:89:LEU:HB3	4:a:90:PRO:HD3	1.98	0.46
4:c:15:ARG:CG	4:c:45:MET:HE1	2.46	0.46
4:d:106:GLN:HB2	4:f:42:TYR:OH	2.15	0.46
4:e:105:ASN:ND2	4:g:37:GLN:HE21	2.14	0.46
4:y:75:LEU:HG	4:y:173:ILE:HD13	1.98	0.46
1:19:256:LEU:HB2	2:E6:29:GLY:HA2	1.97	0.45
2:A0:136:LEU:HD23	2:A0:167:LEU:HB3	1.97	0.45
3:A3:237:THR:HG22	3:A3:237:THR:O	2.16	0.45
3:A5:206:ALA:HB2	3:A5:302:ALA:HB2	1.97	0.45
2:A6:222:PRO:CG	3:A7:324:LYS:HB2	2.45	0.45
2:A8:395:PHE:CD2	2:A8:422:ARG:HD3	2.51	0.45
3:A9:263:LEU:H	3:A9:263:LEU:HD23	1.81	0.45
2:B8:168:ASN:HD22	2:B8:198:THR:HG21	1.81	0.45
2:C0:224:TYR:HA	2:C0:227:LEU:HD12	1.99	0.45
3:C1:105:HIS:CE1	3:C1:150:LEU:HD13	2.51	0.45
3:C1:139:LEU:HA	3:C1:145:SER:HB2	1.98	0.45
2:C4:137:MET:HB3	2:C4:168:ASN:HA	1.97	0.45
2:C4:221:ARG:HB3	3:C5:322:SER:CB	2.45	0.45
2:C6:28:HIS:HE1	2:C6:243:ARG:HD2	1.80	0.45
3:D3:155:VAL:HG13	3:D3:164:MET:HE2	1.98	0.45
2:D4:306:ASP:HB3	2:D4:309:HIS:CE1	2.52	0.45
3:D5:55:THR:O	3:D5:55:THR:HG23	2.16	0.45
3:D7:299:MET:HE1	3:D7:367:PHE:HD2	1.80	0.45
3:E1:309:ARG:H	3:E1:372:THR:HG22	1.80	0.45
2:E4:406:HIS:CD2	3:E5:261:PRO:HB3	2.51	0.45
2:E6:236:SER:OG	2:E6:243:ARG:NH2	2.49	0.45
3:E9:320:ARG:HH11	3:E9:320:ARG:HD3	1.34	0.45
3:F1:167:PHE:CZ	3:F1:233:MET:HG3	2.51	0.45
4:d:99:MET:HE2	4:d:99:MET:HB3	1.85	0.45
4:e:6:PHE:CZ	4:e:15:ARG:NH2	2.85	0.45
4:f:18:ASN:HD22	4:f:45:MET:HA	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:g:11:ASN:O	4:g:15:ARG:HG3	2.16	0.45
4:k:146:ARG:HG3	4:k:146:ARG:NH1	2.31	0.45
4:n:8:SER:HB2	4:n:147:HIS:ND1	2.31	0.45
4:s:67:HIS:HA	4:u:19:GLU:CD	2.39	0.45
2:A6:212:ILE:HG12	2:A6:275:ILE:HD11	1.99	0.45
3:A7:4:ILE:HD11	3:A7:240:LEU:HD22	1.98	0.45
2:A8:209:ILE:HA	2:A8:212:ILE:HG22	1.98	0.45
2:B6:52:PHE:HD2	2:B6:243:ARG:HD3	1.81	0.45
3:C1:257:LEU:HB3	3:C1:266:PHE:CE1	2.51	0.45
3:C3:270:PHE:O	3:C3:298:ASN:ND2	2.36	0.45
2:C4:167:LEU:HA	2:C4:200:VAL:HG13	1.99	0.45
2:C6:1:MET:HA	2:C6:129:CYS:HB3	1.98	0.45
2:D4:214:ARG:HG3	3:D5:324:LYS:HZ3	1.80	0.45
3:D5:176:SER:OG	3:D5:181:GLU:OE1	2.24	0.45
3:E1:198:GLU:HB2	3:E1:266:PHE:CE2	2.48	0.45
3:E1:396:HIS:HA	3:E1:399:THR:HG22	1.97	0.45
2:E6:336:LYS:HE2	2:E6:336:LYS:HB2	1.64	0.45
2:E8:265:ILE:HD12	2:E8:432:TYR:CE1	2.52	0.45
4:a:96:TYR:OH	4:c:6:PHE:HE2	1.98	0.45
4:e:2:SER:O	4:e:2:SER:OG	2.34	0.45
4:g:56:LYS:O	4:g:126:ARG:NH2	2.50	0.45
4:t:15:ARG:HG2	4:t:45:MET:HE1	1.98	0.45
4:v:58:SER:HB3	4:x:12:VAL:HG21	1.97	0.45
4:v:129:MET:SD	4:v:131:TRP:NE1	2.90	0.45
2:A0:164:LYS:HD2	2:A0:164:LYS:HA	1.69	0.45
2:A0:229:ARG:HH11	2:A0:229:ARG:HG3	1.81	0.45
2:A0:282:TYR:HB2	4:a:202:ARG:HH21	1.78	0.45
3:A1:274:THR:HG21	3:A1:282:ARG:HD2	1.98	0.45
2:A4:71:GLU:HB2	2:A4:98:ASP:HB2	1.98	0.45
2:B0:88:HIS:HB3	2:B0:91:GLN:HG2	1.98	0.45
2:B2:318:MET:HE3	2:B2:318:MET:HB3	1.83	0.45
3:B3:397:TRP:HA	3:B3:397:TRP:CE3	2.51	0.45
3:B5:336:LYS:HA	3:B5:336:LYS:CE	2.47	0.45
3:C3:202:ILE:HD12	3:C3:300:MET:HE2	1.96	0.45
2:C6:407:TRP:CH2	3:C7:254:ALA:O	2.68	0.45
2:D0:189:LEU:HD11	2:D0:418:PHE:HD1	1.81	0.45
2:D2:241:SER:HB2	2:D2:249:ASN:HB2	1.96	0.45
3:D7:292:GLN:O	3:D7:298:ASN:ND2	2.47	0.45
3:E1:128:ASP:OD1	3:E1:129:CYS:N	2.44	0.45
3:E5:33:THR:O	3:E5:58:ARG:NH2	2.49	0.45
2:F0:328:VAL:HG21	2:F0:355:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:73:VAL:HA	4:e:109:GLU:O	2.16	0.45
4:f:70:GLY:C	4:h:39:PRO:HD3	2.41	0.45
4:f:99:MET:HE2	4:f:99:MET:HB3	1.54	0.45
4:k:8:SER:HA	4:k:9:PRO:HD3	1.83	0.45
4:r:113:VAL:HG13	4:r:141:THR:HG23	1.98	0.45
1:15:257:PRO:HG3	2:D8:26:LEU:O	2.15	0.45
2:A0:11:GLN:HG3	2:A0:74:VAL:HG11	1.98	0.45
2:A4:60:LYS:HE3	2:A4:60:LYS:HB3	1.57	0.45
3:A7:95:THR:OG1	3:A7:96:GLY:N	2.49	0.45
3:A9:1:MET:N	3:A9:128:ASP:OD2	2.42	0.45
3:B1:190:HIS:HB2	3:B1:414:ASN:HD22	1.81	0.45
3:B7:190:HIS:HA	3:B7:193:VAL:HG12	1.98	0.45
3:B9:256:ASN:HD22	3:B9:350:LYS:HD2	1.82	0.45
3:B9:276:ARG:NH2	3:B9:279:GLN:OE1	2.50	0.45
3:C1:105:HIS:O	3:C1:105:HIS:ND1	2.50	0.45
3:C3:169:VAL:HG12	3:C3:202:ILE:HB	1.97	0.45
2:C6:310:GLY:HA3	2:C6:383:ALA:HB2	1.99	0.45
3:C7:321:MET:N	3:C7:321:MET:SD	2.90	0.45
2:C8:319:TYR:CD2	2:C8:375:VAL:HG22	2.51	0.45
3:D7:323:THR:HA	3:D7:326:VAL:HG12	1.97	0.45
3:D9:318:ARG:HG2	3:D9:354:CYS:HB3	1.98	0.45
2:E2:277:SER:OG	2:E2:278:ALA:N	2.50	0.45
2:E4:215:ARG:NH1	2:E4:216:ASN:OD1	2.49	0.45
3:E9:98:GLY:O	2:F0:257:THR:HG21	2.17	0.45
4:b:97:ARG:HH11	4:d:6:PHE:CB	2.07	0.45
4:f:100:ASN:ND2	4:h:6:PHE:CE2	2.85	0.45
4:v:130:PRO:HB2	4:x:7:ALA:HB1	1.97	0.45
1:11:247:TYR:OH	2:D0:82:THR:N	2.47	0.45
1:12:250:GLU:HG3	1:12:251:TYR:CD1	2.51	0.45
2:A2:66:VAL:HG21	2:A2:122:ILE:HD11	1.97	0.45
3:A9:362:LYS:HA	3:A9:362:LYS:HD2	1.69	0.45
3:B1:40:SER:OG	3:B1:43:GLN:OE1	2.33	0.45
3:B5:68:LEU:HG	3:B5:147:MET:HE2	1.98	0.45
2:C8:323:VAL:HG13	2:C8:355:ILE:HG23	1.98	0.45
2:D0:285:GLN:HB3	2:D4:57:GLY:CA	2.47	0.45
3:D1:163:ILE:HG13	3:D1:164:MET:N	2.32	0.45
2:D2:11:GLN:O	2:D2:15:GLN:HG3	2.17	0.45
3:D3:64:ILE:HD12	3:D3:119:VAL:HG22	1.99	0.45
3:D5:281:TYR:O	3:D9:54:ALA:HB1	2.17	0.45
2:D8:223:THR:HG23	2:D8:225:THR:H	1.81	0.45
2:E0:212:ILE:HD11	2:E0:300:SER:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E2:70:LEU:HD12	2:E2:99:ALA:HB2	1.98	0.45
2:E8:313:MET:HE3	2:E8:346:TRP:HZ2	1.81	0.45
3:F1:309:ARG:NH1	3:F1:341:PHE:O	2.48	0.45
4:b:96:TYR:HA	4:b:108:ILE:HD11	1.99	0.45
4:g:14:LYS:HD3	4:g:47:LEU:CD1	2.47	0.45
4:x:105:ASN:OD1	4:y:39:PRO:HG2	2.17	0.45
1:23:245:SER:HB2	3:C5:42:LEU:HD11	1.99	0.45
1:5:248:ARG:NH1	3:B5:42:LEU:HD21	2.32	0.45
2:A8:282:TYR:HD2	2:A8:283:HIS:CE1	2.35	0.45
3:A9:316:MET:HE2	3:A9:366:THR:HG23	1.99	0.45
2:B0:138:PHE:CZ	2:B0:235:ILE:HD12	2.51	0.45
3:B3:46:ARG:HE	3:B3:46:ARG:HB2	1.61	0.45
3:B5:383:ASP:HA	3:B5:386:THR:HG22	1.98	0.45
3:C1:35:THR:OG1	3:C1:36:TYR:N	2.43	0.45
3:C1:86:ARG:HD2	3:C1:88:ASP:HB2	1.98	0.45
2:C4:390:ARG:O	2:C4:394:LYS:N	2.50	0.45
3:D5:209:ASP:OD1	3:D5:213:ARG:NH1	2.45	0.45
3:E1:2:ARG:HB2	3:E1:131:GLN:HB2	1.99	0.45
2:E2:181:VAL:HG12	3:E3:256:ASN:HD22	1.81	0.45
2:E4:119:LEU:HD22	2:E4:157:LEU:HD21	1.97	0.45
2:E4:284:GLU:CG	2:E8:88:HIS:CD2	2.99	0.45
2:E6:192:HIS:ND1	2:E6:424:ASP:OD2	2.50	0.45
3:E7:208:TYR:CE1	3:E7:225:LEU:HD11	2.52	0.45
2:E8:91:GLN:HB3	2:E8:121:ARG:HG2	1.98	0.45
2:E8:296:PHE:HZ	2:E8:317:LEU:HD21	1.81	0.45
4:b:71:LYS:HZ1	4:d:39:PRO:HB3	1.82	0.45
4:f:58:SER:HA	4:f:126:ARG:HH22	1.81	0.45
4:f:69:LYS:HB2	4:f:69:LYS:HE3	1.59	0.45
4:h:96:TYR:CD1	4:j:159:TYR:OH	2.70	0.45
4:n:171:ILE:HG22	4:n:182:PHE:HA	1.99	0.45
4:n:172:VAL:HG12	4:n:181:GLN:HG2	1.99	0.45
4:x:181:GLN:NE2	4:x:200:ASP:OD1	2.49	0.45
1:18:254:LYS:CE	2:E4:364:PRO:HD2	2.46	0.45
3:A1:32:PRO:O	3:A1:83:GLN:NE2	2.49	0.45
3:A5:226:ASN:HA	3:A5:229:VAL:HG12	1.99	0.45
3:A9:70:PRO:HD2	2:B0:2:ARG:HH12	1.81	0.45
2:B4:268:MET:HE2	2:B4:268:MET:HB3	1.91	0.45
3:C1:73:MET:HB3	3:C1:77:ARG:NH2	2.32	0.45
3:C3:253:LEU:HD11	3:C3:368:VAL:HG21	1.97	0.45
2:C4:319:TYR:HB3	2:C4:323:VAL:HG21	1.98	0.45
2:D4:279:GLU:OE2	4:r:198:ARG:CG	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D7:238:CYS:SG	3:D7:318:ARG:NE	2.90	0.45
2:E4:214:ARG:CG	3:E5:324:LYS:NZ	2.72	0.45
3:E5:105:HIS:CD2	3:E5:150:LEU:HB2	2.51	0.45
3:E5:209:ASP:CG	3:E5:213:ARG:HH21	2.24	0.45
3:E9:7:VAL:HG22	3:E9:64:ILE:HB	1.98	0.45
4:b:68:LEU:HD21	4:b:111:ILE:HD11	1.97	0.45
4:c:100:ASN:ND2	4:e:6:PHE:CZ	2.85	0.45
4:h:105:ASN:ND2	4:j:39:PRO:HG2	2.32	0.45
4:j:117:ARG:HD2	4:j:117:ARG:HA	1.71	0.45
4:s:106:GLN:HG2	4:u:42:TYR:OH	2.15	0.45
4:t:63:ILE:CG2	4:v:16:ARG:HG3	2.47	0.45
4:v:67:HIS:HB3	4:x:19:GLU:OE2	2.17	0.45
3:A1:193:VAL:HG12	3:A1:265:PHE:HE2	1.82	0.45
2:A2:208:ALA:HB2	2:A2:304:LYS:HB2	1.98	0.45
3:A5:23:VAL:HG11	3:A5:230:SER:HB2	1.98	0.45
3:A5:167:PHE:CE2	3:A5:233:MET:HG2	2.52	0.45
3:B5:281:TYR:C	3:B9:54:ALA:HB1	2.42	0.45
3:C1:326:VAL:O	3:C1:330:MET:HG2	2.16	0.45
2:C2:155:GLU:HG2	2:C2:197:HIS:CD2	2.52	0.45
2:C2:425:LEU:HD23	2:C2:425:LEU:HA	1.82	0.45
3:C3:136:THR:HG23	3:C3:167:PHE:HB2	1.98	0.45
2:C4:7:ILE:HG21	2:C4:153:LEU:HD23	1.99	0.45
3:C9:299:MET:HE3	3:C9:305:PRO:HG3	1.98	0.45
2:D2:277:SER:OG	2:D2:278:ALA:N	2.49	0.45
3:D3:350:LYS:NZ	3:D3:352:SER:OG	2.49	0.45
2:E0:66:VAL:HG21	2:E0:122:ILE:HD11	1.99	0.45
2:E0:177:VAL:HA	3:E1:347:ASN:ND2	2.31	0.45
3:E3:239:CYS:SG	3:E3:248:SER:N	2.83	0.45
3:E3:385:PHE:CE2	3:E3:412:GLU:HB3	2.52	0.45
3:E5:99:ASN:HB2	2:E6:257:THR:HG21	1.98	0.45
2:F0:219:ILE:HG13	2:F0:222:PRO:HD3	1.97	0.45
4:f:18:ASN:ND2	4:f:46:ASP:H	2.15	0.45
4:f:146:ARG:NH2	4:f:156:VAL:HB	2.31	0.45
4:g:75:LEU:O	4:g:170:VAL:HA	2.16	0.45
4:g:89:LEU:O	4:g:93:LEU:HG	2.17	0.45
4:n:78:ALA:HB3	4:n:112:PHE:HE1	1.81	0.45
4:q:5:VAL:HB	4:q:161:TYR:HE2	1.82	0.45
4:x:117:ARG:CZ	4:x:117:ARG:HB3	2.46	0.45
2:A0:241:SER:HB3	2:A0:249:ASN:HB3	1.99	0.45
3:A1:6:HIS:CD2	3:A1:134:GLN:HG3	2.51	0.45
2:A4:208:ALA:HB2	2:A4:304:LYS:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A5:203:ASP:OD2	3:A5:302:ALA:N	2.38	0.45
2:A6:27:GLU:HG3	2:A6:361:THR:HG21	1.99	0.45
2:A6:204:LEU:HD22	2:A6:302:MET:HE2	1.99	0.45
3:A7:178:THR:O	3:A7:181:GLU:HG2	2.17	0.45
3:A9:149:THR:OG1	3:A9:191:GLN:OE1	2.27	0.45
2:B2:277:SER:OG	2:B2:278:ALA:N	2.49	0.45
2:B4:298:PRO:HB3	2:B4:307:PRO:HD2	1.99	0.45
2:B6:70:LEU:HD12	2:B6:99:ALA:HB2	1.98	0.45
2:C0:320:ARG:NH2	2:C0:358:GLN:OE1	2.50	0.45
2:C2:277:SER:OG	2:C2:278:ALA:N	2.50	0.45
3:C3:274:THR:OG1	3:C3:279:GLN:OE1	2.31	0.45
3:C5:327:ASP:OD1	3:C5:327:ASP:N	2.45	0.45
3:C7:149:THR:HG23	3:C7:152:ILE:HD12	1.97	0.45
2:D0:119:LEU:HA	2:D0:122:ILE:HG22	1.99	0.45
2:D0:156:ARG:HG2	2:D0:156:ARG:HH21	1.82	0.45
2:E0:18:ASN:HD21	2:E0:78:VAL:HG22	1.81	0.45
2:E0:406:HIS:HA	2:E0:409:VAL:HG12	1.97	0.45
3:E1:113:ILE:HD11	3:E1:151:LEU:HD13	1.99	0.45
2:E4:182:VAL:HG22	2:E4:182:VAL:O	2.17	0.45
2:E4:222:PRO:O	3:E5:323:THR:N	2.50	0.45
2:E6:285:GLN:HG2	2:F0:56:THR:HA	1.99	0.45
3:E9:175:VAL:HG23	2:F0:332:VAL:HG11	1.99	0.45
2:F0:222:PRO:HB3	2:F0:226:ASN:HD22	1.81	0.45
4:d:15:ARG:O	4:d:19:GLU:HB2	2.17	0.45
4:h:66:SER:O	4:j:23:LEU:HD11	2.16	0.45
4:j:71:LYS:HZ3	4:l:39:PRO:HG3	1.81	0.45
4:k:198:ARG:HG2	4:k:198:ARG:NH1	2.19	0.45
4:x:57:ASN:HA	4:x:132:LEU:HD23	1.98	0.45
4:x:127:ALA:O	4:y:157:PRO:CG	2.64	0.45
4:y:185:ILE:HD11	4:y:196:LEU:HD12	1.99	0.45
1:8:256:LEU:HA	1:8:257:PRO:HD3	1.87	0.45
2:A0:139:ASN:OD1	2:A0:139:ASN:N	2.48	0.45
2:A0:172:TRP:N	2:A0:204:LEU:O	2.45	0.45
2:A4:328:VAL:O	2:A4:332:VAL:HG23	2.17	0.45
3:A9:213:ARG:HE	3:A9:297:LYS:HG3	1.81	0.45
3:A9:217:LEU:HD23	3:A9:217:LEU:HA	1.86	0.45
3:B3:27:GLU:OE2	3:B3:318:ARG:NH2	2.35	0.45
3:B5:147:MET:HE3	3:B5:147:MET:HB3	1.77	0.45
2:B6:326:LYS:HD2	2:B6:326:LYS:HA	1.57	0.45
2:B8:164:LYS:HD3	2:B8:164:LYS:HA	1.78	0.45
3:C3:222:TYR:HA	3:C3:225:LEU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C6:88:HIS:HB3	2:C6:91:GLN:OE1	2.17	0.45
3:C7:404:ASP:OD1	3:C7:405:GLU:N	2.45	0.45
2:C8:98:ASP:OD1	2:C8:99:ALA:N	2.50	0.45
3:C9:282:ARG:NH1	3:C9:292:GLN:OE1	2.50	0.45
2:D2:181:VAL:HG22	3:D3:256:ASN:HA	1.99	0.45
3:D3:191:GLN:HA	3:D3:194:GLU:HG2	1.98	0.45
2:D6:209:ILE:HG21	2:D6:227:LEU:HG	1.98	0.45
3:D7:179:VAL:HG11	2:D8:258:ASN:O	2.17	0.45
3:D9:63:ALA:O	3:D9:89:ASN:ND2	2.50	0.45
2:E2:269:LEU:HG	2:E2:384:ILE:HD11	1.99	0.45
3:E3:7:VAL:HB	3:E3:135:ILE:HG13	1.99	0.45
3:E5:290:THR:HA	3:E5:293:MET:HE3	1.98	0.45
3:E7:25:SER:HB3	3:E7:30:ILE:HB	1.99	0.45
2:E8:69:ASP:OD1	2:E8:70:LEU:N	2.49	0.45
2:E8:137:MET:HB3	2:E8:168:ASN:HA	1.99	0.45
3:E9:113:ILE:HG13	3:E9:150:LEU:HD22	1.99	0.45
3:E9:229:VAL:HG12	3:E9:233:MET:HE2	1.98	0.45
4:e:97:ARG:HG3	4:e:161:TYR:CZ	2.52	0.45
4:e:100:ASN:ND2	4:g:6:PHE:CE2	2.84	0.45
4:g:55:LEU:HA	4:g:55:LEU:HD23	1.84	0.45
4:p:141:THR:O	4:p:145:LYS:HG2	2.17	0.45
4:x:99:MET:HE2	4:x:108:ILE:HG23	1.98	0.45
2:A0:356:ASN:OD1	2:A0:357:TYR:N	2.50	0.44
3:A1:22:GLU:OE2	3:A1:81:PHE:HB2	2.17	0.44
3:A1:100:ASN:HB3	3:A1:103:LYS:HB2	1.99	0.44
3:A1:122:LYS:HE3	3:A1:122:LYS:HB3	1.75	0.44
2:A6:318:MET:HE3	2:A6:318:MET:HB3	1.92	0.44
2:B0:306:ASP:HB3	2:B0:309:HIS:CE1	2.52	0.44
3:B1:238:CYS:HB3	3:B1:318:ARG:NH1	2.32	0.44
2:B2:154:LEU:CD1	2:B2:166:LYS:HD2	2.47	0.44
2:B2:234:VAL:HG21	2:B2:302:MET:HE1	1.98	0.44
2:B4:240:ALA:O	2:B4:356:ASN:ND2	2.49	0.44
2:B4:285:GLN:HG2	2:B8:56:THR:HA	1.99	0.44
2:B6:123:ARG:HH12	2:B6:160:ASP:CG	2.25	0.44
2:B8:188:VAL:HG23	2:B8:189:LEU:HD12	1.99	0.44
2:C0:1:MET:N	2:C0:129:CYS:SG	2.75	0.44
3:C3:192:LEU:HD21	3:C3:199:VAL:HG11	1.99	0.44
3:C3:403:MET:HA	3:C3:403:MET:HE2	1.98	0.44
2:C4:175:PRO:HG3	2:C4:304:LYS:HG2	1.98	0.44
3:C5:239:CYS:SG	3:C5:248:SER:N	2.83	0.44
3:C5:259:PRO:HB2	3:C5:260:PHE:CD1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C8:337:THR:O	2:C8:339:ARG:NH1	2.49	0.44
2:D2:181:VAL:HG22	3:D3:256:ASN:HD22	1.82	0.44
2:D2:191:THR:HG21	2:D2:425:LEU:HD13	1.99	0.44
2:D2:259:LEU:HD21	2:D2:316:CYS:HB2	1.98	0.44
2:D4:7:ILE:HG22	2:D4:9:VAL:HG23	1.99	0.44
3:D9:135:ILE:HG22	3:D9:137:HIS:CD2	2.52	0.44
3:E1:19:LYS:NZ	3:E1:223:GLY:O	2.50	0.44
3:E1:122:LYS:HD3	3:E1:122:LYS:HA	1.78	0.44
2:E2:269:LEU:HD13	2:E2:301:MET:HE2	1.99	0.44
2:E4:217:LEU:HD21	2:E4:367:ASP:CG	2.42	0.44
3:E5:112:LEU:HD23	3:E5:112:LEU:O	2.16	0.44
2:E6:222:PRO:HD2	3:E7:324:LYS:HB3	1.98	0.44
2:E6:265:ILE:HG23	2:E6:432:TYR:CZ	2.51	0.44
2:E8:172:TRP:N	2:E8:204:LEU:O	2.42	0.44
4:f:36:ILE:HG13	4:f:37:GLN:H	1.82	0.44
4:j:63:ILE:HD13	4:l:16:ARG:HD2	1.97	0.44
4:k:129:MET:C	4:m:159:TYR:HE2	2.24	0.44
4:n:84:LYS:HD3	4:n:84:LYS:HA	1.84	0.44
2:A0:35:GLN:O	2:A0:35:GLN:HG3	2.17	0.44
3:A5:176:SER:HB2	2:A6:349:THR:HB	1.99	0.44
3:A9:258:ILE:HD11	3:A9:266:PHE:HZ	1.83	0.44
3:B1:114:ASP:OD1	3:B1:114:ASP:N	2.49	0.44
3:B1:149:THR:OG1	3:B1:191:GLN:OE1	2.22	0.44
2:B2:156:ARG:HA	2:B2:159:VAL:HG12	1.99	0.44
2:B4:178:SER:OG	2:B4:179:THR:N	2.49	0.44
2:B8:269:LEU:CD1	2:B8:303:ALA:HB3	2.45	0.44
2:B8:286:LEU:O	2:B8:373:ARG:NH1	2.40	0.44
3:C1:211:CYS:HA	3:C1:215:LEU:HB2	1.99	0.44
3:C5:219:THR:HB	2:C6:324:VAL:CG1	2.28	0.44
3:C7:330:MET:HB3	3:C7:349:MET:HG3	1.99	0.44
3:C7:417:ASP:O	3:C7:420:SER:OG	2.26	0.44
2:C8:282:TYR:O	2:D2:60:LYS:NZ	2.33	0.44
2:D8:422:ARG:HD2	2:D8:422:ARG:HA	1.61	0.44
2:E8:53:PHE:HB3	2:E8:61:HIS:HB3	1.99	0.44
3:E9:70:PRO:HD2	2:F0:2:ARG:HH11	1.81	0.44
3:E9:167:PHE:CE1	3:E9:233:MET:HG2	2.51	0.44
4:c:75:LEU:O	4:c:170:VAL:HA	2.17	0.44
4:g:8:SER:HB2	4:g:147:HIS:HA	1.99	0.44
4:q:2:SER:O	4:q:2:SER:OG	2.34	0.44
4:q:53:GLY:HA2	4:q:62:VAL:HG21	1.99	0.44
4:u:7:ALA:N	4:u:161:TYR:OH	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:v:127:ALA:HB1	4:x:157:PRO:HG3	1.99	0.44
2:A0:402:ARG:HD3	2:A0:402:ARG:HA	1.69	0.44
2:A4:103:PHE:H	2:A4:408:TYR:HE1	1.66	0.44
2:A4:134:GLY:CA	2:A4:164:LYS:HZ3	2.31	0.44
2:A8:27:GLU:OE2	2:A8:243:ARG:NH2	2.49	0.44
3:B1:230:SER:HA	3:B1:233:MET:HG2	1.99	0.44
3:B5:8:GLN:OE1	3:B5:17:GLY:HA3	2.18	0.44
3:B5:66:MET:HE3	3:B5:147:MET:CE	2.47	0.44
3:B5:330:MET:HE3	3:B5:349:MET:HB3	1.98	0.44
2:C2:141:VAL:HG21	2:C2:172:TRP:CZ3	2.52	0.44
3:D3:23:VAL:HG11	3:D3:230:SER:HB2	2.00	0.44
3:D3:266:PHE:HB3	3:D3:368:VAL:HG13	1.99	0.44
2:D4:174:SER:HB2	2:D4:177:VAL:O	2.18	0.44
2:D4:176:GLN:HG3	2:D4:177:VAL:HG23	1.99	0.44
3:D7:112:LEU:HA	3:D7:112:LEU:HD12	1.83	0.44
3:D9:64:ILE:HD12	3:D9:119:VAL:HG12	1.99	0.44
2:E6:306:ASP:HB3	2:E6:309:HIS:CE1	2.53	0.44
2:E6:417:GLU:HA	2:E6:420:GLU:HG3	1.99	0.44
2:F0:176:GLN:CD	3:F1:331:LEU:HD21	2.42	0.44
2:F0:195:LEU:HD21	2:F0:428:LEU:HD22	1.99	0.44
3:F1:42:LEU:HD11	3:F1:243:PRO:HG3	1.99	0.44
4:e:96:TYR:HA	4:e:108:ILE:HD11	1.99	0.44
4:f:110:ILE:O	4:f:131:TRP:HB2	2.17	0.44
4:j:15:ARG:O	4:j:19:GLU:HG3	2.17	0.44
4:l:139:PRO:O	4:l:143:ILE:HG12	2.18	0.44
4:p:170:VAL:HG23	4:p:183:LEU:HB2	2.00	0.44
4:q:64:PRO:HD2	4:q:67:HIS:CE1	2.53	0.44
4:q:106:GLN:NE2	4:s:6:PHE:HZ	2.16	0.44
4:r:191:GLU:HG3	4:r:194:ARG:HB3	2.00	0.44
4:t:110:ILE:O	4:t:131:TRP:HB2	2.15	0.44
4:t:153:GLU:HG3	4:t:154:TYR:H	1.83	0.44
4:x:191:GLU:HB2	4:x:195:ALA:HB2	1.98	0.44
2:A0:222:PRO:HD2	3:A1:324:LYS:HB3	1.99	0.44
3:A1:13:GLY:HA2	3:A1:16:ILE:HG22	1.99	0.44
2:A6:265:ILE:HG23	2:A6:432:TYR:CZ	2.53	0.44
3:A9:73:MET:HE1	3:A9:90:PHE:CG	2.53	0.44
3:B1:91:VAL:HG21	3:B1:116:VAL:HG12	1.98	0.44
3:B1:237:THR:HA	3:B1:240:LEU:HD13	2.00	0.44
2:B6:397:LEU:HD23	2:B6:397:LEU:HA	1.89	0.44
2:C4:362:VAL:HG11	2:C4:369:ALA:C	2.43	0.44
3:C5:174:LYS:HZ2	2:C6:333:ALA:HB1	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C6:181:VAL:CG2	3:C7:256:ASN:OD1	2.66	0.44
2:C8:217:LEU:HD13	2:C8:277:SER:HB3	1.98	0.44
3:C9:103:LYS:O	3:C9:108:GLU:HB3	2.17	0.44
3:C9:220:PRO:HD2	2:D0:326:LYS:HG3	1.99	0.44
3:E1:13:GLY:HA2	3:E1:136:THR:HG22	1.99	0.44
2:E4:27:GLU:HB3	2:E4:361:THR:HG21	1.99	0.44
2:E6:8:HIS:HE1	2:E6:21:TRP:HE1	1.64	0.44
3:E9:207:LEU:HB3	3:E9:225:LEU:HD22	1.99	0.44
3:F1:33:THR:O	3:F1:58:ARG:NH2	2.51	0.44
4:h:170:VAL:HG23	4:h:183:LEU:HB2	1.98	0.44
4:q:67:HIS:HA	4:s:23:LEU:HD11	2.00	0.44
4:x:106:GLN:OE1	4:y:6:PHE:CE1	2.71	0.44
1:19:256:LEU:HA	2:E6:26:LEU:CD2	2.48	0.44
2:A0:363:VAL:HG23	2:A0:366:GLY:HA3	2.00	0.44
2:A2:205:ASP:OD1	2:A2:206:ASN:N	2.50	0.44
3:A7:113:ILE:HG13	3:A7:117:LEU:HD23	2.00	0.44
2:A8:53:PHE:HB3	2:A8:61:HIS:HB3	1.99	0.44
2:A8:116:ASP:N	2:A8:116:ASP:OD1	2.49	0.44
3:B3:175:VAL:HG11	2:B4:329:ASN:ND2	2.32	0.44
2:C4:269:LEU:CD1	2:C4:384:ILE:HD11	2.47	0.44
2:C4:279:GLU:OE1	4:m:197:LEU:HD12	2.16	0.44
2:C8:28:HIS:CE1	2:C8:243:ARG:HH11	2.35	0.44
2:D0:103:PHE:HD2	2:D0:413:MET:HE1	1.82	0.44
2:D0:306:ASP:HB3	2:D0:309:HIS:CE1	2.53	0.44
3:D1:371:SER:OG	3:D1:372:THR:N	2.50	0.44
2:D4:32:PRO:HB3	2:D4:83:TYR:CD1	2.53	0.44
3:D5:310:TYR:CD1	3:D5:371:SER:HB2	2.52	0.44
2:D6:176:GLN:HB3	3:D7:331:LEU:HD11	1.99	0.44
2:D8:207:GLU:HA	2:D8:210:TYR:HB2	1.98	0.44
3:D9:178:THR:OG1	3:D9:181:GLU:OE2	2.35	0.44
3:E1:33:THR:HG23	3:E1:35:THR:HG23	2.00	0.44
3:E5:181:GLU:HB2	3:E5:182:PRO:HD3	1.99	0.44
3:E5:219:THR:O	3:E5:219:THR:OG1	2.34	0.44
2:E8:80:THR:HG22	2:E8:84:ARG:HH21	1.82	0.44
2:F0:319:TYR:HB3	2:F0:323:VAL:HG11	1.99	0.44
4:a:92:LEU:CD1	4:a:196:LEU:HD11	2.48	0.44
4:j:126:ARG:NH1	4:j:133:SER:HB3	2.32	0.44
4:k:96:TYR:HH	4:m:6:PHE:HE2	1.62	0.44
4:t:127:ALA:O	4:v:157:PRO:HB2	2.17	0.44
2:B0:12:ALA:CB	2:B0:140:ALA:HB2	2.47	0.44
2:B2:319:TYR:N	2:B2:354:GLY:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B7:11:GLN:HA	3:B7:72:THR:HG21	1.99	0.44
2:B8:70:LEU:HD12	2:B8:99:ALA:HB2	2.00	0.44
2:C0:328:VAL:HG11	2:C0:355:ILE:HD11	1.99	0.44
2:C2:9:VAL:HG22	2:C2:68:LEU:HB2	1.98	0.44
2:C2:276:ILE:HG23	2:C2:281:ALA:HB2	2.00	0.44
2:C2:286:LEU:O	2:C2:373:ARG:NH1	2.51	0.44
2:C4:210:TYR:CD1	2:C4:227:LEU:HD21	2.53	0.44
3:C9:99:ASN:HD21	3:C9:178:THR:HG22	1.82	0.44
3:D3:317:PHE:HB3	3:D3:321:MET:SD	2.57	0.44
3:D9:6:HIS:HD2	3:D9:134:GLN:NE2	2.15	0.44
2:E0:100:ALA:O	3:E1:255:VAL:HG11	2.17	0.44
2:E0:352:LYS:HD3	2:E0:352:LYS:HA	1.76	0.44
2:F0:274:PRO:HG3	2:F0:286:LEU:HD13	1.98	0.44
3:F1:151:LEU:HD12	3:F1:151:LEU:HA	1.88	0.44
4:l:75:LEU:HG	4:l:173:ILE:HD13	1.98	0.44
4:u:78:ALA:HB3	4:u:112:PHE:HE1	1.82	0.44
1:8:257:PRO:CG	2:C0:29:GLY:HA2	2.47	0.44
2:A0:9:VAL:HG22	2:A0:68:LEU:HD22	1.98	0.44
2:A2:199:ASP:OD1	2:A2:200:VAL:N	2.50	0.44
3:A3:316:MET:HE2	3:A3:366:THR:HG23	1.99	0.44
2:A4:241:SER:OG	2:A4:250:VAL:O	2.24	0.44
2:B0:90:GLU:HB2	2:B0:121:ARG:NH2	2.33	0.44
3:B3:219:THR:CB	2:B4:324:VAL:HG21	2.42	0.44
3:B3:282:ARG:O	3:B7:55:THR:HG22	2.18	0.44
3:B7:209:ASP:O	3:B7:213:ARG:HG2	2.17	0.44
3:B9:101:TRP:H	3:B9:398:TYR:HE1	1.65	0.44
2:C0:210:TYR:HE1	2:C0:227:LEU:HD11	1.82	0.44
3:C1:149:THR:O	3:C1:191:GLN:NE2	2.51	0.44
3:C1:279:GLN:HG3	3:C1:282:ARG:NH1	2.32	0.44
2:C2:207:GLU:HA	2:C2:210:TYR:HB2	2.00	0.44
2:C2:346:TRP:HZ2	2:C2:435:VAL:HG13	1.82	0.44
2:C6:132:LEU:HD13	2:C6:132:LEU:HA	1.82	0.44
3:C7:200:GLN:HB3	3:C7:266:PHE:HB2	1.99	0.44
2:C8:7:ILE:HG23	2:C8:66:VAL:HG23	2.00	0.44
2:C8:70:LEU:HD12	2:C8:145:THR:HG22	1.98	0.44
3:C9:121:ARG:NH2	3:C9:158:GLU:OE2	2.50	0.44
2:D2:272:TYR:HD2	2:D2:275:ILE:HG12	1.83	0.44
3:D7:130:LEU:HD22	3:D7:162:ARG:HG3	2.00	0.44
2:D8:1:MET:N	2:D8:3:GLU:OE2	2.40	0.44
2:D8:19:ALA:HB3	2:D8:228:ASN:HB3	1.99	0.44
2:D8:393:HIS:O	2:D8:397:LEU:HD13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E0:394:LYS:HE3	3:E1:346:PRO:CG	2.48	0.44
2:E4:406:HIS:HA	2:E4:409:VAL:HG12	2.00	0.44
2:F0:113:GLU:OE1	2:F0:113:GLU:N	2.45	0.44
4:e:9:PRO:HA	4:e:12:VAL:HG22	2.00	0.44
4:e:117:ARG:HG2	4:e:117:ARG:NH1	2.32	0.44
4:k:116:ASP:OD1	4:k:117:ARG:N	2.47	0.44
4:q:175:SER:HA	4:q:206:PHE:CE1	2.52	0.44
4:t:96:TYR:CE2	4:v:6:PHE:CD2	3.06	0.44
5:w:83:PHE:O	5:w:87:ARG:HB2	2.17	0.44
2:A0:292:THR:HG21	2:A0:331:ALA:HB1	1.99	0.44
2:A0:343:PHE:HZ	2:A0:351:PHE:CE1	2.35	0.44
3:A1:415:MET:HE2	3:A1:415:MET:HB3	1.81	0.44
2:A2:277:SER:OG	2:A2:278:ALA:N	2.50	0.44
3:A5:44:LEU:HD11	3:A5:59:PHE:CZ	2.53	0.44
3:A5:54:ALA:HB3	3:A5:58:ARG:HG2	2.00	0.44
3:A9:259:PRO:HB2	3:A9:260:PHE:CD1	2.52	0.44
2:B0:286:LEU:CD1	2:B0:371:VAL:HG23	2.48	0.44
3:B3:68:LEU:HG	3:B3:147:MET:HE2	2.00	0.44
3:B7:326:VAL:O	3:B7:330:MET:HG2	2.18	0.44
2:B8:391:MET:O	2:B8:395:PHE:N	2.50	0.44
3:C1:219:THR:HB	2:C2:324:VAL:HG11	1.99	0.44
2:C2:432:TYR:O	2:C2:436:GLY:N	2.51	0.44
2:C4:210:TYR:CE1	2:C4:227:LEU:HD11	2.53	0.44
3:D3:303:SER:HB3	3:D3:377:MET:HE3	1.99	0.44
3:D5:96:GLY:N	3:D5:108:GLU:OE2	2.50	0.44
3:E1:268:ILE:HD12	3:E1:368:VAL:HG22	1.99	0.44
3:E3:113:ILE:HD11	3:E3:151:LEU:HB2	1.99	0.44
2:E4:217:LEU:HD21	2:E4:367:ASP:OD1	2.17	0.44
2:E4:278:ALA:HA	2:E4:369:ALA:HB2	2.00	0.44
3:E7:86:ARG:HG2	3:E7:88:ASP:H	1.83	0.44
2:E8:181:VAL:HG11	2:E8:404:PHE:CE1	2.52	0.44
4:b:69:LYS:CB	4:d:38:LEU:HD11	2.48	0.44
4:b:89:LEU:HB3	4:b:90:PRO:HD3	2.00	0.44
4:c:97:ARG:CG	4:e:161:TYR:CZ	3.01	0.44
4:f:71:LYS:HG3	4:h:39:PRO:HG3	2.00	0.44
4:h:75:LEU:HD23	4:h:111:ILE:HB	2.00	0.44
4:h:105:ASN:CG	4:j:39:PRO:HG2	2.43	0.44
4:p:106:GLN:HB2	4:r:42:TYR:OH	2.17	0.44
4:q:88:LEU:HD22	4:q:185:ILE:HG21	1.99	0.44
1:19:241:PHE:HE1	3:E7:356:ILE:CG2	2.31	0.44
2:A0:210:TYR:CG	3:A1:324:LYS:HD3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A1:12:CYS:HB3	3:A1:138:SER:HB2	2.00	0.44
2:A4:115:VAL:O	2:A4:119:LEU:HD23	2.18	0.44
2:A4:135:PHE:CE2	2:A4:157:LEU:HD12	2.52	0.44
3:A5:95:THR:OG1	3:A5:96:GLY:N	2.51	0.44
2:A8:277:SER:OG	2:A8:278:ALA:N	2.48	0.44
3:B1:239:CYS:SG	3:B1:248:SER:N	2.90	0.44
3:B7:282:ARG:HB2	3:B7:282:ARG:NH2	2.33	0.44
2:C0:70:LEU:HD21	2:C0:149:LEU:HD22	1.99	0.44
2:C0:166:LYS:HE3	2:C0:166:LYS:HB2	1.90	0.44
3:C1:211:CYS:SG	3:C1:220:PRO:HB3	2.57	0.44
3:C5:69:GLU:OE2	2:C6:2:ARG:NH1	2.50	0.44
3:C9:16:ILE:HD11	3:C9:229:VAL:HG21	2.00	0.44
3:C9:220:PRO:HD2	2:D0:326:LYS:CG	2.48	0.44
2:D2:137:MET:HE3	2:D2:137:MET:HB2	1.92	0.44
3:D3:19:LYS:HE2	3:D3:19:LYS:HB2	1.75	0.44
2:D4:5:ILE:HD13	2:D4:64:ARG:HB3	1.99	0.44
3:D9:6:HIS:HE1	3:D9:8:GLN:HE21	1.64	0.44
2:E0:329:ASN:HA	2:E0:332:VAL:HG12	1.99	0.44
3:E3:253:LEU:HD11	3:E3:368:VAL:HG21	1.99	0.44
2:E4:178:SER:OG	2:E4:180:ALA:O	2.35	0.44
2:E4:210:TYR:CZ	3:E5:323:THR:O	2.71	0.44
2:E4:309:HIS:NE2	2:E4:386:GLU:OE1	2.41	0.44
3:E9:69:GLU:CD	2:F0:2:ARG:HH12	2.23	0.44
3:E9:311:LEU:HD12	3:E9:342:VAL:HG11	2.00	0.44
2:F0:65:CYS:O	2:F0:91:GLN:HG3	2.17	0.44
2:F0:107:HIS:NE2	2:F0:151:CYS:SG	2.84	0.44
4:f:152:LYS:HG3	4:f:153:GLU:N	2.32	0.44
4:o:95:TYR:CZ	4:o:99:MET:HE3	2.53	0.44
4:q:181:GLN:HE22	4:q:199:TRP:HA	1.83	0.44
2:A0:228:ASN:HA	2:A0:231:ILE:HG22	1.99	0.43
2:A0:301:MET:HE1	2:A0:304:LYS:N	2.33	0.43
2:A6:296:PHE:CE2	2:A6:335:ILE:HG21	2.53	0.43
2:A8:138:PHE:CZ	2:A8:235:ILE:HD13	2.52	0.43
2:A8:139:ASN:N	2:A8:139:ASN:OD1	2.51	0.43
3:B5:67:ASP:OD1	3:B5:68:LEU:N	2.49	0.43
3:B5:287:PRO:HA	3:B5:290:THR:HG22	2.00	0.43
3:B7:294:PHE:HZ	3:B7:349:MET:HE1	1.83	0.43
2:C2:51:THR:HG21	2:C2:243:ARG:HG2	2.00	0.43
2:C2:241:SER:OG	2:C2:250:VAL:O	2.25	0.43
3:C7:273:LEU:HD23	3:C7:273:LEU:HA	1.77	0.43
2:D0:221:ARG:HH22	4:p:190:GLU:HG3	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D4:116:ASP:OD1	2:D4:116:ASP:N	2.49	0.43
3:D5:180:VAL:HG22	3:D5:183:TYR:HB2	2.00	0.43
2:E2:107:HIS:NE2	2:E2:151:CYS:SG	2.87	0.43
2:E4:221:ARG:HH11	2:E4:221:ARG:HD2	1.67	0.43
3:E5:403:MET:HB2	3:E5:403:MET:HE3	1.81	0.43
2:E6:111:GLY:O	2:E6:115:VAL:HG23	2.17	0.43
2:E6:286:LEU:O	2:E6:373:ARG:NH1	2.44	0.43
2:E8:325:PRO:HA	2:E8:328:VAL:HG12	1.99	0.43
3:F1:149:THR:HA	3:F1:152:ILE:HD12	2.00	0.43
3:F1:237:THR:O	3:F1:241:ARG:NH1	2.51	0.43
4:c:96:TYR:HA	4:c:108:ILE:HD11	1.99	0.43
4:l:63:ILE:HG22	4:n:16:ARG:CD	2.47	0.43
1:12:254:LYS:HE3	2:D2:364:PRO:O	2.18	0.43
1:21:242:ASN:HD22	4:y:163:SER:HB2	1.83	0.43
3:A5:316:MET:HE3	3:A5:316:MET:HB3	1.86	0.43
2:A8:172:TRP:HB3	2:A8:205:ASP:OD1	2.18	0.43
3:B1:181:GLU:HB2	3:B1:182:PRO:HD3	2.00	0.43
2:B4:141:VAL:O	2:B4:147:SER:OG	2.36	0.43
2:B4:212:ILE:HD11	2:B4:300:SER:HA	2.00	0.43
3:B5:13:GLY:HA2	3:B5:16:ILE:HG22	2.00	0.43
2:B6:73:THR:HA	3:B7:46:ARG:HH11	1.83	0.43
2:B8:274:PRO:HB2	2:B8:276:ILE:HG12	2.00	0.43
2:C4:93:ILE:HD12	2:C4:114:ILE:HG13	1.99	0.43
2:C8:262:TYR:HB3	2:C8:263:PRO:HD2	1.99	0.43
2:D0:224:TYR:H	3:D1:245:GLN:HE22	1.66	0.43
3:D1:164:MET:HE3	3:D1:164:MET:HB2	1.82	0.43
3:D5:67:ASP:HB3	3:D5:73:MET:HE2	1.99	0.43
2:D6:64:ARG:HG2	2:D6:125:LEU:HD11	1.99	0.43
2:D8:398:MET:HE2	3:D9:345:ILE:HG23	2.00	0.43
3:D9:87:PRO:HA	3:D9:90:PHE:HD1	1.83	0.43
2:E0:394:LYS:HB3	3:E1:346:PRO:HG3	2.00	0.43
2:E4:109:THR:HG23	2:E4:411:GLU:OE1	2.19	0.43
3:E5:293:MET:HE3	3:E5:293:MET:HB3	1.81	0.43
2:E6:32:PRO:HG3	2:E6:83:TYR:HE1	1.83	0.43
2:E6:177:VAL:HG22	3:E7:331:LEU:HD13	2.00	0.43
2:F0:274:PRO:HG2	2:F0:371:VAL:HG11	1.99	0.43
4:a:68:LEU:HD21	4:a:111:ILE:HD11	2.00	0.43
4:b:97:ARG:HH12	4:d:6:PHE:CB	2.06	0.43
4:k:139:PRO:O	4:k:143:ILE:HG12	2.18	0.43
4:v:59:ASN:ND2	4:x:143:ILE:CD1	2.81	0.43
4:x:111:ILE:HD13	4:x:132:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:21:240:PRO:HG3	4:y:154:TYR:CZ	2.53	0.43
2:A0:259:LEU:HD21	2:A0:316:CYS:HB2	2.00	0.43
3:A3:113:ILE:HA	3:A3:116:VAL:HG22	2.00	0.43
3:A3:187:LEU:HD11	3:A3:408:PHE:CE1	2.52	0.43
2:A4:28:HIS:CD2	2:A4:53:PHE:HE2	2.36	0.43
3:B1:192:LEU:HD21	3:B1:199:VAL:HG21	2.00	0.43
3:B7:109:GLY:HA2	3:B7:147:MET:HE2	1.99	0.43
3:B9:67:ASP:OD1	3:B9:68:LEU:N	2.51	0.43
2:C0:70:LEU:HD12	2:C0:99:ALA:HB2	2.00	0.43
2:C0:278:ALA:HA	2:C0:369:ALA:HB2	2.00	0.43
2:C4:14:ILE:O	2:C4:18:ASN:N	2.48	0.43
2:C4:396:ASP:N	2:C4:396:ASP:OD1	2.50	0.43
2:D2:188:VAL:HG22	2:D2:425:LEU:HD22	1.99	0.43
3:D3:385:PHE:HE2	3:D3:412:GLU:HB2	1.83	0.43
3:D5:141:GLY:O	3:D5:145:SER:OG	2.31	0.43
3:D5:274:THR:HG22	3:D5:282:ARG:HH21	1.83	0.43
2:E0:12:ALA:HB3	2:E0:140:ALA:HB2	2.00	0.43
2:E0:100:ALA:HB2	3:E1:251:ARG:HD2	1.99	0.43
2:E0:306:ASP:OD1	2:E0:308:ARG:NH1	2.51	0.43
3:E3:113:ILE:HA	3:E3:116:VAL:HG12	2.00	0.43
2:E6:280:LYS:NZ	2:F0:89:PRO:HB2	2.34	0.43
3:E7:8:GLN:OE1	3:E7:17:GLY:HA3	2.19	0.43
2:E8:306:ASP:N	2:E8:386:GLU:OE2	2.51	0.43
3:E9:27:GLU:O	3:E9:359:LYS:NZ	2.35	0.43
3:E9:70:PRO:HD2	2:F0:2:ARG:NH1	2.33	0.43
3:E9:206:ALA:HB2	3:E9:302:ALA:HB2	2.01	0.43
4:b:78:ALA:HB3	4:b:112:PHE:CE1	2.50	0.43
4:e:105:ASN:OD1	4:e:106:GLN:N	2.51	0.43
4:f:14:LYS:HD3	4:f:47:LEU:HD12	2.01	0.43
4:k:111:ILE:HD13	4:k:132:LEU:HB2	2.00	0.43
4:n:183:LEU:HA	4:n:184:PRO:HD3	1.77	0.43
4:r:201:TRP:CD1	4:r:201:TRP:H	2.36	0.43
4:x:63:ILE:HG22	4:y:16:ARG:HG3	1.99	0.43
4:x:154:TYR:HE1	4:x:158:THR:HG22	1.83	0.43
1:21:256:LEU:HD21	2:F0:31:GLN:HA	2.00	0.43
1:6:240:PRO:CG	4:i:154:TYR:HB3	2.49	0.43
3:A1:47:ILE:HG12	3:A1:51:TYR:HB2	2.00	0.43
3:A1:392:LYS:CE	3:A1:395:LEU:HD22	2.48	0.43
3:A3:167:PHE:CE2	3:A3:233:MET:HG3	2.54	0.43
3:A3:414:ASN:HD22	3:A3:414:ASN:C	2.26	0.43
2:A4:340:THR:HG23	2:A4:341:ILE:HG13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A7:216:LYS:HE2	3:A7:216:LYS:HA	2.00	0.43
2:A8:262:TYR:HB2	2:A8:265:ILE:HD12	1.99	0.43
3:A9:36:TYR:CD2	3:A9:44:LEU:HD12	2.54	0.43
2:B6:250:VAL:CG1	2:B6:318:MET:HE1	2.49	0.43
3:C5:293:MET:HB2	3:C5:293:MET:HE2	1.70	0.43
2:C6:151:CYS:SG	2:C6:193:SER:OG	2.52	0.43
3:C9:164:MET:HE3	3:C9:164:MET:HB2	1.82	0.43
3:C9:252:LYS:O	3:C9:256:ASN:ND2	2.34	0.43
3:D3:12:CYS:HB3	3:D3:138:SER:HB2	2.01	0.43
2:D4:261:PRO:HG3	2:D4:313:MET:CE	2.49	0.43
2:E0:179:THR:O	2:E0:180:ALA:HB2	2.18	0.43
3:E5:396:HIS:HA	3:E5:399:THR:HG22	2.00	0.43
3:E7:362:LYS:HD2	3:E7:363:MET:HB2	2.01	0.43
3:F1:216:LYS:HA	3:F1:216:LYS:HD3	1.84	0.43
4:j:191:GLU:OE1	4:j:194:ARG:NH2	2.51	0.43
4:n:167:VAL:HA	4:n:168:PRO:HA	1.76	0.43
4:v:96:TYR:OH	4:x:6:PHE:CE2	2.69	0.43
4:y:19:GLU:HB3	4:y:40:PRO:HD2	2.00	0.43
1:2:245:SER:HB2	3:A9:42:LEU:CD2	2.47	0.43
2:A2:91:GLN:HA	2:A2:121:ARG:NH1	2.33	0.43
3:A3:180:VAL:O	3:A3:184:ASN:ND2	2.51	0.43
2:A4:309:HIS:NE2	2:A4:386:GLU:OE1	2.51	0.43
3:A7:73:MET:HB3	3:A7:73:MET:HE3	1.75	0.43
3:B1:103:LYS:HB2	3:B1:108:GLU:OE1	2.19	0.43
3:B9:68:LEU:HD23	3:B9:112:LEU:HD13	2.00	0.43
3:C3:73:MET:HB3	3:C3:77:ARG:NH2	2.33	0.43
3:C3:316:MET:HE1	3:C3:368:VAL:HG13	2.01	0.43
3:C7:90:PHE:HB3	3:C7:92:PHE:CE1	2.53	0.43
3:C9:281:TYR:HE1	3:D3:58:ARG:CZ	2.30	0.43
2:D0:285:GLN:HB3	2:D4:57:GLY:HA2	2.00	0.43
3:D1:281:TYR:HA	3:D5:58:ARG:HD3	2.00	0.43
2:D4:265:ILE:HD11	2:D4:435:VAL:HG21	2.01	0.43
3:D5:139:LEU:HD12	3:D5:170:PHE:HE1	1.83	0.43
3:D5:318:ARG:HD3	3:D5:358:PRO:HD3	1.99	0.43
2:E4:132:LEU:O	2:E4:164:LYS:NZ	2.52	0.43
2:E4:306:ASP:HB3	2:E4:309:HIS:CE1	2.54	0.43
2:E6:115:VAL:HG12	2:E6:156:ARG:HE	1.83	0.43
2:E6:179:THR:O	2:E6:180:ALA:HB2	2.18	0.43
3:E7:391:ARG:HD2	3:E7:391:ARG:HA	1.74	0.43
4:b:115:LEU:HD21	4:b:145:LYS:CE	2.48	0.43
4:d:28:LYS:HD3	4:d:28:LYS:HA	1.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:h:100:ASN:HB3	4:j:6:PHE:CE1	2.52	0.43
4:k:55:LEU:HD22	4:k:111:ILE:HD12	2.00	0.43
4:x:70:GLY:O	4:y:39:PRO:HD3	2.18	0.43
1:7:256:LEU:HD11	2:B8:31:GLN:N	2.34	0.43
3:A7:404:ASP:OD1	3:A7:405:GLU:N	2.51	0.43
2:B4:223:THR:HG1	3:B5:245:GLN:CD	2.13	0.43
2:B8:36:MET:HA	2:B8:37:PRO:HD3	1.83	0.43
3:C1:287:PRO:O	3:C1:291:GLN:HG2	2.19	0.43
2:C4:2:ARG:HB3	2:C4:133:GLN:NE2	2.31	0.43
2:C4:268:MET:SD	2:C4:380:ASN:ND2	2.92	0.43
3:C5:10:GLY:O	3:C5:14:ASN:ND2	2.52	0.43
3:C9:363:MET:HB2	3:C9:363:MET:HE2	1.74	0.43
2:D2:75:VAL:HG11	2:D2:94:SER:HB3	2.01	0.43
2:D2:121:ARG:HD2	2:D2:121:ARG:HA	1.82	0.43
3:D9:287:PRO:HA	3:D9:290:THR:HG22	2.00	0.43
3:D9:290:THR:HG21	3:D9:329:GLN:HB3	2.00	0.43
2:E0:216:ASN:HB3	2:E0:275:ILE:O	2.19	0.43
3:E1:19:LYS:HD2	3:E1:227:HIS:ND1	2.33	0.43
3:E3:213:ARG:HH21	3:E3:216:LYS:HE3	1.83	0.43
2:E4:238:LEU:HD13	2:E4:318:MET:HE3	2.01	0.43
3:E5:156:ARG:HA	3:E5:156:ARG:HD2	1.81	0.43
3:E5:379:LYS:O	3:E5:383:ASP:N	2.47	0.43
4:e:110:ILE:O	4:e:131:TRP:HB2	2.18	0.43
4:f:41:ASN:O	4:f:45:MET:HG2	2.19	0.43
4:h:11:ASN:HD22	4:h:14:LYS:HE2	1.83	0.43
4:i:115:LEU:HD21	4:i:145:LYS:HD3	2.01	0.43
4:x:20:GLU:HG3	4:x:24:MET:HE3	2.00	0.43
1:2:248:ARG:HH22	2:A8:82:THR:N	2.17	0.43
1:20:241:PHE:HE1	3:E9:356:ILE:HG21	1.84	0.43
1:21:257:PRO:O	2:F0:29:GLY:HA3	2.19	0.43
3:A1:7:VAL:HG11	3:A1:151:LEU:HD23	2.01	0.43
3:A1:104:GLY:HA3	3:A1:146:GLY:HA3	2.01	0.43
3:A1:220:PRO:HD2	2:A2:326:LYS:NZ	2.33	0.43
2:A8:68:LEU:HD23	2:A8:93:ILE:HB	1.99	0.43
2:A8:160:ASP:OD1	2:A8:161:TYR:N	2.51	0.43
2:A8:356:ASN:OD1	2:A8:357:TYR:N	2.51	0.43
3:B1:5:VAL:HG23	3:B1:130:LEU:HD11	1.99	0.43
2:B2:208:ALA:HB2	2:B2:304:LYS:HB2	2.00	0.43
2:B4:356:ASN:OD1	2:B4:357:TYR:N	2.52	0.43
2:B6:119:LEU:HG	2:B6:156:ARG:HG2	1.99	0.43
2:B8:280:LYS:HA	2:B8:280:LYS:HD3	1.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C0:275:ILE:HD12	2:C0:368:LEU:HD11	2.01	0.43
3:C7:165:GLU:HG3	3:C7:198:GLU:HG3	2.00	0.43
3:C9:65:LEU:HB3	3:C9:73:MET:HE2	2.01	0.43
3:D1:66:MET:CE	3:D1:151:LEU:HD22	2.38	0.43
2:D2:297:GLU:HA	2:D2:298:PRO:HD3	1.89	0.43
3:D3:247:ASN:O	3:D3:252:LYS:HE2	2.18	0.43
2:D6:154:LEU:HB3	2:D6:197:HIS:HB3	2.01	0.43
3:D9:6:HIS:CE1	3:D9:8:GLN:HE21	2.37	0.43
3:E1:272:PRO:HG3	3:E1:284:LEU:HD11	2.01	0.43
3:E3:218:THR:HG23	3:E3:219:THR:HG23	2.01	0.43
2:E4:269:LEU:HD23	2:E4:303:ALA:HB3	2.01	0.43
2:E6:222:PRO:HD2	3:E7:324:LYS:CB	2.49	0.43
2:E6:345:ASP:OD1	2:E6:346:TRP:N	2.52	0.43
2:F0:51:THR:HG23	2:F0:52:PHE:CD2	2.53	0.43
4:d:18:ASN:CB	4:d:45:MET:HG2	2.48	0.43
4:d:170:VAL:HG22	4:d:185:ILE:HD11	2.00	0.43
4:k:198:ARG:NH1	4:k:198:ARG:CG	2.81	0.43
4:p:50:PHE:HB3	4:p:55:LEU:HD23	2.01	0.43
4:q:92:LEU:HD12	4:q:92:LEU:HA	1.88	0.43
5:w:36:LEU:HD23	5:w:72:ILE:HB	2.01	0.43
4:y:175:SER:HA	4:y:206:PHE:CE1	2.54	0.43
2:A0:3:GLU:HB2	2:A0:64:ARG:HH11	1.84	0.43
2:A2:313:MET:HE1	2:A2:435:VAL:HG11	2.00	0.43
3:A5:216:LYS:HA	3:A5:216:LYS:HD2	1.81	0.43
3:A9:67:ASP:OD1	3:A9:68:LEU:N	2.50	0.43
3:B7:121:ARG:NH1	3:B7:158:GLU:OE2	2.41	0.43
2:C0:168:ASN:HD22	2:C0:198:THR:HG21	1.84	0.43
3:C3:154:LYS:HB2	3:C3:154:LYS:HE3	1.72	0.43
2:C4:356:ASN:OD1	2:C4:357:TYR:N	2.51	0.43
2:C8:306:ASP:HB3	2:C8:309:HIS:CE1	2.54	0.43
2:C8:399:TYR:OH	2:C8:415:GLU:OE1	2.30	0.43
3:D1:282:ARG:NH1	3:D1:292:GLN:OE1	2.52	0.43
2:D4:343:PHE:CE2	2:D4:350:GLY:HA3	2.54	0.43
2:D8:388:PHE:HB2	2:D8:429:GLU:OE2	2.18	0.43
3:D9:296:ALA:HB2	3:D9:305:PRO:HD2	2.01	0.43
3:E7:67:ASP:OD1	3:E7:68:LEU:N	2.50	0.43
2:F0:154:LEU:HG	2:F0:197:HIS:HB3	2.00	0.43
3:F1:30:ILE:HD12	3:F1:51:TYR:HE2	1.82	0.43
4:a:105:ASN:ND2	4:c:37:GLN:HE22	2.16	0.43
4:d:106:GLN:HG3	4:f:6:PHE:CE1	2.54	0.43
4:f:8:SER:HA	4:f:9:PRO:HD3	1.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:f:154:TYR:HE1	4:f:158:THR:HG22	1.83	0.43
4:h:14:LYS:HD3	4:h:47:LEU:CD1	2.45	0.43
4:v:14:LYS:HD2	4:v:47:LEU:HD23	2.01	0.43
1:6:247:TYR:OH	2:B6:81:GLY:HA3	2.18	0.43
2:A0:306:ASP:HB3	2:A0:309:HIS:CE1	2.54	0.43
3:A3:67:ASP:OD1	3:A3:68:LEU:N	2.47	0.43
3:A5:139:LEU:HD12	3:A5:170:PHE:CE1	2.54	0.43
3:A9:208:TYR:HD1	2:B0:326:LYS:HZ2	1.65	0.43
2:B2:432:TYR:HD1	2:B2:432:TYR:HA	1.72	0.43
2:B4:250:VAL:HG13	2:B4:318:MET:HE1	2.00	0.43
3:B5:6:HIS:HE2	3:B5:8:GLN:HB3	1.84	0.43
2:B6:192:HIS:ND1	2:B6:424:ASP:OD2	2.49	0.43
2:B6:238:LEU:HD12	2:B6:238:LEU:HA	1.83	0.43
3:B7:375:GLN:HE22	3:B7:419:VAL:HA	1.84	0.43
2:C0:283:HIS:CD2	2:C4:60:LYS:NZ	2.87	0.43
3:C3:184:ASN:OD1	3:C3:398:TYR:OH	2.32	0.43
2:C4:105:ARG:HG2	2:C4:411:GLU:HG2	2.01	0.43
2:C4:121:ARG:HH12	2:C4:124:LYS:HE3	1.84	0.43
2:C4:277:SER:C	2:C4:369:ALA:HB2	2.43	0.43
3:C5:177:ASP:OD2	3:C5:178:THR:HG23	2.19	0.43
2:C8:28:HIS:NE2	2:C8:243:ARG:HD2	2.34	0.43
3:C9:167:PHE:HZ	3:C9:236:VAL:HG11	1.83	0.43
2:D0:394:LYS:CG	3:D1:346:PRO:HG3	2.46	0.43
3:D1:53:GLU:OE2	3:D1:55:THR:N	2.52	0.43
3:D3:65:LEU:HB3	3:D3:73:MET:HE2	2.00	0.43
3:D3:68:LEU:HA	3:D3:93:GLY:HA3	2.01	0.43
3:D5:404:ASP:OD1	3:D5:405:GLU:N	2.51	0.43
3:D7:167:PHE:CE1	3:D7:233:MET:HG2	2.54	0.43
2:E2:244:PHE:HB2	2:E2:356:ASN:HD21	1.83	0.43
3:E5:1:MET:N	3:E5:128:ASP:OD2	2.41	0.43
2:E6:195:LEU:HD21	2:E6:428:LEU:HD22	2.01	0.43
2:F0:174:SER:HB3	2:F0:177:VAL:O	2.18	0.43
4:e:48:ILE:O	4:e:48:ILE:HG13	2.17	0.43
4:f:56:LYS:HE2	4:f:56:LYS:HB2	1.87	0.43
4:m:79:ASP:HB2	4:m:167:VAL:HG21	2.01	0.43
2:A0:285:GLN:OE1	2:A4:57:GLY:HA2	2.19	0.43
2:A4:28:HIS:CE1	2:A4:243:ARG:HD2	2.53	0.43
2:A4:96:LYS:HZ2	3:A5:128:ASP:CG	2.27	0.43
3:A5:248:SER:HA	3:A5:252:LYS:HD2	2.00	0.43
2:A8:394:LYS:HD3	3:A9:346:PRO:CG	2.49	0.43
3:B1:5:VAL:CG2	3:B1:130:LEU:HD11	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B2:90:GLU:HG2	2:B2:121:ARG:HH21	1.84	0.43
3:B3:207:LEU:HB3	3:B3:225:LEU:HD22	2.00	0.43
2:B4:338:LYS:HG2	2:B4:340:THR:HG22	2.00	0.43
3:B9:103:LYS:HA	3:B9:107:THR:HG22	2.00	0.43
3:B9:321:MET:HE3	3:B9:363:MET:SD	2.58	0.43
2:C0:188:VAL:HG12	2:C0:425:LEU:HD13	2.01	0.43
2:C0:256:GLN:O	2:C0:260:VAL:HG22	2.19	0.43
3:C3:220:PRO:HB2	3:C3:225:LEU:HD21	2.01	0.43
3:C3:257:LEU:HD21	3:C3:314:SER:HB2	2.01	0.43
2:C4:141:VAL:HG11	2:C4:172:TRP:CE3	2.54	0.43
2:C4:298:PRO:HA	2:C4:301:MET:HE1	2.01	0.43
3:C7:318:ARG:C	3:C7:321:MET:HE1	2.44	0.43
2:D0:283:HIS:HA	2:D4:60:LYS:CE	2.48	0.43
3:D1:248:SER:HA	3:D1:252:LYS:HG3	2.01	0.43
3:D1:334:GLN:HE22	3:D1:347:ASN:HA	1.84	0.43
3:D5:1:MET:N	3:D5:128:ASP:OD2	2.44	0.43
3:D5:316:MET:HE3	3:D5:316:MET:HB2	1.89	0.43
2:D6:319:TYR:CD2	2:D6:375:VAL:HG22	2.54	0.43
3:D7:211:CYS:HB2	2:D8:326:LYS:NZ	2.33	0.43
3:D7:281:TYR:CE1	3:E1:58:ARG:NE	2.87	0.43
3:D9:8:GLN:NE2	3:D9:17:GLY:HA3	2.34	0.43
3:D9:14:ASN:HD22	3:D9:72:THR:HG23	1.84	0.43
3:D9:124:ALA:HB1	3:D9:130:LEU:HD22	2.00	0.43
3:E1:84:LEU:HD12	3:E1:84:LEU:HA	1.90	0.43
2:E4:194:LEU:O	2:E4:198:THR:HG22	2.18	0.43
3:E9:167:PHE:CZ	3:E9:233:MET:HG2	2.54	0.43
3:E9:349:MET:C	3:E9:350:LYS:HD2	2.43	0.43
3:F1:198:GLU:OE2	3:F1:200:GLN:NE2	2.46	0.43
4:f:71:LYS:HE3	4:f:106:GLN:OE1	2.19	0.43
4:i:63:ILE:HA	4:k:16:ARG:HD2	2.01	0.43
4:j:71:LYS:HZ2	4:j:106:GLN:HB2	1.84	0.43
4:t:51:PRO:HD2	4:t:54:SER:OG	2.19	0.43
2:A0:71:GLU:HB3	2:A0:98:ASP:HB2	2.01	0.42
2:A0:315:CYS:HB2	2:A0:351:PHE:CD1	2.54	0.42
3:A1:49:VAL:HG11	3:A1:241:ARG:HG2	2.01	0.42
2:A2:282:TYR:CE2	2:A6:60:LYS:NZ	2.84	0.42
3:A5:91:VAL:HG21	3:A5:116:VAL:HG22	2.01	0.42
2:A6:133:GLN:NE2	2:A6:133:GLN:HA	2.32	0.42
3:A7:200:GLN:HG2	3:A7:268:ILE:HD11	2.01	0.42
3:A9:225:LEU:HD21	2:B0:326:LYS:NZ	2.34	0.42
3:B1:60:VAL:HA	3:B1:61:PRO:HD3	1.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B1:155:VAL:HG13	3:B1:164:MET:HE1	2.01	0.42
2:B2:28:HIS:CE1	2:B2:243:ARG:HD2	2.53	0.42
3:B3:98:GLY:O	2:B4:257:THR:HG21	2.18	0.42
3:B3:219:THR:CA	2:B4:324:VAL:HG21	2.49	0.42
2:B4:296:PHE:CE1	2:B4:377:MET:HE1	2.53	0.42
3:B7:282:ARG:HB2	3:B7:282:ARG:CZ	2.49	0.42
2:B8:262:TYR:HB3	2:B8:263:PRO:HD2	2.01	0.42
2:B8:265:ILE:HG23	2:B8:432:TYR:CE1	2.54	0.42
2:C0:262:TYR:HB2	2:C0:265:ILE:HG22	2.01	0.42
3:C1:280:GLN:OE1	3:C1:280:GLN:HA	2.18	0.42
3:C5:219:THR:CB	2:C6:324:VAL:HG11	2.29	0.42
2:C6:217:LEU:HD21	2:C6:367:ASP:OD2	2.19	0.42
2:D4:52:PHE:HD2	2:D4:243:ARG:HD3	1.84	0.42
2:D4:203:MET:HE2	2:D4:267:PHE:HB3	2.01	0.42
3:D5:66:MET:CG	3:D5:147:MET:HE2	2.49	0.42
2:D6:269:LEU:CD1	2:D6:384:ILE:HD11	2.48	0.42
2:E4:98:ASP:OD1	2:E4:99:ALA:N	2.52	0.42
3:E5:174:LYS:HA	3:E5:174:LYS:HD2	1.68	0.42
3:E7:44:LEU:HG	3:E7:44:LEU:O	2.18	0.42
4:e:2:SER:N	4:e:11:ASN:OD1	2.52	0.42
4:g:184:PRO:HB2	4:g:189:LEU:HB2	2.00	0.42
4:l:12:VAL:HG12	4:l:15:ARG:NH1	2.34	0.42
4:n:148:PHE:O	4:n:149:ARG:HG2	2.19	0.42
4:r:57:ASN:HA	4:r:132:LEU:HD23	2.01	0.42
4:x:106:GLN:CD	4:y:6:PHE:HZ	2.24	0.42
1:18:250:GLU:HB2	2:E4:229:ARG:HH22	1.84	0.42
1:3:247:TYR:OH	2:B0:81:GLY:HA3	2.19	0.42
3:A1:229:VAL:O	3:A1:233:MET:HB2	2.19	0.42
3:A1:299:MET:HE1	3:A1:367:PHE:CE2	2.54	0.42
2:A2:133:GLN:NE2	2:A2:251:ASP:HB3	2.34	0.42
3:A7:206:ALA:HB2	3:A7:302:ALA:HB2	2.00	0.42
2:B4:277:SER:OG	2:B4:278:ALA:N	2.52	0.42
3:B5:8:GLN:HE21	3:B5:65:LEU:HD11	1.84	0.42
2:B6:392:ASP:CG	2:B6:422:ARG:HH22	2.23	0.42
2:B8:285:GLN:CG	2:B8:285:GLN:O	2.67	0.42
2:C0:265:ILE:HG13	2:C0:432:TYR:CZ	2.54	0.42
2:C4:3:GLU:HG3	2:C4:51:THR:HA	2.01	0.42
3:C5:397:TRP:CH2	2:C6:260:VAL:HB	2.54	0.42
3:D1:128:ASP:OD1	3:D1:129:CYS:N	2.42	0.42
3:D1:268:ILE:HG23	3:D1:300:MET:SD	2.59	0.42
3:D3:112:LEU:HD23	3:D3:147:MET:HE1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D3:383:ASP:HA	3:D3:386:THR:HG22	2.01	0.42
2:D4:151:CYS:SG	2:D4:193:SER:OG	2.64	0.42
3:D7:186:THR:HG22	3:D7:411:ALA:HB1	2.02	0.42
3:D7:383:ASP:HA	3:D7:386:THR:HG22	2.01	0.42
2:E0:88:HIS:HB3	2:E0:91:GLN:HB2	2.01	0.42
3:E3:165:GLU:OE1	3:E3:200:GLN:NE2	2.52	0.42
3:E5:67:ASP:OD1	3:E5:68:LEU:N	2.53	0.42
2:E8:269:LEU:CD2	2:E8:384:ILE:HD11	2.49	0.42
3:F1:205:GLU:HA	3:F1:208:TYR:HB2	2.00	0.42
4:b:53:GLY:HA2	4:b:62:VAL:HG21	2.00	0.42
4:d:74:ALA:HB2	4:d:172:VAL:HG12	2.01	0.42
4:l:185:ILE:HD13	4:l:195:ALA:HB3	2.01	0.42
4:r:101:GLU:OE2	4:t:161:TYR:OH	2.31	0.42
4:x:130:PRO:HB2	4:y:7:ALA:CB	2.48	0.42
4:y:12:VAL:HG12	4:y:15:ARG:NH1	2.34	0.42
1:1:247:TYR:HH	2:A6:82:THR:H	1.54	0.42
1:10:257:PRO:HG3	2:C8:26:LEU:O	2.19	0.42
1:13:253:ALA:CB	2:D4:32:PRO:HG3	2.48	0.42
1:18:241:PHE:CZ	3:E5:356:ILE:HD12	2.54	0.42
1:4:244:GLN:CD	3:B3:320:ARG:HH12	2.26	0.42
2:A0:185:TYR:HE2	2:A0:398:MET:HE2	1.83	0.42
2:A2:137:MET:HB3	2:A2:168:ASN:HA	2.00	0.42
2:A2:143:GLY:O	2:A2:186:ASN:ND2	2.53	0.42
2:A8:273:ALA:HA	2:A8:274:PRO:HA	1.86	0.42
3:A9:54:ALA:C	3:A9:56:GLY:H	2.27	0.42
3:A9:166:THR:HG23	3:A9:199:VAL:HG13	2.02	0.42
2:B2:69:ASP:OD1	2:B2:70:LEU:N	2.52	0.42
3:B3:152:ILE:HG12	3:B3:164:MET:HE1	2.00	0.42
2:B4:69:ASP:OD1	2:B4:70:LEU:N	2.52	0.42
2:B4:210:TYR:CE2	3:B5:327:ASP:OD2	2.72	0.42
2:B8:278:ALA:HA	2:B8:369:ALA:HB2	2.00	0.42
2:C0:206:ASN:O	2:C0:210:TYR:N	2.51	0.42
2:C0:223:THR:HG23	2:C0:225:THR:HG22	2.02	0.42
3:C3:103:LYS:HB3	3:C3:103:LYS:HE2	1.84	0.42
3:C5:167:PHE:CE2	3:C5:233:MET:HG2	2.55	0.42
2:C6:135:PHE:HB2	2:C6:166:LYS:HA	2.00	0.42
2:C8:352:LYS:HA	2:C8:352:LYS:HD3	1.78	0.42
3:C9:190:HIS:HB2	3:C9:414:ASN:HD21	1.84	0.42
2:D0:298:PRO:HB3	2:D0:307:PRO:HD2	2.01	0.42
2:D2:10:GLY:HA2	2:D2:145:THR:HG23	2.02	0.42
2:D4:261:PRO:HG3	2:D4:313:MET:HE2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D5:32:PRO:HD3	3:D5:81:PHE:CZ	2.53	0.42
3:D5:310:TYR:HD1	3:D5:371:SER:HB2	1.84	0.42
2:E0:195:LEU:HD13	2:E0:264:ARG:HH21	1.85	0.42
2:E0:208:ALA:O	2:E0:212:ILE:HG12	2.19	0.42
2:E0:220:GLU:O	3:E1:325:GLU:OE2	2.38	0.42
2:E0:274:PRO:HG3	2:E0:286:LEU:HD12	2.01	0.42
3:E1:273:LEU:H	3:E1:292:GLN:HE22	1.67	0.42
3:E3:68:LEU:HD23	3:E3:112:LEU:HD22	2.01	0.42
2:E4:221:ARG:HD2	2:E4:221:ARG:HA	1.54	0.42
2:E4:230:LEU:HD22	2:E4:275:ILE:HD12	2.01	0.42
3:E5:211:CYS:SG	3:E5:220:PRO:HB3	2.58	0.42
2:E8:2:ARG:NE	2:E8:133:GLN:HE21	2.15	0.42
3:F1:30:ILE:HD12	3:F1:51:TYR:CE2	2.55	0.42
4:e:110:ILE:HB	4:e:131:TRP:CG	2.55	0.42
4:g:95:TYR:CZ	4:g:99:MET:HE3	2.55	0.42
4:l:79:ASP:OD2	4:l:152:LYS:NZ	2.42	0.42
1:0:254:LYS:HA	1:0:255:PRO:HD3	1.88	0.42
2:A0:152:LEU:HD21	2:A0:156:ARG:HH11	1.85	0.42
2:A6:271:SER:OG	2:A6:377:MET:HB3	2.19	0.42
2:A8:298:PRO:HG2	2:A8:308:ARG:NH2	2.34	0.42
2:A8:298:PRO:HB3	2:A8:307:PRO:HD2	2.02	0.42
2:A8:394:LYS:HD3	3:A9:346:PRO:HG3	2.01	0.42
3:A9:318:ARG:HG2	3:A9:354:CYS:HB3	2.01	0.42
3:A9:415:MET:O	3:A9:419:VAL:HG23	2.18	0.42
3:B1:281:TYR:CD2	3:B5:87:PRO:HD3	2.54	0.42
2:C0:133:GLN:HG3	2:C0:252:VAL:HG22	2.00	0.42
2:C0:338:LYS:HZ3	2:C0:339:ARG:H	1.67	0.42
2:C0:406:HIS:CD2	3:C1:261:PRO:HD3	2.55	0.42
3:C1:281:TYR:HA	3:C5:58:ARG:HD3	2.00	0.42
2:C2:187:SER:O	2:C2:191:THR:OG1	2.34	0.42
2:C2:209:ILE:HG22	2:C2:227:LEU:HG	2.01	0.42
3:C7:318:ARG:O	3:C7:321:MET:HE1	2.20	0.42
2:C8:250:VAL:HG13	2:C8:255:PHE:HE1	1.84	0.42
3:C9:135:ILE:HD12	3:C9:152:ILE:HG12	2.01	0.42
3:C9:281:TYR:HE1	3:D3:58:ARG:NH2	2.17	0.42
3:D3:10:GLY:HA2	3:D3:143:THR:HG23	2.01	0.42
3:D3:101:TRP:HE3	3:D3:403:MET:HE1	1.84	0.42
3:D3:155:VAL:HG13	3:D3:164:MET:CE	2.49	0.42
2:D6:183:GLU:HA	2:D6:186:ASN:HD22	1.84	0.42
2:D6:297:GLU:HA	2:D6:298:PRO:HD3	1.94	0.42
3:D9:239:CYS:SG	3:D9:248:SER:N	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D9:301:CYS:SG	3:D9:302:ALA:N	2.93	0.42
2:E0:229:ARG:NH1	2:E0:229:ARG:CG	2.83	0.42
2:E0:283:HIS:ND1	2:E4:60:LYS:CE	2.72	0.42
2:E2:265:ILE:HG23	2:E2:432:TYR:CE1	2.55	0.42
2:E4:4:VAL:HG21	2:E4:136:LEU:HD13	2.00	0.42
2:E8:238:LEU:HD12	2:E8:238:LEU:HA	1.83	0.42
3:E9:293:MET:SD	3:E9:367:PHE:HB2	2.59	0.42
2:F0:12:ALA:HB3	2:F0:140:ALA:HB2	2.01	0.42
2:F0:319:TYR:HB2	2:F0:355:ILE:HG12	2.00	0.42
4:e:99:MET:HB2	4:e:99:MET:HE3	1.57	0.42
4:m:97:ARG:NH1	4:m:101:GLU:OE1	2.52	0.42
4:o:18:ASN:HD21	4:o:46:ASP:H	1.66	0.42
4:v:67:HIS:CB	4:x:19:GLU:OE2	2.67	0.42
4:x:63:ILE:HG22	4:y:16:ARG:CG	2.50	0.42
1:0:254:LYS:H	1:0:254:LYS:HG2	1.43	0.42
1:19:250:GLU:HB3	2:E6:229:ARG:HH21	1.83	0.42
2:A0:224:TYR:O	2:A0:228:ASN:ND2	2.52	0.42
2:A0:242:LEU:HD21	2:A0:251:ASP:HA	2.00	0.42
3:A1:326:VAL:O	3:A1:330:MET:HG2	2.19	0.42
2:A4:98:ASP:O	2:A4:105:ARG:NH1	2.49	0.42
3:A5:7:VAL:HG11	3:A5:151:LEU:HD21	2.01	0.42
3:A9:167:PHE:CD1	3:A9:200:GLN:HB2	2.54	0.42
3:B5:314:SER:OG	3:B5:315:ALA:N	2.51	0.42
3:B9:15:GLN:O	3:B9:226:ASN:ND2	2.53	0.42
3:C1:49:VAL:HG11	3:C1:241:ARG:HG2	2.02	0.42
3:C1:102:ALA:HB1	3:C1:401:GLU:HB2	2.01	0.42
3:C1:283:ALA:O	3:C1:288:GLU:HG2	2.18	0.42
2:C6:135:PHE:HB2	2:C6:166:LYS:HG2	2.01	0.42
2:C6:191:THR:OG1	2:C6:425:LEU:HD21	2.20	0.42
2:C6:325:PRO:HA	2:C6:328:VAL:HB	2.00	0.42
2:C6:328:VAL:HG21	2:C6:355:ILE:HD11	2.02	0.42
3:D5:113:ILE:O	3:D5:117:LEU:HB2	2.19	0.42
2:D6:4:VAL:HG12	2:D6:133:GLN:HB3	2.01	0.42
3:D7:117:LEU:HD23	3:D7:121:ARG:NH2	2.33	0.42
3:D9:128:ASP:OD1	3:D9:128:ASP:N	2.50	0.42
2:E0:132:LEU:HB3	2:E0:164:LYS:HZ3	1.84	0.42
2:E4:97:GLU:CG	3:E5:129:CYS:SG	3.08	0.42
3:E5:186:THR:HG22	3:E5:415:MET:CE	2.46	0.42
3:E5:260:PHE:HE2	3:E5:425:TYR:CE2	2.37	0.42
3:E5:286:VAL:HG23	3:E5:287:PRO:HD3	2.00	0.42
3:E7:139:LEU:HB2	3:E7:171:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F0:320:ARG:HG2	2:F0:360:PRO:HG3	2.01	0.42
4:i:185:ILE:HD13	4:i:185:ILE:HA	1.86	0.42
4:l:110:ILE:O	4:l:131:TRP:HB2	2.19	0.42
4:n:201:TRP:CD1	4:n:201:TRP:H	2.37	0.42
4:o:18:ASN:ND2	4:o:46:ASP:H	2.18	0.42
4:p:115:LEU:HD23	4:p:115:LEU:HA	1.85	0.42
5:w:38:PHE:HB2	5:w:130:LEU:HB3	2.00	0.42
4:y:139:PRO:O	4:y:143:ILE:HG12	2.19	0.42
2:A2:306:ASP:HB3	2:A2:309:HIS:CE1	2.55	0.42
2:A6:203:MET:HE2	2:A6:267:PHE:HB3	2.02	0.42
2:A6:296:PHE:HE2	2:A6:335:ILE:HG21	1.84	0.42
2:A8:212:ILE:HG12	2:A8:275:ILE:HD11	2.00	0.42
2:B2:422:ARG:HD2	2:B2:422:ARG:HA	1.92	0.42
3:B5:357:PRO:HB2	3:B5:361:LEU:O	2.19	0.42
2:B6:285:GLN:HB3	2:C0:57:GLY:HA3	2.01	0.42
3:B9:165:GLU:OE2	3:B9:200:GLN:NE2	2.51	0.42
3:B9:192:LEU:HD21	3:B9:199:VAL:HG21	2.01	0.42
3:B9:383:ASP:HA	3:B9:386:THR:HG22	2.01	0.42
3:C1:97:ALA:HB3	3:C1:143:THR:HG22	2.02	0.42
2:C4:76:ASP:OD1	2:C4:77:GLU:N	2.52	0.42
2:C6:340:THR:HG23	2:C6:341:ILE:HG13	2.02	0.42
2:D0:273:ALA:HA	2:D0:274:PRO:HA	1.85	0.42
2:D6:98:ASP:OD1	2:D6:99:ALA:N	2.52	0.42
2:D6:430:LYS:HZ2	2:D6:430:LYS:HG2	1.63	0.42
2:E0:65:CYS:SG	2:E0:66:VAL:N	2.92	0.42
2:E0:163:LYS:HA	2:E0:163:LYS:CE	2.49	0.42
3:E1:388:MET:HG2	2:E2:346:TRP:O	2.19	0.42
3:E3:122:LYS:HD3	3:E3:122:LYS:HA	1.84	0.42
3:E3:289:LEU:HD23	3:E3:289:LEU:HA	1.85	0.42
2:E4:181:VAL:HG21	3:E5:312:THR:HG22	2.01	0.42
2:E6:335:ILE:HG23	2:E6:341:ILE:HD11	2.01	0.42
3:E7:216:LYS:HD3	3:E7:216:LYS:HA	1.89	0.42
3:E7:276:ARG:NH2	3:E7:279:GLN:OE1	2.44	0.42
4:e:10:LEU:HG	4:e:143:ILE:HG22	2.01	0.42
4:h:63:ILE:HG23	4:h:67:HIS:ND1	2.35	0.42
4:m:10:LEU:HB2	4:m:147:HIS:CE1	2.55	0.42
4:n:150:VAL:HG13	4:n:165:THR:HG23	2.02	0.42
4:r:12:VAL:HG12	4:r:15:ARG:NH1	2.34	0.42
4:r:77:PHE:HE2	4:r:171:ILE:HD12	1.84	0.42
1:18:254:LYS:NZ	2:E4:364:PRO:HD2	2.35	0.42
2:A0:209:ILE:HA	2:A0:212:ILE:HB	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A2:103:PHE:CD2	2:A2:413:MET:HE1	2.55	0.42
3:A3:135:ILE:HD13	3:A3:152:ILE:HD11	2.02	0.42
2:A4:282:TYR:O	2:A8:60:LYS:HE2	2.20	0.42
2:A8:205:ASP:O	2:A8:209:ILE:HG13	2.20	0.42
2:B0:30:ILE:HG21	2:B0:61:HIS:HD2	1.84	0.42
2:B0:73:THR:OG1	3:B1:2:ARG:NH2	2.52	0.42
3:B5:200:GLN:HB3	3:B5:268:ILE:HD11	2.02	0.42
2:B6:276:ILE:HB	2:B6:280:LYS:HB3	2.00	0.42
3:B7:63:ALA:O	3:B7:89:ASN:ND2	2.52	0.42
2:B8:274:PRO:HG3	2:B8:286:LEU:HD12	2.00	0.42
2:C0:357:TYR:HD1	2:C0:357:TYR:HA	1.76	0.42
3:C5:100:ASN:HB3	3:C5:103:LYS:HG2	2.01	0.42
2:C6:76:ASP:OD2	3:C7:46:ARG:NH1	2.49	0.42
2:C8:370:LYS:O	2:C8:370:LYS:HG3	2.18	0.42
3:C9:187:LEU:HD23	3:C9:187:LEU:HA	1.90	0.42
3:C9:309:ARG:NH1	3:C9:341:PHE:O	2.52	0.42
2:D4:324:VAL:HA	2:D4:325:PRO:HD3	1.90	0.42
3:D5:172:SER:HB3	3:D5:205:GLU:CG	2.48	0.42
3:D9:200:GLN:CG	3:D9:268:ILE:HD11	2.47	0.42
2:E0:269:LEU:HD22	2:E0:384:ILE:HD11	2.01	0.42
3:E3:349:MET:HE2	3:E3:349:MET:HB3	1.92	0.42
3:E5:20:PHE:HA	3:E5:230:SER:OG	2.19	0.42
2:E6:27:GLU:OE2	2:E6:320:ARG:NH2	2.52	0.42
3:E9:42:LEU:O	3:E9:42:LEU:HG	2.19	0.42
3:F1:292:GLN:O	3:F1:298:ASN:ND2	2.39	0.42
4:b:164:ARG:HG3	4:b:165:THR:HG23	2.02	0.42
4:f:110:ILE:HB	4:f:131:TRP:CG	2.55	0.42
4:i:9:PRO:HA	4:i:12:VAL:HG22	2.02	0.42
4:n:59:ASN:HD21	4:p:9:PRO:CB	2.26	0.42
4:o:73:VAL:HG12	4:o:109:GLU:HB3	2.02	0.42
4:p:100:ASN:ND2	4:r:6:PHE:CZ	2.88	0.42
4:s:70:GLY:HA3	4:u:38:LEU:C	2.35	0.42
4:s:176:ASP:OD1	4:s:176:ASP:N	2.52	0.42
1:20:245:SER:HB3	1:20:248:ARG:HD3	2.01	0.42
2:A0:240:ALA:HA	2:A0:243:ARG:HE	1.85	0.42
2:A6:125:LEU:HD23	2:A6:125:LEU:HA	1.90	0.42
2:A8:268:MET:HB3	2:A8:378:ILE:HG23	2.01	0.42
2:B6:282:TYR:HB3	2:B6:283:HIS:ND1	2.35	0.42
3:B7:141:GLY:O	3:B7:145:SER:OG	2.33	0.42
2:B8:65:CYS:SG	2:B8:66:VAL:N	2.93	0.42
2:B8:238:LEU:HD12	2:B8:238:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:377:MET:SD	2:C2:379:SER:OG	2.73	0.42
3:C5:73:MET:HE3	3:C5:92:PHE:HA	2.02	0.42
2:C6:179:THR:OG1	3:C7:246:LEU:HD21	2.20	0.42
3:C7:66:MET:HE2	3:C7:116:VAL:HG11	2.01	0.42
2:D2:108:TYR:O	2:D2:112:LYS:NZ	2.40	0.42
3:D3:100:ASN:ND2	3:D3:397:TRP:O	2.50	0.42
2:D4:172:TRP:CD1	2:D4:173:PRO:HD2	2.54	0.42
3:D9:107:THR:HG1	3:D9:108:GLU:CD	2.25	0.42
2:E0:282:TYR:HB2	2:E0:283:HIS:CD2	2.55	0.42
3:E7:349:MET:HB2	3:E7:349:MET:HE2	1.78	0.42
2:E8:345:ASP:OD1	2:E8:346:TRP:N	2.52	0.42
2:F0:60:LYS:HE3	2:F0:60:LYS:HB3	1.82	0.42
3:F1:256:ASN:ND2	3:F1:350:LYS:HG3	2.35	0.42
4:f:63:ILE:HD11	4:f:132:LEU:HD13	2.01	0.42
4:h:100:ASN:ND2	4:j:6:PHE:CE2	2.78	0.42
4:j:118:ASP:OD1	4:j:118:ASP:N	2.53	0.42
4:l:181:GLN:NE2	4:l:200:ASP:OD1	2.52	0.42
4:m:74:ALA:HB2	4:m:172:VAL:HG12	2.02	0.42
4:u:187:SER:OG	4:u:188:GLY:N	2.47	0.42
1:19:243:ALA:CB	3:E7:356:ILE:HA	2.49	0.42
1:6:247:TYR:CZ	2:B6:81:GLY:HA3	2.54	0.42
1:7:256:LEU:CD1	2:B8:31:GLN:HB3	2.49	0.42
3:A5:40:SER:HB3	3:A5:43:GLN:HG3	2.01	0.42
3:A9:320:ARG:HG3	3:A9:320:ARG:NH1	2.32	0.42
3:B1:27:GLU:OE2	3:B1:241:ARG:NH1	2.39	0.42
3:B3:31:ASP:HB3	3:B3:32:PRO:HD2	2.01	0.42
2:B6:339:ARG:HA	2:B6:339:ARG:HD2	1.67	0.42
3:B7:50:PHE:CD2	3:B7:241:ARG:HD3	2.55	0.42
3:B7:112:LEU:O	3:B7:112:LEU:HD23	2.20	0.42
3:B7:383:ASP:HA	3:B7:386:THR:HG22	2.01	0.42
2:B8:156:ARG:HH21	2:B8:156:ARG:HD2	1.60	0.42
2:C0:7:ILE:HG22	2:C0:9:VAL:HG23	2.01	0.42
2:C2:296:PHE:HD1	2:C2:377:MET:HE2	1.85	0.42
2:C2:324:VAL:HA	2:C2:325:PRO:HD3	1.91	0.42
3:C3:289:LEU:HD12	3:C3:365:VAL:CG1	2.48	0.42
2:D6:138:PHE:CZ	2:D6:235:ILE:HD12	2.47	0.42
2:D6:401:LYS:HD2	3:D7:344:TRP:CE3	2.55	0.42
3:D7:2:ARG:HH11	3:D7:240:LEU:HD22	1.84	0.42
2:E0:166:LYS:N	2:E0:199:ASP:OD2	2.50	0.42
2:E0:176:GLN:CB	3:E1:331:LEU:CD1	2.81	0.42
3:E1:156:ARG:NH1	3:E1:162:ARG:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E3:48:ASN:OD1	3:E3:48:ASN:N	2.53	0.42
3:E5:258:ILE:HD12	3:E5:264:HIS:HA	2.00	0.42
2:E6:174:SER:OG	2:E6:177:VAL:O	2.20	0.42
2:E6:258:ASN:HB3	2:E6:352:LYS:CE	2.48	0.42
2:E6:316:CYS:HA	2:E6:352:LYS:HB2	2.01	0.42
3:F1:398:TYR:HB3	3:F1:403:MET:HG3	2.02	0.42
4:e:105:ASN:HD22	4:g:37:GLN:HE21	1.67	0.42
4:e:175:SER:HA	4:e:206:PHE:CE1	2.55	0.42
4:h:10:LEU:HD21	4:h:49:LEU:HD11	2.00	0.42
4:v:71:LYS:CE	4:v:109:GLU:HG2	2.50	0.42
5:w:35:ALA:HB2	5:w:133:VAL:HG12	2.02	0.42
5:w:153:VAL:HA	5:w:156:ARG:HB2	2.01	0.42
1:10:254:LYS:H	1:10:254:LYS:HG2	1.46	0.42
2:A0:359:PRO:HA	2:A0:360:PRO:HD3	1.94	0.42
2:A2:204:LEU:HD23	2:A2:231:ILE:HD12	2.02	0.42
2:A4:3:GLU:OE1	2:A4:132:LEU:HD13	2.20	0.42
3:B1:156:ARG:HH21	3:B1:164:MET:HB2	1.85	0.42
3:B5:49:VAL:HG21	3:B5:241:ARG:HG2	2.02	0.42
3:B5:139:LEU:HA	3:B5:145:SER:HB3	2.01	0.42
2:B8:280:LYS:NZ	2:C2:89:PRO:HB2	2.35	0.42
2:C2:288:VAL:HA	2:C2:291:ILE:HG12	2.00	0.42
3:C5:313:ALA:HA	3:C5:369:GLY:HA2	2.02	0.42
3:C7:6:HIS:CD2	3:C7:134:GLN:HG3	2.54	0.42
3:D3:200:GLN:HB3	3:D3:268:ILE:HD11	2.00	0.42
2:D4:248:LEU:HD22	2:D4:354:GLY:HA2	2.02	0.42
2:D4:338:LYS:HB2	2:D4:338:LYS:HE3	1.87	0.42
3:D5:135:ILE:HB	3:D5:166:THR:HG22	2.01	0.42
2:D6:402:ARG:HH21	2:D6:402:ARG:HG2	1.85	0.42
3:D7:281:TYR:HE1	3:E1:58:ARG:HH21	1.65	0.42
3:D9:228:LEU:HD21	3:D9:273:LEU:HD21	2.01	0.42
2:E0:36:MET:HE3	2:E0:61:HIS:NE2	2.34	0.42
3:E1:51:TYR:HB3	3:E1:59:PHE:HB3	2.02	0.42
2:E2:36:MET:HE1	2:E2:49:PHE:CD2	2.55	0.42
2:E4:23:LEU:HD11	2:E4:361:THR:HG23	2.01	0.42
3:E5:3:GLU:HA	3:E5:49:VAL:HA	2.02	0.42
2:E6:12:ALA:HB3	2:E6:140:ALA:HB2	2.00	0.42
2:F0:173:PRO:HG2	2:F0:391:MET:HE1	2.02	0.42
2:F0:223:THR:OG1	2:F0:224:TYR:N	2.52	0.42
3:F1:20:PHE:HA	3:F1:230:SER:HB2	2.00	0.42
3:F1:258:ILE:O	3:F1:258:ILE:HG13	2.19	0.42
4:c:97:ARG:O	4:c:101:GLU:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:h:9:PRO:HB2	4:h:143:ILE:HD12	2.02	0.42
4:j:106:GLN:HG3	4:l:42:TYR:OH	2.20	0.42
4:k:189:LEU:HB3	4:k:191:GLU:OE1	2.20	0.42
4:m:183:LEU:HA	4:m:184:PRO:HD3	1.83	0.42
4:p:72:SER:OG	4:p:199:TRP:NE1	2.50	0.42
5:w:103:LYS:HA	5:w:103:LYS:HD2	1.84	0.42
1:11:241:PHE:HZ	3:D1:356:ILE:HG23	1.85	0.41
1:19:254:LYS:HD3	1:19:254:LYS:HA	1.91	0.41
1:3:248:ARG:HG3	3:B1:42:LEU:HD11	2.01	0.41
3:A5:201:VAL:HG11	3:A5:374:ILE:HD11	2.01	0.41
2:A8:384:ILE:HB	2:A8:432:TYR:CE2	2.55	0.41
3:A9:132:GLY:HA2	3:A9:162:ARG:HB3	2.02	0.41
2:B0:221:ARG:CB	3:B1:322:SER:CB	2.73	0.41
3:B5:117:LEU:HD12	3:B5:117:LEU:HA	1.84	0.41
3:B9:281:TYR:O	3:C3:54:ALA:HB1	2.20	0.41
2:C0:137:MET:HE2	2:C0:154:LEU:HD21	2.02	0.41
3:C5:121:ARG:NH1	3:C5:158:GLU:OE1	2.45	0.41
3:C9:77:ARG:HH21	3:C9:92:PHE:HZ	1.67	0.41
2:D0:189:LEU:HD11	2:D0:418:PHE:CE1	2.55	0.41
3:D3:219:THR:HB	2:D4:324:VAL:HG11	2.02	0.41
2:D4:69:ASP:OD1	2:D4:70:LEU:N	2.53	0.41
3:D7:282:ARG:HH12	3:D7:292:GLN:HG3	1.85	0.41
3:D7:317:PHE:CD1	3:D7:326:VAL:HG23	2.55	0.41
2:D8:105:ARG:O	2:D8:110:ILE:HG22	2.20	0.41
3:D9:200:GLN:CB	3:D9:268:ILE:HD11	2.49	0.41
2:E0:132:LEU:HB3	2:E0:164:LYS:NZ	2.34	0.41
3:E1:406:MET:HE2	3:E1:406:MET:HB2	1.88	0.41
2:E6:256:GLN:O	2:E6:260:VAL:HG22	2.20	0.41
3:E7:66:MET:HB3	3:E7:147:MET:HE1	2.02	0.41
3:E9:46:ARG:HG3	3:E9:49:VAL:HG13	2.00	0.41
3:E9:257:LEU:HD12	3:E9:266:PHE:HE1	1.85	0.41
2:F0:99:ALA:O	2:F0:105:ARG:HD3	2.20	0.41
4:c:130:PRO:HB3	4:e:159:TYR:CD2	2.55	0.41
4:d:126:ARG:HD3	4:d:133:SER:HB3	2.01	0.41
4:f:198:ARG:NH1	4:f:198:ARG:CG	2.83	0.41
4:g:15:ARG:O	4:g:19:GLU:HB3	2.19	0.41
4:i:63:ILE:CD1	4:k:16:ARG:HD2	2.33	0.41
4:l:154:TYR:HE1	4:l:158:THR:HG22	1.84	0.41
4:n:139:PRO:O	4:n:143:ILE:HG12	2.20	0.41
4:x:71:LYS:HE3	4:x:106:GLN:HG2	2.02	0.41
4:y:115:LEU:HG	4:y:145:LYS:HE3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:11:245:SER:OG	3:D1:42:LEU:CD2	2.59	0.41
1:18:247:TYR:CE2	2:E4:18:ASN:OD1	2.73	0.41
1:21:256:LEU:HD11	2:F0:31:GLN:N	2.35	0.41
1:23:257:PRO:HG2	2:C4:26:LEU:HD13	2.01	0.41
2:A0:210:TYR:HD1	2:A0:210:TYR:HA	1.74	0.41
2:A0:210:TYR:CE1	2:A0:227:LEU:HD21	2.51	0.41
2:A4:36:MET:HA	2:A4:37:PRO:HD3	1.76	0.41
2:A6:291:ILE:HD12	2:A6:375:VAL:HG23	2.01	0.41
2:A6:413:MET:HE2	2:A6:413:MET:HB3	1.57	0.41
2:B0:324:VAL:HA	2:B0:325:PRO:HD3	1.94	0.41
3:B1:248:SER:HA	3:B1:252:LYS:HG2	2.01	0.41
2:B6:345:ASP:OD1	2:B6:346:TRP:N	2.53	0.41
3:B7:105:HIS:CD2	3:B7:150:LEU:HD12	2.55	0.41
2:C2:172:TRP:CG	2:C2:173:PRO:HD2	2.55	0.41
2:C4:377:MET:SD	2:C4:379:SER:HB3	2.60	0.41
2:C6:231:ILE:HD13	2:C6:302:MET:CE	2.50	0.41
2:C8:205:ASP:O	2:C8:209:ILE:HG13	2.20	0.41
3:C9:23:VAL:HG11	3:C9:230:SER:HB2	2.01	0.41
2:D4:90:GLU:HB3	2:D4:121:ARG:HD3	2.01	0.41
3:D5:377:MET:O	3:D5:381:VAL:HG23	2.20	0.41
2:D8:99:ALA:O	2:D8:105:ARG:HD3	2.20	0.41
2:E0:189:LEU:HD11	2:E0:418:PHE:HE1	1.84	0.41
2:E0:219:ILE:HG21	2:E0:219:ILE:HD13	1.75	0.41
2:E0:311:LYS:NZ	2:E0:342:GLN:OE1	2.49	0.41
3:E7:113:ILE:HA	3:E7:116:VAL:HG12	2.02	0.41
2:F0:101:ASN:HB3	2:F0:182:VAL:HG21	2.01	0.41
4:g:187:SER:OG	4:g:188:GLY:N	2.50	0.41
4:j:48:ILE:HD12	4:j:48:ILE:HA	1.81	0.41
4:m:148:PHE:O	4:m:149:ARG:HG2	2.20	0.41
4:p:15:ARG:HG2	4:p:45:MET:HE1	2.01	0.41
4:r:8:SER:OG	4:r:11:ASN:ND2	2.53	0.41
4:r:9:PRO:HA	4:r:12:VAL:HG22	2.02	0.41
4:u:176:ASP:OD1	4:u:176:ASP:N	2.43	0.41
4:y:57:ASN:HB3	4:y:132:LEU:HD23	2.02	0.41
1:10:250:GLU:O	1:10:250:GLU:HG2	2.20	0.41
1:18:254:LYS:CB	2:E4:26:LEU:HD13	2.50	0.41
3:A5:262:ARG:HD3	3:A5:421:GLU:OE2	2.20	0.41
2:B0:259:LEU:HD11	2:B0:316:CYS:HB2	2.02	0.41
2:B4:66:VAL:HG21	2:B4:122:ILE:HD11	2.02	0.41
2:B4:185:TYR:CD2	2:B4:395:PHE:HE1	2.37	0.41
2:B4:240:ALA:HB1	2:B4:356:ASN:HD22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B4:397:LEU:HD23	2:B4:397:LEU:HA	1.92	0.41
3:B5:324:LYS:O	3:B5:328:GLU:N	2.45	0.41
3:B7:11:GLN:HG2	3:B7:12:CYS:N	2.34	0.41
2:B8:422:ARG:NH1	2:B8:426:ALA:HB2	2.35	0.41
2:C0:71:GLU:HB3	2:C0:98:ASP:HB3	2.02	0.41
3:C1:148:GLY:O	3:C1:152:ILE:HG13	2.21	0.41
3:C1:164:MET:H	3:C1:197:ASP:HB3	1.85	0.41
2:C2:214:ARG:HG3	3:C3:324:LYS:HZ2	1.84	0.41
3:C3:420:SER:O	3:C3:424:GLN:N	2.54	0.41
2:C6:282:TYR:CE2	4:n:201:TRP:HZ2	2.37	0.41
3:C7:28:HIS:NE2	3:C7:241:ARG:HD2	2.35	0.41
3:C9:347:ASN:OD1	3:C9:349:MET:HB3	2.20	0.41
2:D0:98:ASP:OD1	2:D0:99:ALA:N	2.53	0.41
2:D0:241:SER:HB2	2:D0:249:ASN:HB2	2.03	0.41
2:D0:259:LEU:HB3	2:D0:268:MET:HE3	2.01	0.41
3:D1:135:ILE:HD12	3:D1:152:ILE:HG12	2.03	0.41
2:D2:173:PRO:HG2	2:D2:391:MET:HE1	2.01	0.41
2:D4:394:LYS:HG2	3:D5:346:PRO:HG3	2.02	0.41
2:D8:392:ASP:OD1	2:D8:422:ARG:NH2	2.46	0.41
3:E1:131:GLN:OE1	3:E1:163:ILE:HD11	2.21	0.41
2:E2:336:LYS:HB2	2:E2:336:LYS:HE2	1.75	0.41
3:E5:213:ARG:HH12	3:E5:297:LYS:HB3	1.85	0.41
2:E8:274:PRO:HG2	2:E8:371:VAL:HG11	2.03	0.41
3:E9:47:ILE:HD12	3:E9:47:ILE:HA	1.96	0.41
4:i:106:GLN:CG	4:k:42:TYR:OH	2.68	0.41
4:m:10:LEU:HG	4:m:143:ILE:CG2	2.50	0.41
4:n:45:MET:HE3	4:n:45:MET:HB3	1.96	0.41
4:r:53:GLY:HA2	4:r:62:VAL:CG2	2.48	0.41
4:s:8:SER:HB2	4:s:147:HIS:HA	2.02	0.41
4:x:105:ASN:HB2	4:y:41:ASN:ND2	2.36	0.41
1:16:256:LEU:HD12	2:E0:29:GLY:HA2	1.98	0.41
3:A1:166:THR:OG1	3:A1:199:VAL:HG22	2.20	0.41
3:A1:252:LYS:O	3:A1:256:ASN:ND2	2.54	0.41
3:A1:299:MET:HE1	3:A1:367:PHE:HE2	1.85	0.41
2:A2:306:ASP:HB3	2:A2:309:HIS:HE1	1.84	0.41
3:A3:41:ASP:OD1	3:A3:41:ASP:N	2.54	0.41
3:A3:86:ARG:HA	3:A3:87:PRO:HD3	1.97	0.41
3:A5:178:THR:O	3:A5:181:GLU:HG2	2.20	0.41
3:A7:54:ALA:C	3:A7:56:GLY:H	2.29	0.41
3:A7:114:ASP:OD1	3:A7:115:SER:N	2.54	0.41
2:A8:157:LEU:HD23	2:A8:157:LEU:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A8:221:ARG:HA	3:A9:322:SER:OG	2.21	0.41
2:B0:3:GLU:HA	2:B0:51:THR:HA	2.03	0.41
3:B1:249:ASP:H	3:B1:252:LYS:CB	2.33	0.41
2:B4:208:ALA:HB2	2:B4:304:LYS:HB2	2.02	0.41
2:B4:311:LYS:H	2:B4:382:THR:CG2	2.33	0.41
2:B4:395:PHE:HD2	2:B4:422:ARG:HD2	1.85	0.41
3:B5:190:HIS:CE1	3:B5:414:ASN:HD22	2.39	0.41
3:B7:208:TYR:HB3	2:B8:326:LYS:CE	2.51	0.41
3:B9:256:ASN:ND2	3:B9:350:LYS:HD2	2.35	0.41
3:C1:117:LEU:CD1	3:C1:154:LYS:HG2	2.50	0.41
2:C2:219:ILE:HG22	2:C2:222:PRO:HD3	2.01	0.41
2:C2:223:THR:OG1	3:C3:245:GLN:OE1	2.28	0.41
2:C8:28:HIS:HE1	2:C8:243:ARG:HH11	1.68	0.41
3:C9:53:GLU:OE2	3:C9:54:ALA:N	2.53	0.41
2:D0:344:VAL:HG22	2:D0:345:ASP:N	2.35	0.41
2:E0:155:GLU:HG3	2:E0:197:HIS:NE2	2.36	0.41
2:E4:406:HIS:ND1	3:E5:261:PRO:HD3	2.35	0.41
3:E7:309:ARG:H	3:E7:372:THR:HG22	1.84	0.41
3:E9:156:ARG:HH22	3:E9:197:ASP:HB2	1.85	0.41
2:F0:313:MET:HE3	2:F0:346:TRP:HZ2	1.85	0.41
4:a:183:LEU:O	4:a:185:ILE:N	2.52	0.41
4:n:110:ILE:HB	4:n:131:TRP:CG	2.55	0.41
4:p:142:GLU:O	4:p:146:ARG:HG2	2.20	0.41
4:q:75:LEU:O	4:q:170:VAL:HA	2.21	0.41
4:q:99:MET:HE2	4:q:99:MET:HB3	1.99	0.41
4:s:2:SER:O	4:s:2:SER:OG	2.37	0.41
4:x:89:LEU:HB3	4:x:90:PRO:HD3	2.03	0.41
4:y:116:ASP:OD1	4:y:117:ARG:N	2.49	0.41
1:23:246:CYS:SG	3:C5:355:ASP:OD2	2.78	0.41
2:A0:264:ARG:HG3	2:A0:264:ARG:NH1	2.31	0.41
3:A1:257:LEU:HD21	3:A1:314:SER:HB2	2.02	0.41
2:A2:103:PHE:HD2	2:A2:413:MET:HE1	1.86	0.41
2:A4:11:GLN:HG3	2:A4:74:VAL:HG21	2.03	0.41
2:A4:28:HIS:HD2	2:A4:53:PHE:HE2	1.67	0.41
2:A4:71:GLU:CD	3:A5:247:ASN:HD21	2.28	0.41
2:A8:2:ARG:HG3	2:A8:51:THR:HG22	2.02	0.41
2:A8:36:MET:HA	2:A8:37:PRO:HD3	1.89	0.41
2:A8:123:ARG:NH2	2:A8:160:ASP:OD2	2.49	0.41
2:B2:119:LEU:HD13	2:B2:156:ARG:CD	2.37	0.41
2:B2:298:PRO:HB3	2:B2:307:PRO:HD2	2.02	0.41
2:B4:88:HIS:HA	2:B4:89:PRO:HD3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B6:342:GLN:OE1	2:B6:342:GLN:HA	2.21	0.41
2:C2:53:PHE:O	2:C2:64:ARG:NH2	2.53	0.41
2:C2:414:GLU:HG2	2:C2:417:GLU:OE2	2.20	0.41
3:C3:238:CYS:SG	3:C3:239:CYS:N	2.93	0.41
3:C7:150:LEU:O	3:C7:154:LYS:HG2	2.20	0.41
2:C8:60:LYS:NZ	2:C8:61:HIS:O	2.48	0.41
3:D1:253:LEU:O	3:D1:257:LEU:HB2	2.21	0.41
3:D5:23:VAL:CG1	3:D5:230:SER:HB2	2.48	0.41
2:D6:105:ARG:HH11	2:D6:110:ILE:HD13	1.86	0.41
3:D7:3:GLU:HA	3:D7:49:VAL:HA	2.02	0.41
3:D7:229:VAL:HA	3:D7:300:MET:HE1	2.02	0.41
2:D8:419:SER:O	2:D8:423:GLU:HG2	2.21	0.41
3:E3:44:LEU:HG	3:E3:44:LEU:O	2.21	0.41
2:E6:370:LYS:HB2	2:E6:370:LYS:HE2	1.75	0.41
3:E9:128:ASP:N	3:E9:128:ASP:OD1	2.50	0.41
3:E9:198:GLU:HG3	3:E9:266:PHE:CE2	2.55	0.41
3:E9:238:CYS:SG	3:E9:239:CYS:N	2.92	0.41
3:E9:257:LEU:HD13	3:E9:312:THR:HG23	2.02	0.41
4:a:172:VAL:HG13	4:a:180:ALA:HB3	2.02	0.41
4:b:70:GLY:HA3	4:d:38:LEU:O	2.21	0.41
4:c:70:GLY:O	4:e:39:PRO:HD3	2.20	0.41
4:f:35:ASN:HD22	4:f:35:ASN:N	2.18	0.41
4:q:73:VAL:HA	4:q:109:GLU:O	2.21	0.41
1:7:242:ASN:OD1	1:7:242:ASN:N	2.54	0.41
2:A2:100:ALA:O	3:A3:255:VAL:HG11	2.21	0.41
2:A6:298:PRO:HG3	2:A6:308:ARG:HH22	1.85	0.41
2:A6:397:LEU:HG	3:A7:344:TRP:HB2	2.02	0.41
2:A8:223:THR:HB	3:A9:245:GLN:OE1	2.21	0.41
3:A9:283:ALA:HA	3:B3:55:THR:CG2	2.51	0.41
2:B0:173:PRO:HG3	2:B0:187:SER:OG	2.20	0.41
2:B4:31:GLN:NE2	2:B4:37:PRO:HG3	2.36	0.41
3:B5:324:LYS:HB2	3:B5:324:LYS:HE3	1.79	0.41
3:B7:403:MET:HE2	3:B7:403:MET:HB3	1.94	0.41
2:B8:215:ARG:HH12	2:B8:299:ALA:HB1	1.86	0.41
2:C0:411:GLU:OE1	2:C0:411:GLU:N	2.54	0.41
2:C4:423:GLU:HA	2:C4:426:ALA:HB3	2.02	0.41
3:C5:321:MET:SD	3:C5:321:MET:N	2.93	0.41
2:C6:66:VAL:HG12	2:C6:91:GLN:HB2	2.03	0.41
3:D3:100:ASN:ND2	3:D3:401:GLU:OE2	2.53	0.41
3:D5:215:LEU:HB3	3:D5:217:LEU:HD13	2.02	0.41
2:E0:12:ALA:CB	2:E0:140:ALA:HB2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E3:295:ASP:OD2	3:E3:297:LYS:HG2	2.20	0.41
3:E5:2:ARG:HD3	3:E5:131:GLN:OE1	2.20	0.41
2:E8:191:THR:CG2	2:E8:425:LEU:HD21	2.50	0.41
3:E9:28:HIS:CE1	3:E9:241:ARG:HE	2.37	0.41
3:F1:249:ASP:OD1	3:F1:250:LEU:N	2.54	0.41
4:e:5:VAL:HG23	4:e:8:SER:HB3	2.03	0.41
4:k:79:ASP:OD2	4:k:152:LYS:NZ	2.42	0.41
4:m:53:GLY:HA2	4:m:62:VAL:HG21	2.02	0.41
4:s:95:TYR:CZ	4:s:99:MET:HE2	2.56	0.41
4:v:71:LYS:HE2	4:v:109:GLU:HG2	2.03	0.41
5:w:45:LYS:O	5:w:49:ILE:HG12	2.21	0.41
4:y:181:GLN:NE2	4:y:200:ASP:OD1	2.53	0.41
1:4:240:PRO:CB	4:g:154:TYR:CA	2.99	0.41
2:A0:428:LEU:HD12	2:A0:428:LEU:HA	1.92	0.41
3:A1:215:LEU:HD11	3:A1:273:LEU:HD22	2.03	0.41
2:A2:77:GLU:HA	2:A2:80:THR:HG22	2.02	0.41
3:A3:252:LYS:O	3:A3:256:ASN:ND2	2.54	0.41
2:A4:68:LEU:HD21	2:A4:149:LEU:HD21	2.03	0.41
2:A4:121:ARG:HD2	2:A4:121:ARG:HA	1.82	0.41
2:A6:154:LEU:HD23	2:A6:154:LEU:HA	1.91	0.41
3:A7:10:GLY:HA2	3:A7:143:THR:HG23	2.02	0.41
3:A9:135:ILE:HG21	3:A9:152:ILE:HD11	2.03	0.41
2:B0:124:LYS:HE3	2:B0:124:LYS:HB2	1.82	0.41
3:B3:77:ARG:HH22	3:B3:92:PHE:HZ	1.69	0.41
2:B4:367:ASP:OD1	2:B4:367:ASP:N	2.49	0.41
2:B4:402:ARG:HD3	2:B4:402:ARG:HA	1.92	0.41
3:B7:386:THR:O	3:B7:390:ARG:HG2	2.21	0.41
3:C1:309:ARG:O	3:C1:372:THR:HG22	2.21	0.41
3:C1:330:MET:HB3	3:C1:349:MET:HG2	2.01	0.41
3:C3:206:ALA:O	3:C3:210:ILE:HG12	2.21	0.41
3:C3:256:ASN:HD22	3:C3:350:LYS:HD2	1.86	0.41
2:C4:23:LEU:HD11	2:C4:233:GLN:OE1	2.21	0.41
3:D1:16:ILE:HD11	3:D1:229:VAL:HB	2.02	0.41
2:D4:137:MET:HE3	2:D4:137:MET:HB2	1.91	0.41
3:D7:289:LEU:HD22	3:D7:365:VAL:HG12	2.03	0.41
3:D9:374:ILE:HD11	3:D9:422:TYR:CZ	2.56	0.41
3:D9:396:HIS:HA	3:D9:399:THR:HG22	2.03	0.41
2:E0:50:ASN:O	2:E0:64:ARG:NH2	2.54	0.41
3:E1:207:LEU:HB3	3:E1:225:LEU:HD22	2.01	0.41
3:E5:101:TRP:CE3	3:E5:187:LEU:HD23	2.55	0.41
3:E9:375:GLN:NE2	3:E9:423:GLN:HB2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F1:51:TYR:HB3	3:F1:59:PHE:HB3	2.02	0.41
4:b:92:LEU:HA	4:b:92:LEU:HD23	1.82	0.41
4:f:99:MET:HE1	4:f:201:TRP:CD2	2.56	0.41
4:k:181:GLN:NE2	4:k:200:ASP:OD1	2.53	0.41
4:m:10:LEU:HB2	4:m:147:HIS:ND1	2.35	0.41
4:r:152:LYS:HE2	4:r:152:LYS:HB3	1.72	0.41
4:u:112:PHE:CG	4:u:129:MET:HE1	2.56	0.41
4:x:96:TYR:CZ	4:y:6:PHE:CE2	3.09	0.41
1:17:253:ALA:HB1	2:E2:32:PRO:HG2	2.03	0.41
1:19:250:GLU:O	2:E6:229:ARG:NH2	2.53	0.41
2:A0:182:VAL:HG22	2:A0:185:TYR:HB2	2.01	0.41
3:A1:263:LEU:HD12	3:A1:370:ASN:HD21	1.84	0.41
2:A4:291:ILE:HD12	2:A4:375:VAL:HG23	2.02	0.41
3:A5:211:CYS:O	2:A6:326:LYS:NZ	2.53	0.41
3:A7:139:LEU:HD12	3:A7:170:PHE:CE1	2.54	0.41
2:A8:173:PRO:HG2	2:A8:391:MET:HE3	2.03	0.41
3:B1:39:ASP:HA	4:d:90:PRO:HG3	2.01	0.41
3:B1:362:LYS:HE2	3:B1:362:LYS:HB2	1.52	0.41
3:B3:375:GLN:HG3	3:B3:419:VAL:HG13	2.01	0.41
2:B6:217:LEU:O	2:B6:218:ASP:HB3	2.21	0.41
3:B7:54:ALA:HB3	3:B7:58:ARG:HG2	2.03	0.41
3:B7:283:ALA:HA	3:C1:55:THR:CG2	2.50	0.41
2:B8:254:GLU:HG2	2:B8:352:LYS:HE2	2.01	0.41
3:B9:50:PHE:CE2	3:B9:241:ARG:HD3	2.56	0.41
3:B9:141:GLY:O	3:B9:145:SER:OG	2.29	0.41
2:C0:54:SER:OG	2:C0:55:GLU:N	2.53	0.41
3:C1:262:ARG:HA	3:C1:262:ARG:HD2	1.79	0.41
3:C3:107:THR:OG1	3:C3:108:GLU:N	2.54	0.41
3:C5:32:PRO:HD3	3:C5:81:PHE:CZ	2.56	0.41
3:C5:295:ASP:HB3	3:C5:298:ASN:HB2	2.03	0.41
3:C9:72:THR:O	3:C9:75:SER:OG	2.37	0.41
3:C9:204:ASN:HB3	3:C9:208:TYR:CE2	2.55	0.41
2:D2:319:TYR:CD2	2:D2:375:VAL:HG22	2.55	0.41
3:D3:113:ILE:HD12	3:D3:113:ILE:HA	1.97	0.41
3:D3:141:GLY:O	3:D3:145:SER:OG	2.33	0.41
3:D5:87:PRO:HA	3:D5:90:PHE:CD1	2.56	0.41
3:D5:311:LEU:HD23	3:D5:311:LEU:HA	1.95	0.41
3:D9:237:THR:HG23	3:D9:241:ARG:HH21	1.85	0.41
2:E4:383:ALA:O	2:E4:386:GLU:HG2	2.21	0.41
2:E6:230:LEU:CD2	2:E6:368:LEU:HD11	2.51	0.41
2:E6:261:PRO:HG3	2:E6:313:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E7:267:LEU:CD1	3:E7:301:CYS:HB3	2.51	0.41
2:E8:141:VAL:HG11	2:E8:172:TRP:CZ3	2.56	0.41
2:F0:218:ASP:OD2	2:F0:280:LYS:NZ	2.39	0.41
2:F0:231:ILE:O	2:F0:235:ILE:HG12	2.21	0.41
2:F0:313:MET:HE3	2:F0:346:TRP:CZ2	2.56	0.41
3:F1:203:ASP:OD1	3:F1:377:MET:HE1	2.21	0.41
4:h:201:TRP:CD1	4:h:201:TRP:H	2.37	0.41
4:j:175:SER:HA	4:j:206:PHE:CE1	2.54	0.41
4:t:139:PRO:O	4:t:143:ILE:HG12	2.20	0.41
4:y:189:LEU:HB3	4:y:191:GLU:OE1	2.20	0.41
1:0:239:LEU:HA	1:0:240:PRO:HD3	1.87	0.41
1:18:241:PHE:CZ	3:E5:356:ILE:CG2	3.03	0.41
1:19:241:PHE:HB2	3:E7:43:GLN:NE2	2.22	0.41
1:4:253:ALA:HB1	2:B2:32:PRO:HG2	2.02	0.41
1:5:257:PRO:HD3	2:B4:26:LEU:HD11	2.03	0.41
1:7:253:ALA:HB2	2:B8:82:THR:HG21	2.03	0.41
2:A0:185:TYR:CE2	2:A0:398:MET:HE2	2.55	0.41
3:A1:43:GLN:HA	3:A1:242:PHE:HE1	1.85	0.41
3:A1:212:PHE:CE1	2:A2:326:LYS:HB3	2.56	0.41
2:A2:370:LYS:HB3	2:A2:370:LYS:HE3	1.71	0.41
2:A4:2:ARG:H	2:A4:2:ARG:HG2	1.75	0.41
3:A5:239:CYS:SG	3:A5:247:ASN:HA	2.61	0.41
3:A5:317:PHE:HB3	3:A5:321:MET:SD	2.61	0.41
2:A6:238:LEU:HD12	2:A6:238:LEU:HA	1.88	0.41
2:A6:262:TYR:HB3	2:A6:263:PRO:HD2	2.03	0.41
2:A8:117:LEU:HD23	2:A8:117:LEU:HA	1.96	0.41
2:A8:219:ILE:HD13	2:A8:219:ILE:HG21	1.79	0.41
3:A9:396:HIS:CE1	2:B0:261:PRO:O	2.69	0.41
2:B0:102:ASN:HA	2:B0:408:TYR:HE1	1.85	0.41
2:B0:241:SER:OG	2:B0:250:VAL:O	2.31	0.41
3:B1:118:ASP:O	3:B1:122:LYS:HG2	2.21	0.41
3:B1:382:SER:OG	3:B1:412:GLU:OE2	2.34	0.41
2:B2:8:HIS:CD2	2:B2:138:PHE:HD2	2.39	0.41
3:B3:103:LYS:HA	3:B3:107:THR:HG22	2.03	0.41
2:B4:359:PRO:HA	2:B4:360:PRO:HD3	1.93	0.41
3:B5:330:MET:CE	3:B5:349:MET:HB3	2.51	0.41
2:B6:52:PHE:CD2	2:B6:243:ARG:HD3	2.55	0.41
2:B6:357:TYR:HD1	2:B6:357:TYR:HA	1.75	0.41
3:B7:267:LEU:HB3	3:B7:299:MET:CE	2.51	0.41
2:B8:215:ARG:HH22	2:B8:299:ALA:C	2.28	0.41
2:B8:367:ASP:OD1	2:B8:368:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C1:220:PRO:HG2	2:C2:326:LYS:HB2	2.03	0.41
3:C1:281:TYR:CE1	3:C5:58:ARG:NH1	2.89	0.41
3:C1:318:ARG:HD3	3:C1:358:PRO:HD3	2.03	0.41
3:C3:263:LEU:HD12	3:C3:370:ASN:HD21	1.86	0.41
2:C4:279:GLU:OE2	4:m:197:LEU:CD1	2.69	0.41
2:C4:287:SER:N	2:C4:290:GLU:OE2	2.46	0.41
3:C5:52:ASN:ND2	3:C5:123:GLU:OE2	2.42	0.41
2:C6:121:ARG:HH11	2:C6:121:ARG:HD2	1.77	0.41
2:C8:203:MET:HE3	2:C8:267:PHE:HD2	1.86	0.41
2:D0:319:TYR:N	2:D0:354:GLY:O	2.49	0.41
3:D1:167:PHE:CE2	3:D1:233:MET:HG3	2.56	0.41
3:D1:286:VAL:N	3:D1:287:PRO:HD2	2.35	0.41
3:D1:321:MET:HE2	3:D1:321:MET:HB3	2.02	0.41
3:D1:422:TYR:HD1	3:D1:422:TYR:HA	1.78	0.41
3:D3:117:LEU:HA	3:D3:117:LEU:HD23	1.88	0.41
2:D4:218:ASP:OD1	4:r:194:ARG:NH2	2.53	0.41
3:D5:169:VAL:HG12	3:D5:202:ILE:HB	2.03	0.41
2:D6:101:ASN:HB2	3:D7:255:VAL:HG21	2.03	0.41
2:D6:222:PRO:CD	3:D7:324:LYS:NZ	2.82	0.41
2:D6:402:ARG:HD3	2:D6:405:VAL:HG11	2.03	0.41
2:D8:109:THR:OG1	2:D8:411:GLU:O	2.39	0.41
3:D9:164:MET:HE2	3:D9:164:MET:HB2	1.97	0.41
2:E2:319:TYR:CE1	2:E2:375:VAL:HG22	2.55	0.41
3:E3:55:THR:O	3:E3:55:THR:HG23	2.20	0.41
2:E4:402:ARG:HG2	2:E4:402:ARG:HH21	1.86	0.41
3:E5:64:ILE:HD12	3:E5:119:VAL:HG12	2.03	0.41
2:E6:72:PRO:O	2:E6:76:ASP:HB2	2.21	0.41
2:E6:270:SER:OG	2:E6:302:MET:HB3	2.20	0.41
2:E6:404:PHE:CE1	3:E7:259:PRO:HA	2.56	0.41
3:E7:28:HIS:HA	3:E7:43:GLN:HG2	2.03	0.41
2:E8:173:PRO:HG2	2:E8:391:MET:HE3	2.03	0.41
3:E9:183:TYR:OH	3:E9:388:MET:O	2.22	0.41
2:F0:258:ASN:ND2	2:F0:352:LYS:HD2	2.36	0.41
3:F1:156:ARG:HD3	3:F1:164:MET:HE3	2.01	0.41
3:F1:382:SER:HA	3:F1:415:MET:HE1	2.03	0.41
4:a:129:MET:HG2	4:a:131:TRP:CZ2	2.56	0.41
4:d:46:ASP:OD1	4:d:46:ASP:N	2.54	0.41
4:d:75:LEU:O	4:d:170:VAL:HA	2.20	0.41
4:e:129:MET:SD	4:e:131:TRP:NE1	2.94	0.41
4:g:151:MET:HE1	4:g:158:THR:HG21	2.03	0.41
4:h:189:LEU:HD23	4:h:189:LEU:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:105:ASN:HB2	4:l:39:PRO:HG2	2.03	0.41
4:j:115:LEU:HD12	4:j:167:VAL:HB	2.03	0.41
4:j:130:PRO:HG3	4:l:159:TYR:CB	2.50	0.41
4:n:10:LEU:HB2	4:n:147:HIS:ND1	2.36	0.41
4:n:172:VAL:HG21	4:n:199:TRP:HE1	1.86	0.41
4:o:82:ASP:OD1	4:o:83:PRO:HD2	2.21	0.41
4:p:130:PRO:HB3	4:r:159:TYR:CE1	2.56	0.41
4:q:12:VAL:HG12	4:q:15:ARG:NH1	2.36	0.41
4:s:139:PRO:O	4:s:143:ILE:HG12	2.21	0.41
4:t:8:SER:HA	4:t:9:PRO:HD3	1.90	0.41
4:t:106:GLN:OE1	4:v:15:ARG:CD	2.69	0.41
4:v:97:ARG:O	4:v:101:GLU:HG2	2.20	0.41
4:x:75:LEU:HG	4:x:173:ILE:HD13	2.01	0.41
4:y:63:ILE:HA	4:y:64:PRO:HD3	1.94	0.41
1:10:254:LYS:HZ3	2:C8:22:GLU:HG2	1.82	0.41
1:17:253:ALA:CB	2:E2:32:PRO:HG2	2.51	0.41
3:A1:193:VAL:HG12	3:A1:265:PHE:CZ	2.56	0.41
3:A1:219:THR:CG2	3:A1:219:THR:O	2.69	0.41
3:A1:365:VAL:HG22	3:A1:366:THR:N	2.35	0.41
2:A2:356:ASN:OD1	2:A2:357:TYR:N	2.54	0.41
2:A6:69:ASP:OD1	2:A6:70:LEU:N	2.54	0.41
3:A9:361:LEU:HD23	3:A9:361:LEU:HA	1.95	0.41
2:B0:397:LEU:CD2	3:B1:344:TRP:O	2.69	0.41
3:B7:86:ARG:HA	3:B7:87:PRO:HD3	1.96	0.41
2:B8:174:SER:OG	2:B8:205:ASP:OD1	2.37	0.41
3:B9:392:LYS:HD2	3:B9:395:LEU:HD22	2.03	0.41
3:C3:21:TRP:CH2	3:C3:61:PRO:HB3	2.55	0.41
3:C3:167:PHE:HE1	3:C3:200:GLN:NE2	2.19	0.41
3:C5:209:ASP:CG	3:C5:213:ARG:HH21	2.29	0.41
3:C7:385:PHE:HZ	3:C7:408:PHE:HD2	1.69	0.41
3:C9:246:LEU:HD12	3:C9:246:LEU:HA	1.90	0.41
2:D0:12:ALA:HB3	2:D0:140:ALA:HB2	2.03	0.41
3:D1:7:VAL:CG1	3:D1:66:MET:HE3	2.51	0.41
2:D2:6:SER:OG	2:D2:8:HIS:NE2	2.54	0.41
2:D2:276:ILE:HD11	2:D2:286:LEU:HD11	2.02	0.41
2:D6:264:ARG:HH11	2:D6:264:ARG:HD2	1.67	0.41
3:D9:155:VAL:HG13	3:D9:164:MET:HE1	2.02	0.41
2:E4:256:GLN:HE21	2:E4:256:GLN:N	2.19	0.41
2:E6:217:LEU:HD23	2:E6:219:ILE:HG13	2.03	0.41
2:E8:157:LEU:HD23	2:E8:157:LEU:HA	1.95	0.41
2:E8:319:TYR:HB2	2:E8:355:ILE:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E8:339:ARG:HD2	2:E8:339:ARG:HA	1.81	0.41
2:F0:214:ARG:NH2	2:F0:220:GLU:HA	2.36	0.41
3:F1:42:LEU:O	3:F1:42:LEU:HG	2.21	0.41
3:F1:205:GLU:OE1	3:F1:205:GLU:N	2.54	0.41
4:g:75:LEU:HD23	4:g:111:ILE:HB	2.03	0.41
4:j:127:ALA:O	4:l:157:PRO:HG3	2.22	0.41
4:l:175:SER:HA	4:l:206:PHE:CE1	2.55	0.41
4:n:14:LYS:HB2	4:n:47:LEU:HD22	2.03	0.41
4:n:48:ILE:O	4:n:48:ILE:HG23	2.21	0.41
4:t:191:GLU:HB2	4:t:195:ALA:HB2	2.02	0.41
4:y:198:ARG:CG	4:y:198:ARG:NH1	2.73	0.41
1:10:244:GLN:NE2	4:o:162:GLY:HA3	2.36	0.40
3:A1:117:LEU:HD13	3:A1:154:LYS:HZ1	1.83	0.40
2:A4:272:TYR:HB3	2:A4:275:ILE:HD11	2.03	0.40
3:A9:182:PRO:HD2	3:A9:388:MET:HE1	2.03	0.40
3:A9:391:ARG:O	3:A9:391:ARG:HG3	2.22	0.40
3:B5:253:LEU:O	3:B5:257:LEU:HB2	2.21	0.40
2:B6:406:HIS:HA	2:B6:409:VAL:HG12	2.01	0.40
3:B7:10:GLY:HA2	3:B7:143:THR:HG23	2.02	0.40
3:B9:186:THR:HG22	3:B9:415:MET:SD	2.61	0.40
3:C1:292:GLN:HG2	3:C1:298:ASN:HD22	1.85	0.40
3:C7:133:PHE:HB2	3:C7:164:MET:HB3	2.02	0.40
3:C9:22:GLU:HG3	3:C9:81:PHE:CD2	2.56	0.40
3:C9:236:VAL:HG13	3:C9:237:THR:HG23	2.03	0.40
3:C9:240:LEU:HD21	3:C9:249:ASP:HB2	2.02	0.40
2:D2:164:LYS:HD2	2:D2:164:LYS:HA	1.87	0.40
3:D3:60:VAL:HA	3:D3:61:PRO:HD3	1.97	0.40
3:D5:21:TRP:CZ3	3:D5:61:PRO:HB3	2.57	0.40
3:D5:21:TRP:HA	3:D5:24:ILE:HG22	2.03	0.40
2:D8:221:ARG:HB3	3:D9:322:SER:HB3	2.02	0.40
2:D8:251:ASP:H	2:D8:254:GLU:HG3	1.86	0.40
3:E1:326:VAL:O	3:E1:330:MET:HG2	2.21	0.40
3:E5:25:SER:HB3	3:E5:30:ILE:HB	2.03	0.40
3:E9:105:HIS:HB3	3:E9:106:TYR:CD1	2.56	0.40
4:c:67:HIS:CE1	4:e:20:GLU:OE1	2.75	0.40
4:e:107:LYS:HB2	4:e:107:LYS:HE2	1.64	0.40
4:l:8:SER:HA	4:l:9:PRO:HD3	1.86	0.40
4:l:146:ARG:HD3	4:l:156:VAL:CG2	2.44	0.40
4:s:82:ASP:HB3	4:s:85:CYS:SG	2.61	0.40
4:t:12:VAL:HG12	4:t:15:ARG:NH1	2.37	0.40
4:u:172:VAL:O	4:u:180:ALA:N	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:v:75:LEU:O	4:v:170:VAL:HA	2.21	0.40
4:x:106:GLN:OE1	4:y:6:PHE:CZ	2.74	0.40
3:A1:136:THR:HG22	3:A1:167:PHE:HD2	1.85	0.40
2:A2:141:VAL:HG11	2:A2:172:TRP:CE3	2.56	0.40
3:A5:2:ARG:NH2	3:A5:249:ASP:OD2	2.55	0.40
3:A7:137:HIS:NE2	3:A7:168:SER:OG	2.53	0.40
3:B1:284:LEU:H	3:B5:55:THR:HB	1.87	0.40
2:B8:259:LEU:HD21	2:B8:316:CYS:HB2	2.03	0.40
2:B8:262:TYR:HB2	2:B8:265:ILE:HD12	2.01	0.40
2:C0:254:GLU:HA	2:C0:257:THR:HG22	2.04	0.40
2:C0:306:ASP:HB2	2:C0:309:HIS:NE2	2.37	0.40
3:C3:141:GLY:O	3:C3:184:ASN:ND2	2.48	0.40
2:C4:10:GLY:O	2:C4:14:ILE:HG12	2.21	0.40
3:C5:154:LYS:HB3	3:C5:154:LYS:HE2	1.64	0.40
2:C6:296:PHE:CD2	2:C6:335:ILE:HG21	2.56	0.40
3:C7:374:ILE:HD11	3:C7:422:TYR:OH	2.21	0.40
3:D1:193:VAL:HG13	3:D1:194:GLU:HG3	2.03	0.40
2:D2:207:GLU:HG3	2:D2:304:LYS:HG3	2.03	0.40
2:D2:217:LEU:HD11	2:D2:275:ILE:HG22	2.02	0.40
2:D2:407:TRP:HZ2	3:D3:258:ILE:HD11	1.87	0.40
3:D3:228:LEU:HG	3:D3:300:MET:HE2	2.03	0.40
3:D3:283:ALA:HA	3:D7:54:ALA:O	2.21	0.40
3:D3:313:ALA:HB1	3:D3:367:PHE:HE1	1.85	0.40
3:D3:330:MET:HE3	3:D3:349:MET:HB3	2.03	0.40
2:D4:229:ARG:NH1	2:D4:229:ARG:HG3	2.35	0.40
3:D5:13:GLY:HA2	3:D5:16:ILE:HG22	2.04	0.40
3:D5:289:LEU:HD23	3:D5:289:LEU:HA	1.95	0.40
2:E0:174:SER:HB3	2:E0:177:VAL:O	2.21	0.40
2:E2:212:ILE:HD11	2:E2:300:SER:HA	2.02	0.40
3:E3:202:ILE:HG12	3:E3:300:MET:HE3	2.03	0.40
2:E6:250:VAL:HG12	2:E6:254:GLU:HG2	2.02	0.40
2:E8:211:ASP:OD1	2:E8:211:ASP:N	2.52	0.40
2:F0:261:PRO:HG3	2:F0:313:MET:CE	2.52	0.40
4:c:187:SER:H	4:c:190:GLU:HB3	1.86	0.40
4:e:130:PRO:HB3	4:g:7:ALA:HB1	2.03	0.40
4:g:106:GLN:NE2	4:i:6:PHE:CZ	2.89	0.40
4:k:82:ASP:HB3	4:k:85:CYS:SG	2.61	0.40
4:k:96:TYR:OH	4:m:6:PHE:HE2	2.03	0.40
4:l:111:ILE:HD13	4:l:132:LEU:HB2	2.03	0.40
4:o:48:ILE:HD12	4:o:48:ILE:HA	1.91	0.40
4:o:149:ARG:NH1	4:o:162:GLY:O	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:o:164:ARG:HG2	4:o:164:ARG:NH1	2.35	0.40
4:t:153:GLU:O	4:t:155:GLU:HG3	2.22	0.40
4:t:183:LEU:HD23	4:t:183:LEU:HA	1.87	0.40
4:v:36:ILE:HD12	4:v:36:ILE:HA	1.96	0.40
4:y:55:LEU:HD22	4:y:111:ILE:HD12	2.03	0.40
1:1:254:LYS:HG3	2:A6:364:PRO:HB2	2.04	0.40
1:18:246:CYS:HB2	3:E5:245:GLN:HG2	2.02	0.40
3:A1:233:MET:HE2	3:A1:233:MET:HB3	1.87	0.40
3:A3:113:ILE:HG23	3:A3:117:LEU:HD23	2.04	0.40
3:A5:219:THR:CG2	2:A6:324:VAL:HG21	2.50	0.40
3:A5:257:LEU:HD21	3:A5:314:SER:HB2	2.03	0.40
2:A6:121:ARG:HH12	2:A6:125:LEU:HG	1.86	0.40
2:B2:262:TYR:HB3	2:B2:263:PRO:HD2	2.02	0.40
2:B6:269:LEU:HD21	2:B6:384:ILE:HD11	2.03	0.40
3:B7:152:ILE:HG22	3:B7:195:ASN:HB3	2.04	0.40
3:B7:213:ARG:HD3	3:B7:297:LYS:NZ	2.36	0.40
2:B8:305:CYS:HG	2:B8:309:HIS:HE2	1.66	0.40
2:C2:214:ARG:HG3	3:C3:324:LYS:NZ	2.37	0.40
2:C4:30:ILE:HD13	2:C4:53:PHE:CE2	2.56	0.40
3:C5:105:HIS:ND1	3:C5:150:LEU:HB2	2.37	0.40
3:C7:10:GLY:HA2	3:C7:143:THR:OG1	2.21	0.40
2:C8:147:SER:HB2	2:C8:190:SER:HB3	2.02	0.40
2:C8:402:ARG:HA	2:C8:402:ARG:HD3	1.95	0.40
3:C9:281:TYR:CD1	3:D3:58:ARG:CZ	3.04	0.40
2:D0:137:MET:HE2	2:D0:137:MET:HB3	1.89	0.40
2:D0:231:ILE:O	2:D0:235:ILE:HG12	2.21	0.40
2:D0:258:ASN:HD22	2:D0:258:ASN:HA	1.64	0.40
2:D2:208:ALA:HB2	2:D2:304:LYS:HG2	2.04	0.40
2:D2:221:ARG:HB3	3:D3:322:SER:HB3	2.03	0.40
3:D3:169:VAL:HG12	3:D3:202:ILE:HB	2.03	0.40
2:E0:64:ARG:HB3	2:E0:125:LEU:HD21	2.03	0.40
2:E2:152:LEU:HD12	2:E2:152:LEU:HA	1.91	0.40
3:E3:60:VAL:HA	3:E3:61:PRO:HD3	1.93	0.40
2:E4:178:SER:HB3	3:E5:347:ASN:CG	2.46	0.40
3:E5:73:MET:HE3	3:E5:73:MET:HB3	1.90	0.40
3:E9:7:VAL:HG11	3:E9:151:LEU:HD23	2.03	0.40
2:F0:319:TYR:CD2	2:F0:375:VAL:HG22	2.56	0.40
4:b:71:LYS:NZ	4:d:39:PRO:HB3	2.36	0.40
4:d:158:THR:OG1	4:d:161:TYR:HB2	2.22	0.40
4:d:196:LEU:HD23	4:d:196:LEU:HA	1.85	0.40
4:g:106:GLN:NE2	4:i:6:PHE:HZ	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:103:GLY:O	4:l:42:TYR:CE2	2.74	0.40
4:t:63:ILE:HG22	4:v:16:ARG:CD	2.50	0.40
5:w:158:ASP:OD1	5:w:160:ARG:NE	2.54	0.40
4:x:110:ILE:O	4:x:131:TRP:HB2	2.20	0.40
4:y:85:CYS:SG	4:y:167:VAL:HG22	2.61	0.40
1:21:238:THR:HG21	3:F1:359:LYS:HZ1	1.87	0.40
2:A0:244:PHE:CD2	2:A0:358:GLN:HG2	2.56	0.40
2:A4:17:GLY:HA2	2:A4:20:CYS:HB2	2.04	0.40
3:A7:7:VAL:HB	3:A7:135:ILE:HG13	2.04	0.40
3:A7:104:GLY:O	3:A7:147:MET:HB3	2.22	0.40
2:B0:9:VAL:HG13	2:B0:139:ASN:HB3	2.04	0.40
2:B0:149:LEU:HD23	2:B0:149:LEU:HA	1.94	0.40
2:B2:3:GLU:OE1	2:B2:64:ARG:NE	2.54	0.40
2:B2:12:ALA:HB3	2:B2:140:ALA:HB2	2.02	0.40
3:B7:297:LYS:HE3	3:B7:297:LYS:HB3	1.79	0.40
3:B9:287:PRO:O	3:B9:291:GLN:HG3	2.22	0.40
2:C2:279:GLU:OE2	4:l:198:ARG:HA	2.22	0.40
2:C6:207:GLU:HA	2:C6:210:TYR:HB2	2.03	0.40
3:C7:5:VAL:HB	3:C7:133:PHE:CD1	2.57	0.40
3:D1:4:ILE:HD11	3:D1:131:GLN:HG2	2.03	0.40
3:D7:281:TYR:CD1	3:E1:58:ARG:NE	2.89	0.40
3:E3:309:ARG:H	3:E3:372:THR:HG22	1.85	0.40
2:E4:210:TYR:OH	3:E5:323:THR:O	2.37	0.40
3:E5:136:THR:HG22	3:E5:167:PHE:HB2	2.03	0.40
2:E6:273:ALA:HA	2:E6:274:PRO:HA	1.84	0.40
2:E8:322:ASP:O	2:E8:373:ARG:NE	2.54	0.40
4:c:11:ASN:HA	4:c:14:LYS:HG2	2.04	0.40
4:c:41:ASN:O	4:c:45:MET:HG3	2.22	0.40
4:h:21:ARG:O	4:h:24:MET:HG3	2.22	0.40
4:i:15:ARG:O	4:i:19:GLU:HG3	2.21	0.40
4:m:10:LEU:HD12	4:m:147:HIS:CD2	2.56	0.40
4:r:28:LYS:HA	4:r:28:LYS:HD3	1.83	0.40
4:s:12:VAL:HG12	4:s:15:ARG:NH1	2.36	0.40
4:x:106:GLN:CD	4:y:6:PHE:CZ	2.99	0.40
4:y:57:ASN:HB3	4:y:132:LEU:HD21	2.04	0.40
1:0:244:GLN:H	3:A5:320:ARG:NH1	2.19	0.40
2:A0:176:GLN:OE1	2:A0:176:GLN:HA	2.21	0.40
2:A0:211:ASP:OD2	2:A0:304:LYS:NZ	2.54	0.40
3:A1:21:TRP:CZ2	3:A1:63:ALA:HB2	2.57	0.40
2:A2:51:THR:HG21	2:A2:243:ARG:HA	2.04	0.40
2:A4:115:VAL:HG21	2:A4:152:LEU:HG	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A6:273:ALA:HA	2:A6:274:PRO:HA	1.76	0.40
2:A6:279:GLU:OE2	4:d:198:ARG:CD	2.69	0.40
3:A7:249:ASP:H	3:A7:252:LYS:HG3	1.87	0.40
3:A9:39:ASP:HB3	4:c:90:PRO:HG2	2.02	0.40
3:A9:214:THR:HG22	3:A9:297:LYS:HG2	2.03	0.40
3:B3:6:HIS:HE1	3:B3:20:PHE:CD2	2.39	0.40
2:B4:221:ARG:HA	3:B5:322:SER:HB2	2.04	0.40
3:B5:136:THR:HG22	3:B5:167:PHE:HB2	2.02	0.40
2:B6:69:ASP:OD2	2:B6:71:GLU:HB3	2.21	0.40
2:B6:280:LYS:HD3	2:B6:280:LYS:HA	1.92	0.40
2:B8:62:VAL:HA	2:B8:63:PRO:HD3	1.88	0.40
2:C0:336:LYS:HE3	2:C0:336:LYS:HB3	1.92	0.40
2:C2:170:CYS:HB2	2:C2:203:MET:HE1	2.04	0.40
3:C3:284:LEU:HA	3:C3:284:LEU:HD12	1.80	0.40
2:C4:132:LEU:HB3	2:C4:164:LYS:NZ	2.36	0.40
3:C5:310:TYR:CD1	3:C5:371:SER:HB2	2.57	0.40
2:C6:309:HIS:HE2	2:C6:386:GLU:CD	2.28	0.40
2:C6:327:ASP:HA	2:C6:330:ALA:HB3	2.04	0.40
2:C6:395:PHE:HZ	2:C6:418:PHE:HB3	1.85	0.40
2:D0:203:MET:HE2	2:D0:267:PHE:HD1	1.87	0.40
3:D1:100:ASN:HB3	3:D1:103:LYS:HG2	2.03	0.40
2:D2:88:HIS:HA	2:D2:89:PRO:HD3	1.92	0.40
2:D4:393:HIS:O	2:D4:397:LEU:HD13	2.22	0.40
3:D7:19:LYS:HD2	3:D7:19:LYS:HA	1.94	0.40
3:D7:117:LEU:CD2	3:D7:121:ARG:HH22	2.33	0.40
2:E2:185:TYR:CE2	2:E2:398:MET:HE3	2.56	0.40
2:E4:64:ARG:HB3	2:E4:125:LEU:HD21	2.04	0.40
2:E4:251:ASP:OD1	2:E4:251:ASP:N	2.52	0.40
3:E5:180:VAL:HB	3:E5:183:TYR:HB2	2.04	0.40
3:E7:77:ARG:HH11	3:E7:77:ARG:HD2	1.67	0.40
4:b:185:ILE:H	4:b:185:ILE:HG12	1.73	0.40
4:e:100:ASN:HB3	4:g:6:PHE:CE1	2.56	0.40
4:g:149:ARG:HB3	4:g:164:ARG:H	1.87	0.40
4:n:8:SER:HA	4:n:9:PRO:HD3	1.82	0.40
4:q:14:LYS:HD3	4:q:47:LEU:HB2	2.03	0.40
4:r:21:ARG:HG2	4:r:21:ARG:NH2	2.36	0.40
4:r:146:ARG:HG3	4:r:146:ARG:HH11	1.87	0.40
4:s:66:SER:C	4:u:23:LEU:HD11	2.35	0.40
4:x:139:PRO:O	4:x:143:ILE:HG12	2.21	0.40
4:y:110:ILE:O	4:y:131:TRP:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	1	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	10	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	11	20/351 (6%)	15 (75%)	5 (25%)	0	100	100
1	12	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	13	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	14	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	15	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	16	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	17	20/351 (6%)	20 (100%)	0	0	100	100
1	18	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	19	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	2	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	20	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	21	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
1	22	18/351 (5%)	14 (78%)	4 (22%)	0	100	100
1	23	18/351 (5%)	15 (83%)	3 (17%)	0	100	100
1	3	20/351 (6%)	18 (90%)	1 (5%)	1 (5%)	1	16
1	4	20/351 (6%)	20 (100%)	0	0	100	100
1	5	20/351 (6%)	19 (95%)	1 (5%)	0	100	100
1	6	20/351 (6%)	20 (100%)	0	0	100	100
1	7	20/351 (6%)	20 (100%)	0	0	100	100
1	8	20/351 (6%)	17 (85%)	3 (15%)	0	100	100
1	9	20/351 (6%)	18 (90%)	2 (10%)	0	100	100
2	A0	424/453 (94%)	397 (94%)	27 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A2	424/453 (94%)	406 (96%)	17 (4%)	1 (0%)	43	78
2	A4	424/453 (94%)	398 (94%)	26 (6%)	0	100	100
2	A6	424/453 (94%)	399 (94%)	25 (6%)	0	100	100
2	A8	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	B0	424/453 (94%)	404 (95%)	20 (5%)	0	100	100
2	B2	424/453 (94%)	406 (96%)	18 (4%)	0	100	100
2	B4	424/453 (94%)	407 (96%)	17 (4%)	0	100	100
2	B6	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
2	B8	424/453 (94%)	404 (95%)	20 (5%)	0	100	100
2	C0	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	C2	424/453 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
2	C4	424/453 (94%)	390 (92%)	33 (8%)	1 (0%)	43	78
2	C6	424/453 (94%)	396 (93%)	28 (7%)	0	100	100
2	C8	424/453 (94%)	393 (93%)	31 (7%)	0	100	100
2	D0	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	D2	424/453 (94%)	405 (96%)	18 (4%)	1 (0%)	43	78
2	D4	424/453 (94%)	406 (96%)	18 (4%)	0	100	100
2	D6	424/453 (94%)	409 (96%)	15 (4%)	0	100	100
2	D8	424/453 (94%)	409 (96%)	15 (4%)	0	100	100
2	E0	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
2	E2	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	E4	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	E6	424/453 (94%)	401 (95%)	23 (5%)	0	100	100
2	E8	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
2	F0	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
3	A1	424/449 (94%)	390 (92%)	34 (8%)	0	100	100
3	A3	424/449 (94%)	402 (95%)	21 (5%)	1 (0%)	43	78
3	A5	424/449 (94%)	388 (92%)	34 (8%)	2 (0%)	24	63
3	A7	424/449 (94%)	394 (93%)	29 (7%)	1 (0%)	43	78
3	A9	424/449 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
3	B1	424/449 (94%)	401 (95%)	23 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B3	424/449 (94%)	397 (94%)	25 (6%)	2 (0%)	24	63
3	B5	424/449 (94%)	394 (93%)	28 (7%)	2 (0%)	24	63
3	B7	424/449 (94%)	399 (94%)	24 (6%)	1 (0%)	43	78
3	B9	424/449 (94%)	405 (96%)	18 (4%)	1 (0%)	43	78
3	C1	424/449 (94%)	399 (94%)	25 (6%)	0	100	100
3	C3	424/449 (94%)	398 (94%)	25 (6%)	1 (0%)	43	78
3	C5	424/449 (94%)	403 (95%)	21 (5%)	0	100	100
3	C7	424/449 (94%)	394 (93%)	29 (7%)	1 (0%)	43	78
3	C9	424/449 (94%)	395 (93%)	28 (7%)	1 (0%)	43	78
3	D1	424/449 (94%)	398 (94%)	25 (6%)	1 (0%)	43	78
3	D3	424/449 (94%)	394 (93%)	28 (7%)	2 (0%)	24	63
3	D5	424/449 (94%)	396 (93%)	26 (6%)	2 (0%)	24	63
3	D7	424/449 (94%)	404 (95%)	20 (5%)	0	100	100
3	D9	424/449 (94%)	398 (94%)	25 (6%)	1 (0%)	43	78
3	E1	424/449 (94%)	402 (95%)	21 (5%)	1 (0%)	43	78
3	E3	424/449 (94%)	400 (94%)	23 (5%)	1 (0%)	43	78
3	E5	424/449 (94%)	396 (93%)	28 (7%)	0	100	100
3	E7	424/449 (94%)	400 (94%)	23 (5%)	1 (0%)	43	78
3	E9	424/449 (94%)	393 (93%)	31 (7%)	0	100	100
3	F1	424/449 (94%)	391 (92%)	32 (8%)	1 (0%)	43	78
4	a	146/220 (66%)	134 (92%)	11 (8%)	1 (1%)	18	56
4	b	146/220 (66%)	134 (92%)	12 (8%)	0	100	100
4	c	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	d	197/220 (90%)	180 (91%)	17 (9%)	0	100	100
4	e	197/220 (90%)	185 (94%)	11 (6%)	1 (0%)	24	63
4	f	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	g	197/220 (90%)	184 (93%)	13 (7%)	0	100	100
4	h	197/220 (90%)	183 (93%)	14 (7%)	0	100	100
4	i	197/220 (90%)	182 (92%)	14 (7%)	1 (0%)	24	63
4	j	197/220 (90%)	182 (92%)	15 (8%)	0	100	100
4	k	197/220 (90%)	183 (93%)	13 (7%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	l	197/220 (90%)	186 (94%)	11 (6%)	0	100	100
4	m	197/220 (90%)	181 (92%)	16 (8%)	0	100	100
4	n	197/220 (90%)	182 (92%)	14 (7%)	1 (0%)	24	63
4	o	197/220 (90%)	180 (91%)	17 (9%)	0	100	100
4	p	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	q	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	r	197/220 (90%)	184 (93%)	12 (6%)	1 (0%)	24	63
4	s	197/220 (90%)	181 (92%)	16 (8%)	0	100	100
4	t	197/220 (90%)	188 (95%)	7 (4%)	2 (1%)	12	48
4	u	197/220 (90%)	188 (95%)	8 (4%)	1 (0%)	24	63
4	v	197/220 (90%)	180 (91%)	17 (9%)	0	100	100
4	x	197/220 (90%)	185 (94%)	12 (6%)	0	100	100
4	y	197/220 (90%)	184 (93%)	12 (6%)	1 (0%)	24	63
5	w	139/189 (74%)	133 (96%)	6 (4%)	0	100	100
All	All	27289/37345 (73%)	25630 (94%)	1620 (6%)	39 (0%)	49	83

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A3	179	VAL
3	A5	55	THR
3	A7	55	THR
3	A9	55	THR
3	B3	55	THR
3	B7	55	THR
3	D1	179	VAL
2	D2	163	LYS
3	D3	55	THR
3	E1	55	THR
1	3	251	TYR
3	B3	179	VAL
3	B5	55	THR
2	C2	58	ALA
3	C3	179	VAL
2	C4	89	PRO
3	C7	39	ASP
3	D3	179	VAL

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Mol	Chain	Res	Type
3	D5	179	VAL
3	E7	55	THR
4	y	154	TYR
3	B5	336	LYS
3	B9	55	THR
3	C9	55	THR
3	D5	55	THR
3	E3	55	THR
4	e	60	ASN
4	t	154	TYR
2	A2	32	PRO
3	D9	39	ASP
3	F1	171	PRO
4	i	159	TYR
4	n	51	PRO
4	u	51	PRO
4	t	51	PRO
4	k	51	PRO
3	A5	259	PRO
4	r	51	PRO
4	a	51	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	0	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	1	20/304 (7%)	20 (100%)	0	100	100
1	10	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	11	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	12	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	13	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	14	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	15	20/304 (7%)	19 (95%)	1 (5%)	22	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	16	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	17	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	18	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	19	20/304 (7%)	17 (85%)	3 (15%)	3	12
1	2	20/304 (7%)	20 (100%)	0	100	100
1	20	20/304 (7%)	20 (100%)	0	100	100
1	21	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	22	18/304 (6%)	18 (100%)	0	100	100
1	23	18/304 (6%)	18 (100%)	0	100	100
1	3	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	4	20/304 (7%)	20 (100%)	0	100	100
1	5	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	6	20/304 (7%)	18 (90%)	2 (10%)	7	24
1	7	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	8	20/304 (7%)	19 (95%)	1 (5%)	22	43
1	9	20/304 (7%)	20 (100%)	0	100	100
2	A0	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	A2	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	A4	359/379 (95%)	347 (97%)	12 (3%)	33	55
2	A6	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	A8	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	B0	359/379 (95%)	349 (97%)	10 (3%)	38	60
2	B2	359/379 (95%)	349 (97%)	10 (3%)	38	60
2	B4	359/379 (95%)	350 (98%)	9 (2%)	42	63
2	B6	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	B8	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	C0	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	C2	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	C4	359/379 (95%)	357 (99%)	2 (1%)	78	83
2	C6	359/379 (95%)	352 (98%)	7 (2%)	50	67
2	C8	359/379 (95%)	350 (98%)	9 (2%)	42	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D0	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	D2	359/379 (95%)	351 (98%)	8 (2%)	45	64
2	D4	359/379 (95%)	355 (99%)	4 (1%)	65	76
2	D6	359/379 (95%)	354 (99%)	5 (1%)	59	72
2	D8	359/379 (95%)	353 (98%)	6 (2%)	53	69
2	E0	359/379 (95%)	357 (99%)	2 (1%)	78	83
2	E2	359/379 (95%)	354 (99%)	5 (1%)	59	72
2	E4	359/379 (95%)	356 (99%)	3 (1%)	73	80
2	E6	359/379 (95%)	357 (99%)	2 (1%)	78	83
2	E8	359/379 (95%)	358 (100%)	1 (0%)	86	86
2	F0	359/379 (95%)	351 (98%)	8 (2%)	45	64
3	A1	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	A3	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	A5	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	A7	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	A9	364/381 (96%)	355 (98%)	9 (2%)	42	63
3	B1	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	B3	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	B5	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	B7	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	B9	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	C1	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	C3	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	C5	364/381 (96%)	356 (98%)	8 (2%)	45	64
3	C7	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	C9	364/381 (96%)	361 (99%)	3 (1%)	73	80
3	D1	364/381 (96%)	359 (99%)	5 (1%)	59	72
3	D3	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	D5	364/381 (96%)	358 (98%)	6 (2%)	55	70
3	D7	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	D9	364/381 (96%)	358 (98%)	6 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E1	364/381 (96%)	355 (98%)	9 (2%)	42	63
3	E3	364/381 (96%)	355 (98%)	9 (2%)	42	63
3	E5	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	E7	364/381 (96%)	357 (98%)	7 (2%)	50	67
3	E9	364/381 (96%)	360 (99%)	4 (1%)	65	76
3	F1	364/381 (96%)	359 (99%)	5 (1%)	59	72
4	a	130/190 (68%)	127 (98%)	3 (2%)	44	64
4	b	130/190 (68%)	128 (98%)	2 (2%)	57	72
4	c	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	d	174/190 (92%)	168 (97%)	6 (3%)	32	54
4	e	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	f	174/190 (92%)	169 (97%)	5 (3%)	37	58
4	g	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	h	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	i	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	j	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	k	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	l	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	m	174/190 (92%)	172 (99%)	2 (1%)	65	76
4	n	174/190 (92%)	170 (98%)	4 (2%)	44	64
4	o	174/190 (92%)	167 (96%)	7 (4%)	28	49
4	p	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	q	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	r	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	s	174/190 (92%)	171 (98%)	3 (2%)	53	69
4	t	174/190 (92%)	173 (99%)	1 (1%)	78	83
4	u	174/190 (92%)	174 (100%)	0	100	100
4	v	174/190 (92%)	169 (97%)	5 (3%)	37	58
4	x	174/190 (92%)	168 (97%)	6 (3%)	32	54
4	y	174/190 (92%)	171 (98%)	3 (2%)	53	69
5	w	127/164 (77%)	124 (98%)	3 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	23489/31780 (74%)	23093 (98%)	396 (2%)	52 69

All (396) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	254	LYS
1	10	254	LYS
1	10	256	LEU
1	11	241	PHE
1	11	246	CYS
1	12	256	LEU
1	13	252	VAL
1	14	248	ARG
1	15	252	VAL
1	16	254	LYS
1	17	252	VAL
1	17	254	LYS
1	18	256	LEU
1	19	238	THR
1	19	248	ARG
1	19	256	LEU
1	21	256	LEU
1	3	256	LEU
1	5	248	ARG
1	6	239	LEU
1	6	256	LEU
1	7	239	LEU
1	8	237	PRO
2	A0	96	LYS
2	A0	119	LEU
2	A0	163	LYS
2	A0	285	GLN
2	A0	326	LYS
2	A0	401	LYS
3	A1	179	VAL
3	A1	297	LYS
3	A1	379	LYS
2	A2	15	GLN
2	A2	85	HIS
2	A2	203	MET
2	A2	285	GLN
2	A2	353	CYS

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Mol	Chain	Res	Type
2	A2	370	LYS
2	A2	402	ARG
3	A3	11	GLN
3	A3	155	VAL
3	A3	174	LYS
3	A3	180	VAL
3	A3	298	ASN
2	A4	7	ILE
2	A4	15	GLN
2	A4	60	LYS
2	A4	85	HIS
2	A4	96	LYS
2	A4	224	TYR
2	A4	257	THR
2	A4	328	VAL
2	A4	338	LYS
2	A4	370	LYS
2	A4	372	MET
2	A4	401	LYS
3	A5	11	GLN
3	A5	320	ARG
3	A5	325	GLU
2	A6	96	LYS
2	A6	214	ARG
2	A6	224	TYR
2	A6	254	GLU
2	A6	323	VAL
2	A6	370	LYS
2	A6	401	LYS
2	A6	413	MET
2	A6	430	LYS
3	A7	11	GLN
3	A7	247	ASN
3	A7	297	LYS
3	A7	336	LYS
3	A7	390	ARG
2	A8	85	HIS
2	A8	92	LEU
2	A8	96	LYS
2	A8	163	LYS
2	A8	164	LYS
2	A8	235	ILE

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Mol	Chain	Res	Type
2	A8	341	ILE
2	A8	353	CYS
3	A9	42	LEU
3	A9	45	GLU
3	A9	46	ARG
3	A9	174	LYS
3	A9	280	GLN
3	A9	324	LYS
3	A9	351	SER
3	A9	379	LYS
3	A9	391	ARG
2	B0	82	THR
2	B0	92	LEU
2	B0	98	ASP
2	B0	117	LEU
2	B0	156	ARG
2	B0	163	LYS
2	B0	257	THR
2	B0	338	LYS
2	B0	372	MET
2	B0	401	LYS
3	B1	193	VAL
3	B1	252	LYS
3	B1	280	GLN
3	B1	362	LYS
2	B2	2	ARG
2	B2	32	PRO
2	B2	163	LYS
2	B2	196	GLU
2	B2	252	VAL
2	B2	297	GLU
2	B2	336	LYS
2	B2	363	VAL
2	B2	370	LYS
2	B2	393	HIS
3	B3	46	ARG
3	B3	154	LYS
3	B3	171	PRO
3	B3	336	LYS
2	B4	60	LYS
2	B4	163	LYS
2	B4	164	LYS

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Mol	Chain	Res	Type
2	B4	221	ARG
2	B4	227	LEU
2	B4	280	LYS
2	B4	336	LYS
2	B4	370	LYS
2	B4	378	ILE
3	B5	16	ILE
3	B5	162	ARG
3	B5	252	LYS
3	B5	324	LYS
3	B5	336	LYS
2	B6	92	LEU
2	B6	285	GLN
2	B6	326	LYS
2	B6	339	ARG
3	B7	11	GLN
3	B7	55	THR
3	B7	122	LYS
3	B7	147	MET
3	B7	256	ASN
3	B7	324	LYS
2	B8	60	LYS
2	B8	92	LEU
2	B8	181	VAL
2	B8	311	LYS
2	B8	372	MET
2	B8	397	LEU
3	B9	46	ARG
3	B9	55	THR
3	B9	157	GLU
3	B9	177	ASP
3	B9	280	GLN
3	B9	359	LYS
3	B9	379	LYS
2	C0	7	ILE
2	C0	96	LYS
2	C0	154	LEU
2	C0	264	ARG
2	C0	326	LYS
2	C0	336	LYS
2	C0	370	LYS
3	C1	45	GLU

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Mol	Chain	Res	Type
3	C1	174	LYS
3	C1	324	LYS
2	C2	96	LYS
2	C2	163	LYS
2	C2	181	VAL
3	C3	95	THR
3	C3	324	LYS
3	C3	388	MET
2	C4	326	LYS
2	C4	401	LYS
3	C5	11	GLN
3	C5	42	LEU
3	C5	83	GLN
3	C5	114	ASP
3	C5	174	LYS
3	C5	291	GLN
3	C5	297	LYS
3	C5	379	LYS
2	C6	31	GLN
2	C6	112	LYS
2	C6	132	LEU
2	C6	338	LYS
2	C6	339	ARG
2	C6	370	LYS
2	C6	401	LYS
3	C7	11	GLN
3	C7	42	LEU
3	C7	88	ASP
3	C7	174	LYS
3	C7	324	LYS
3	C7	334	GLN
3	C7	405	GLU
2	C8	84	ARG
2	C8	96	LYS
2	C8	163	LYS
2	C8	224	TYR
2	C8	285	GLN
2	C8	311	LYS
2	C8	368	LEU
2	C8	390	ARG
2	C8	401	LYS
3	C9	154	LYS

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Mol	Chain	Res	Type
3	C9	291	GLN
3	C9	390	ARG
2	D0	15	GLN
2	D0	35	GLN
2	D0	36	MET
2	D0	84	ARG
2	D0	156	ARG
2	D0	370	LYS
2	D0	401	LYS
2	D0	409	VAL
3	D1	11	GLN
3	D1	99	ASN
3	D1	217	LEU
3	D1	245	GLN
3	D1	343	GLU
2	D2	85	HIS
2	D2	92	LEU
2	D2	124	LYS
2	D2	248	LEU
2	D2	264	ARG
2	D2	311	LYS
2	D2	339	ARG
2	D2	370	LYS
3	D3	19	LYS
3	D3	191	GLN
3	D3	362	LYS
3	D3	379	LYS
2	D4	156	ARG
2	D4	163	LYS
2	D4	401	LYS
2	D4	437	ILE
3	D5	48	ASN
3	D5	55	THR
3	D5	157	GLU
3	D5	216	LYS
3	D5	324	LYS
3	D5	391	ARG
2	D6	33	ASP
2	D6	85	HIS
2	D6	96	LYS
2	D6	218	ASP
2	D6	297	GLU

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Mol	Chain	Res	Type
3	D7	122	LYS
3	D7	164	MET
3	D7	216	LYS
3	D7	279	GLN
2	D8	153	LEU
2	D8	163	LYS
2	D8	219	ILE
2	D8	326	LYS
2	D8	372	MET
2	D8	430	LYS
3	D9	19	LYS
3	D9	32	PRO
3	D9	48	ASN
3	D9	154	LYS
3	D9	216	LYS
3	D9	362	LYS
2	E0	96	LYS
2	E0	163	LYS
3	E1	11	GLN
3	E1	122	LYS
3	E1	147	MET
3	E1	215	LEU
3	E1	287	PRO
3	E1	297	LYS
3	E1	328	GLU
3	E1	361	LEU
3	E1	391	ARG
2	E2	85	HIS
2	E2	130	THR
2	E2	184	PRO
2	E2	397	LEU
2	E2	430	LYS
3	E3	11	GLN
3	E3	55	THR
3	E3	83	GLN
3	E3	130	LEU
3	E3	174	LYS
3	E3	247	ASN
3	E3	336	LYS
3	E3	362	LYS
3	E3	406	MET
2	E4	2	ARG

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Mol	Chain	Res	Type
2	E4	124	LYS
2	E4	256	GLN
3	E5	11	GLN
3	E5	122	LYS
3	E5	359	LYS
3	E5	362	LYS
2	E6	124	LYS
2	E6	338	LYS
3	E7	55	THR
3	E7	122	LYS
3	E7	154	LYS
3	E7	174	LYS
3	E7	189	VAL
3	E7	320	ARG
3	E7	323	THR
2	E8	401	LYS
3	E9	83	GLN
3	E9	88	ASP
3	E9	280	GLN
3	E9	281	TYR
2	F0	124	LYS
2	F0	227	LEU
2	F0	280	LYS
2	F0	282	TYR
2	F0	283	HIS
2	F0	304	LYS
2	F0	336	LYS
2	F0	433	GLU
3	F1	177	ASP
3	F1	252	LYS
3	F1	320	ARG
3	F1	324	LYS
3	F1	359	LYS
4	a	146	ARG
4	a	196	LEU
4	a	202	ARG
4	b	69	LYS
4	b	176	ASP
4	c	63	ILE
4	c	202	ARG
4	d	17	LEU
4	d	28	LYS

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Mol	Chain	Res	Type
4	d	35	ASN
4	d	101	GLU
4	d	191	GLU
4	d	202	ARG
4	e	107	LYS
4	e	120	GLU
4	e	146	ARG
4	e	153	GLU
4	f	35	ASN
4	f	36	ILE
4	f	69	LYS
4	f	84	LYS
4	f	202	ARG
4	g	24	MET
4	g	28	LYS
4	g	130	PRO
4	h	130	PRO
4	i	97	ARG
4	i	152	LYS
4	j	97	ARG
4	k	198	ARG
4	l	3	GLN
4	m	99	MET
4	m	196	LEU
4	n	28	LYS
4	n	62	VAL
4	n	101	GLU
4	n	202	ARG
4	o	24	MET
4	o	63	ILE
4	o	91	PHE
4	o	110	ILE
4	o	117	ARG
4	o	164	ARG
4	o	202	ARG
4	p	97	ARG
4	p	152	LYS
4	p	202	ARG
4	q	97	ARG
4	q	110	ILE
4	q	152	LYS
4	r	117	ARG

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Mol	Chain	Res	Type
4	r	152	LYS
4	r	202	ARG
4	s	63	ILE
4	s	97	ARG
4	s	202	ARG
4	t	173	ILE
4	v	3	GLN
4	v	69	LYS
4	v	94	ASN
4	v	97	ARG
4	v	202	ARG
5	w	25	ARG
5	w	58	LYS
5	w	66	LYS
4	x	17	LEU
4	x	56	LYS
4	x	101	GLU
4	x	117	ARG
4	x	120	GLU
4	x	198	ARG
4	y	47	LEU
4	y	198	ARG
4	y	202	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (409) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	244	GLN
1	10	242	ASN
1	10	244	GLN
1	12	242	ASN
1	15	242	ASN
1	16	242	ASN
1	17	242	ASN
1	18	244	GLN
1	2	242	ASN
1	20	244	GLN
1	3	242	ASN
1	8	244	GLN
2	A0	85	HIS
2	A0	102	ASN
2	A0	228	ASN

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Mol	Chain	Res	Type
2	A0	258	ASN
2	A0	406	HIS
3	A1	43	GLN
3	A1	83	GLN
3	A1	89	ASN
3	A1	247	ASN
3	A1	256	ASN
3	A1	329	GLN
3	A1	347	ASN
3	A1	348	ASN
3	A1	375	GLN
2	A2	85	HIS
2	A2	101	ASN
2	A2	128	ASN
2	A2	228	ASN
2	A2	285	GLN
2	A2	358	GLN
2	A2	393	HIS
3	A3	89	ASN
3	A3	94	GLN
3	A3	256	ASN
3	A3	414	ASN
2	A4	18	ASN
2	A4	28	HIS
2	A4	88	HIS
2	A4	101	ASN
3	A5	43	GLN
3	A5	280	GLN
3	A5	329	GLN
3	A5	347	ASN
3	A5	348	ASN
2	A6	11	GLN
2	A6	18	ASN
2	A6	31	GLN
2	A6	101	ASN
2	A6	102	ASN
2	A6	128	ASN
2	A6	133	GLN
2	A6	168	ASN
2	A6	256	GLN
2	A6	283	HIS
2	A6	285	GLN

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Mol	Chain	Res	Type
2	A6	342	GLN
2	A6	380	ASN
3	A7	131	GLN
3	A7	191	GLN
3	A7	195	ASN
3	A7	204	ASN
3	A7	245	GLN
3	A7	247	ASN
3	A7	329	GLN
2	A8	11	GLN
2	A8	91	GLN
2	A8	101	ASN
2	A8	102	ASN
2	A8	128	ASN
2	A8	258	ASN
2	A8	283	HIS
2	A8	329	ASN
2	A8	380	ASN
2	A8	393	HIS
3	A9	137	HIS
3	A9	190	HIS
3	A9	279	GLN
3	A9	329	GLN
3	A9	396	HIS
2	B0	91	GLN
2	B0	101	ASN
2	B0	102	ASN
2	B0	197	HIS
2	B0	226	ASN
2	B0	233	GLN
2	B0	283	HIS
2	B0	285	GLN
2	B0	380	ASN
3	B1	94	GLN
2	B2	11	GLN
2	B2	91	GLN
2	B2	101	ASN
2	B2	226	ASN
2	B2	256	GLN
2	B2	283	HIS
3	B3	11	GLN
3	B3	99	ASN

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Mol	Chain	Res	Type
3	B3	100	ASN
3	B3	131	GLN
3	B3	190	HIS
3	B3	195	ASN
3	B3	307	HIS
3	B3	347	ASN
3	B3	348	ASN
2	B4	11	GLN
2	B4	216	ASN
2	B4	228	ASN
2	B4	266	HIS
3	B5	14	ASN
3	B5	43	GLN
3	B5	52	ASN
3	B5	99	ASN
3	B5	191	GLN
3	B5	298	ASN
3	B5	329	GLN
3	B5	334	GLN
3	B5	347	ASN
3	B5	348	ASN
2	B6	31	GLN
2	B6	168	ASN
2	B6	256	GLN
3	B7	105	HIS
3	B7	307	HIS
3	B7	396	HIS
3	B7	423	GLN
2	B8	11	GLN
2	B8	107	HIS
2	B8	133	GLN
2	B8	176	GLN
2	B8	206	ASN
2	B8	216	ASN
2	B8	226	ASN
2	B8	258	ASN
2	B8	406	HIS
3	B9	8	GLN
3	B9	137	HIS
3	B9	191	GLN
3	B9	227	HIS
3	B9	245	GLN

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Mol	Chain	Res	Type
2	C0	11	GLN
2	C0	216	ASN
2	C0	258	ASN
2	C0	283	HIS
2	C0	293	ASN
2	C0	406	HIS
3	C1	8	GLN
3	C1	89	ASN
3	C1	195	ASN
3	C1	426	GLN
2	C2	11	GLN
2	C2	28	HIS
2	C2	256	GLN
2	C2	329	ASN
2	C2	380	ASN
3	C3	8	GLN
3	C3	14	ASN
3	C3	43	GLN
3	C3	105	HIS
3	C3	137	HIS
3	C3	190	HIS
3	C3	191	GLN
3	C3	195	ASN
3	C3	335	ASN
3	C3	424	GLN
3	C3	426	GLN
2	C4	31	GLN
2	C4	101	ASN
2	C4	133	GLN
2	C4	206	ASN
3	C5	105	HIS
3	C5	131	GLN
3	C5	226	ASN
3	C5	335	ASN
3	C5	337	ASN
3	C5	348	ASN
2	C6	28	HIS
2	C6	128	ASN
2	C6	168	ASN
2	C6	356	ASN
3	C7	14	ASN
3	C7	131	GLN

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Mol	Chain	Res	Type
3	C7	245	GLN
3	C7	247	ASN
3	C7	332	ASN
3	C7	348	ASN
2	C8	28	HIS
2	C8	206	ASN
2	C8	256	GLN
3	C9	11	GLN
3	C9	94	GLN
3	C9	99	ASN
3	C9	131	GLN
3	C9	264	HIS
3	C9	334	GLN
2	D0	31	GLN
2	D0	139	ASN
2	D0	283	HIS
3	D1	11	GLN
3	D1	99	ASN
3	D1	245	GLN
3	D1	247	ASN
3	D1	337	ASN
3	D1	396	HIS
2	D2	11	GLN
2	D2	15	GLN
2	D2	85	HIS
2	D2	88	HIS
2	D2	258	ASN
2	D2	283	HIS
2	D2	293	ASN
2	D2	356	ASN
2	D2	380	ASN
3	D3	134	GLN
3	D3	195	ASN
3	D3	247	ASN
3	D3	256	ASN
3	D3	279	GLN
3	D3	332	ASN
2	D4	11	GLN
2	D4	216	ASN
2	D4	283	HIS
2	D4	380	ASN
3	D5	6	HIS

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Mol	Chain	Res	Type
3	D5	195	ASN
3	D5	245	GLN
3	D5	334	GLN
3	D5	337	ASN
3	D5	348	ASN
2	D6	91	GLN
2	D6	102	ASN
2	D6	176	GLN
2	D6	186	ASN
2	D6	216	ASN
2	D6	283	HIS
3	D7	99	ASN
3	D7	191	GLN
3	D7	204	ASN
3	D7	279	GLN
3	D7	292	GLN
3	D7	348	ASN
3	D7	375	GLN
3	D7	426	GLN
2	D8	35	GLN
2	D8	50	ASN
2	D8	102	ASN
2	D8	283	HIS
2	D8	356	ASN
3	D9	6	HIS
3	D9	8	GLN
3	D9	14	ASN
3	D9	52	ASN
3	D9	204	ASN
3	D9	348	ASN
2	E0	18	ASN
2	E0	31	GLN
2	E0	102	ASN
2	E0	258	ASN
2	E0	356	ASN
2	E0	406	HIS
3	E1	11	GLN
3	E1	14	ASN
3	E1	43	GLN
3	E1	99	ASN
3	E1	191	GLN
3	E1	245	GLN

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Mol	Chain	Res	Type
3	E1	298	ASN
3	E1	347	ASN
3	E1	348	ASN
2	E2	31	GLN
2	E2	216	ASN
2	E2	228	ASN
2	E2	283	HIS
2	E2	309	HIS
2	E2	406	HIS
3	E3	6	HIS
3	E3	137	HIS
3	E3	247	ASN
3	E3	291	GLN
2	E4	11	GLN
2	E4	31	GLN
2	E4	50	ASN
2	E4	85	HIS
2	E4	91	GLN
2	E4	102	ASN
2	E4	128	ASN
2	E4	197	HIS
2	E4	283	HIS
2	E4	342	GLN
3	E5	11	GLN
3	E5	190	HIS
3	E5	245	GLN
3	E5	247	ASN
3	E5	256	ASN
3	E5	347	ASN
3	E5	348	ASN
3	E5	414	ASN
3	E5	423	GLN
2	E6	11	GLN
2	E6	35	GLN
2	E6	206	ASN
2	E6	216	ASN
2	E6	226	ASN
2	E6	358	GLN
2	E6	406	HIS
3	E7	43	GLN
3	E7	245	GLN
3	E7	375	GLN

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Mol	Chain	Res	Type
3	E7	396	HIS
3	E7	414	ASN
2	E8	8	HIS
2	E8	85	HIS
2	E8	88	HIS
2	E8	128	ASN
2	E8	133	GLN
3	E9	11	GLN
3	E9	204	ASN
3	E9	256	ASN
3	E9	335	ASN
3	E9	347	ASN
3	E9	348	ASN
2	F0	226	ASN
2	F0	258	ASN
2	F0	266	HIS
2	F0	283	HIS
3	F1	15	GLN
3	F1	105	HIS
3	F1	134	GLN
3	F1	291	GLN
3	F1	337	ASN
3	F1	347	ASN
4	a	100	ASN
4	a	105	ASN
4	b	60	ASN
4	b	94	ASN
4	c	65	GLN
4	c	106	GLN
4	c	125	HIS
4	d	35	ASN
4	d	37	GLN
4	d	203	ASN
4	e	3	GLN
4	e	35	ASN
4	e	37	GLN
4	f	18	ASN
4	f	37	GLN
4	g	37	GLN
4	g	106	GLN
4	h	27	GLN
4	h	37	GLN

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Mol	Chain	Res	Type
4	h	67	HIS
4	h	106	GLN
4	i	37	GLN
4	i	67	HIS
4	i	106	GLN
4	i	128	HIS
4	j	3	GLN
4	j	18	ASN
4	j	67	HIS
4	j	125	HIS
4	k	11	ASN
4	k	181	GLN
4	k	203	ASN
4	l	11	ASN
4	l	67	HIS
4	l	181	GLN
4	m	11	ASN
4	m	35	ASN
4	m	59	ASN
4	m	147	HIS
4	n	18	ASN
4	n	35	ASN
4	n	59	ASN
4	n	105	ASN
4	n	125	HIS
4	o	67	HIS
4	p	18	ASN
4	p	37	GLN
4	p	67	HIS
4	p	94	ASN
4	p	105	ASN
4	q	25	GLN
4	q	37	GLN
4	q	60	ASN
4	q	181	GLN
4	r	3	GLN
4	r	11	ASN
4	s	25	GLN
4	t	11	ASN
4	t	94	ASN
4	t	181	GLN
4	u	59	ASN

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Mol	Chain	Res	Type
4	u	67	HIS
4	u	100	ASN
4	u	106	GLN
4	u	181	GLN
4	v	18	ASN
4	v	59	ASN
4	v	67	HIS
4	v	94	ASN
4	v	203	ASN
5	w	43	HIS
4	x	11	ASN
4	x	181	GLN
4	y	11	ASN
4	y	37	GLN
4	y	181	GLN
4	y	203	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

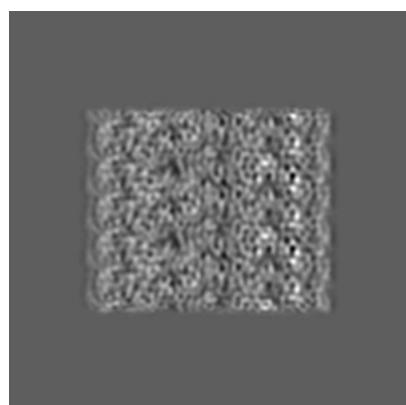
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26019. These allow visual inspection of the internal detail of the map and identification of artifacts.

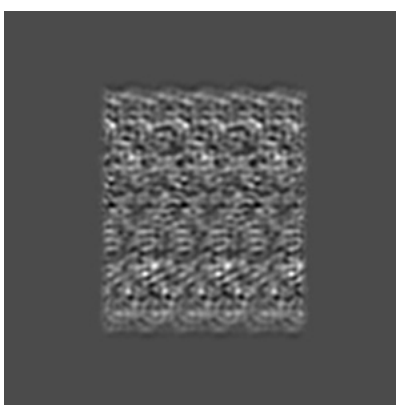
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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: 108



Y Index: 108



Z Index: 108

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: 156



Y Index: 153

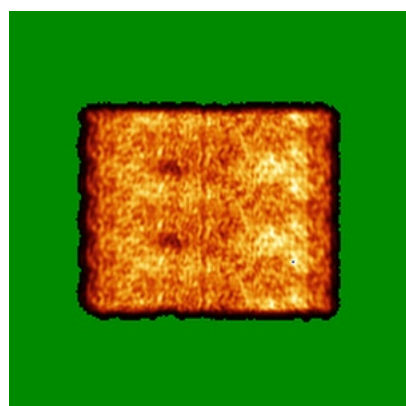


Z Index: 155

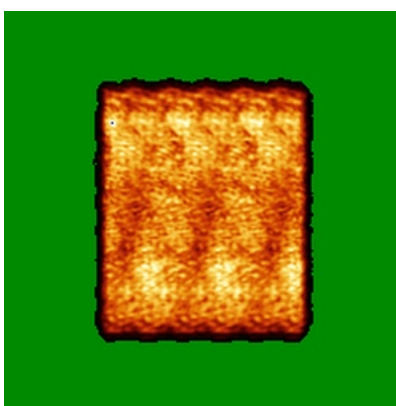
The images above show the largest variance slices of the map in three orthogonal directions.

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

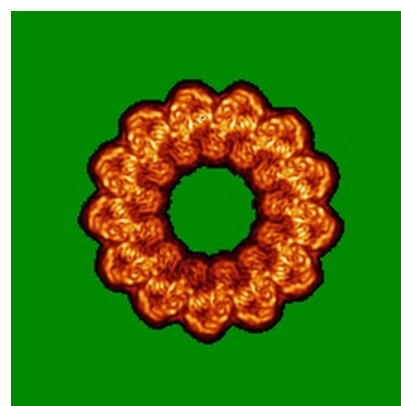
6.4.1 Primary map



X



Y

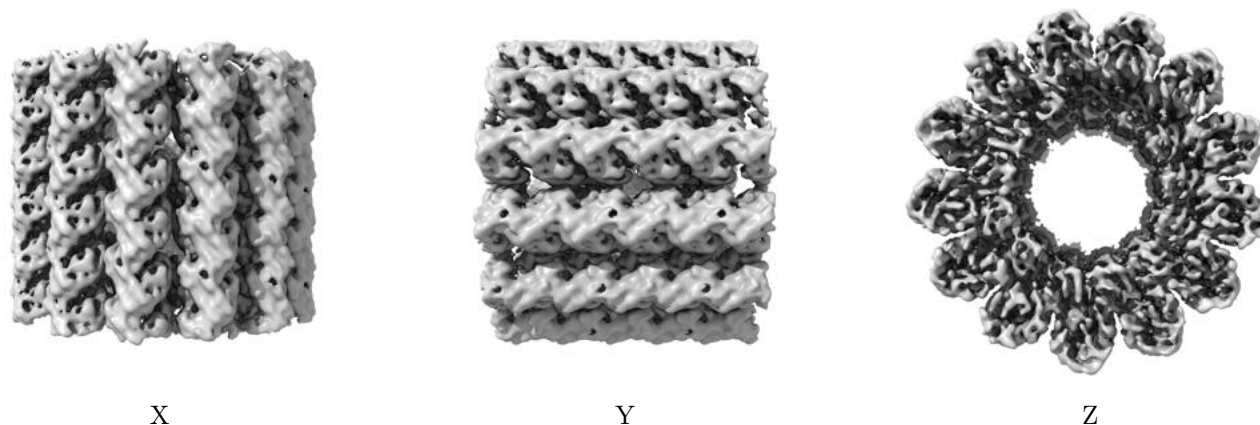


Z

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

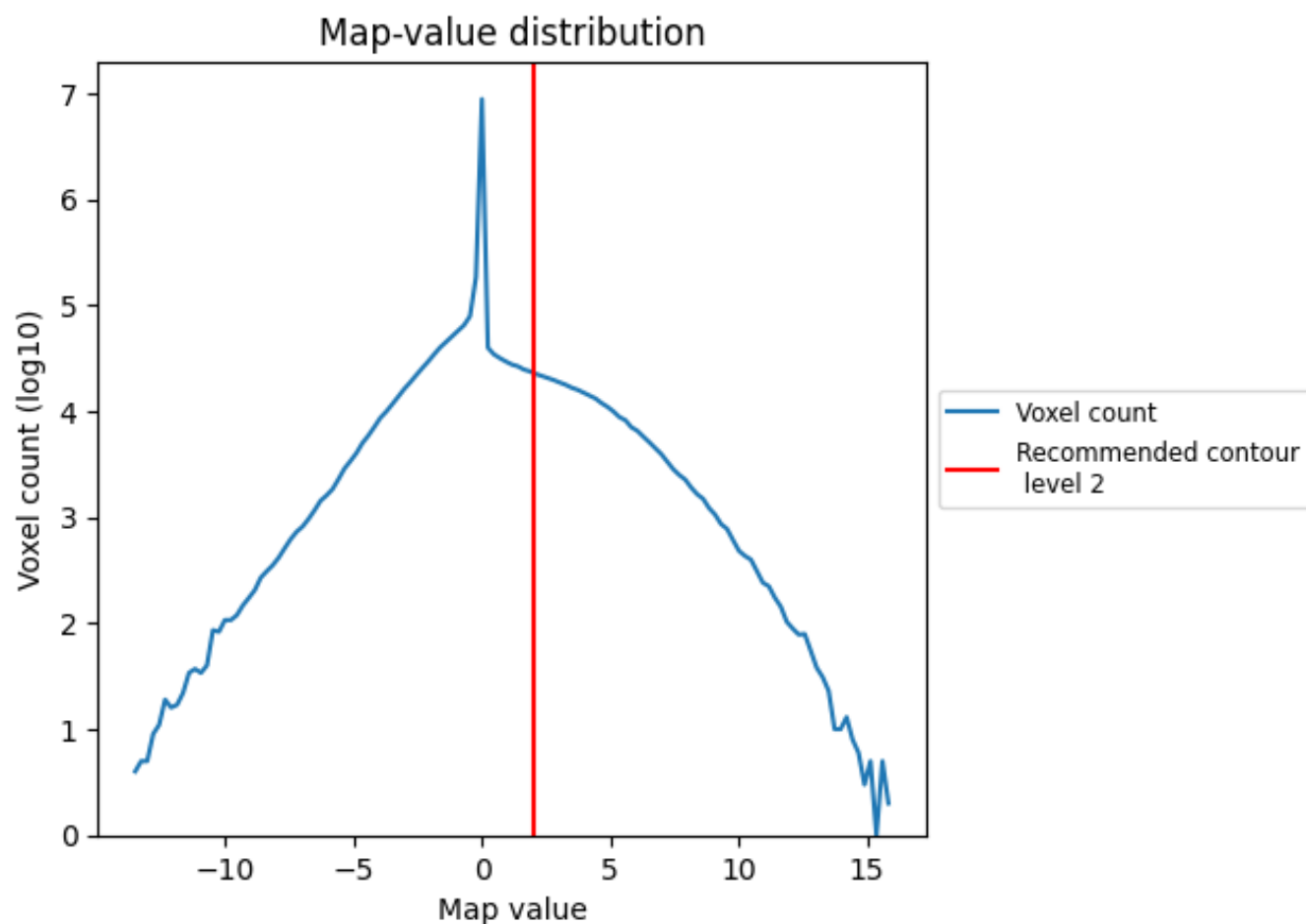
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

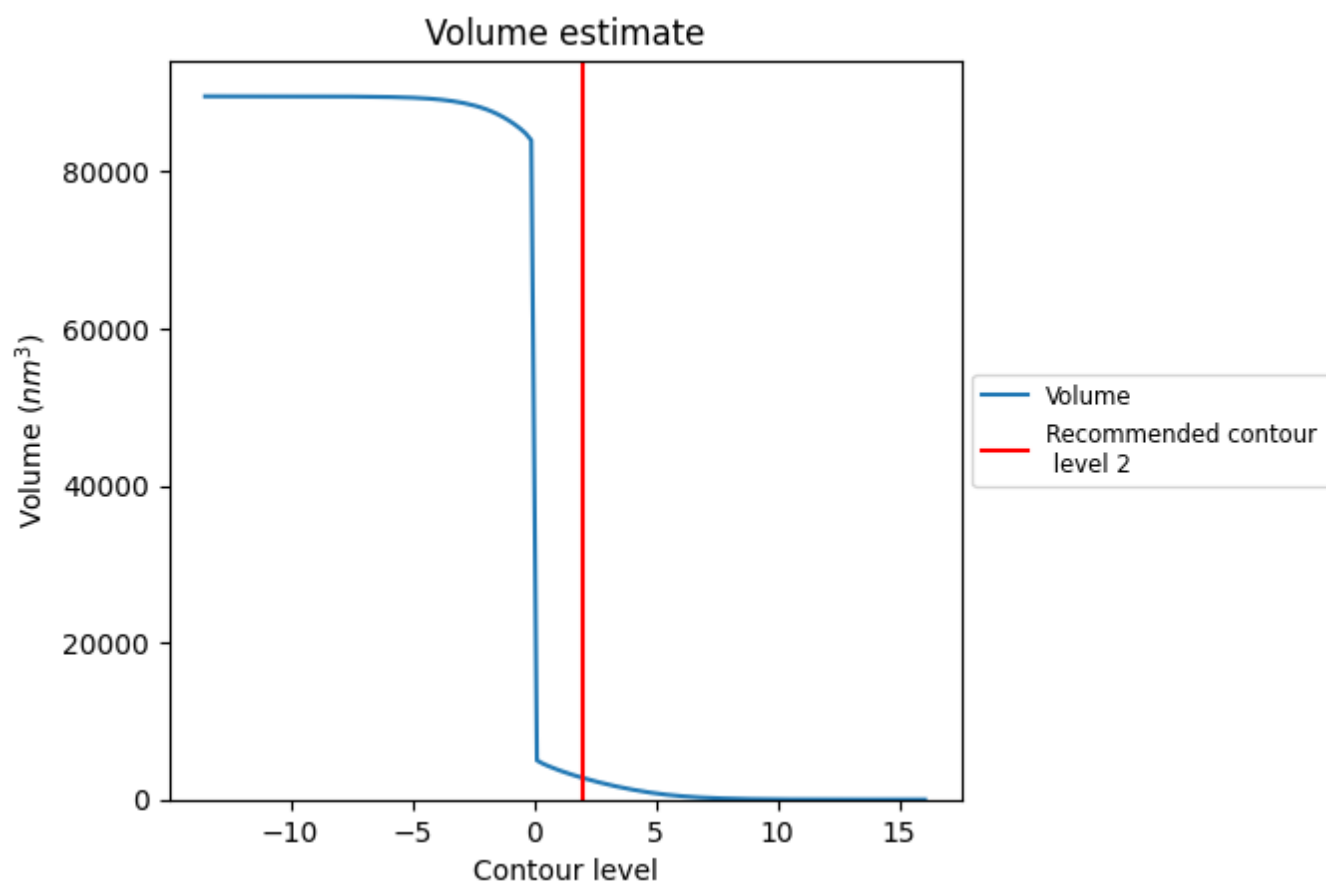
This section contains the results of statistical analysis of the map.

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.

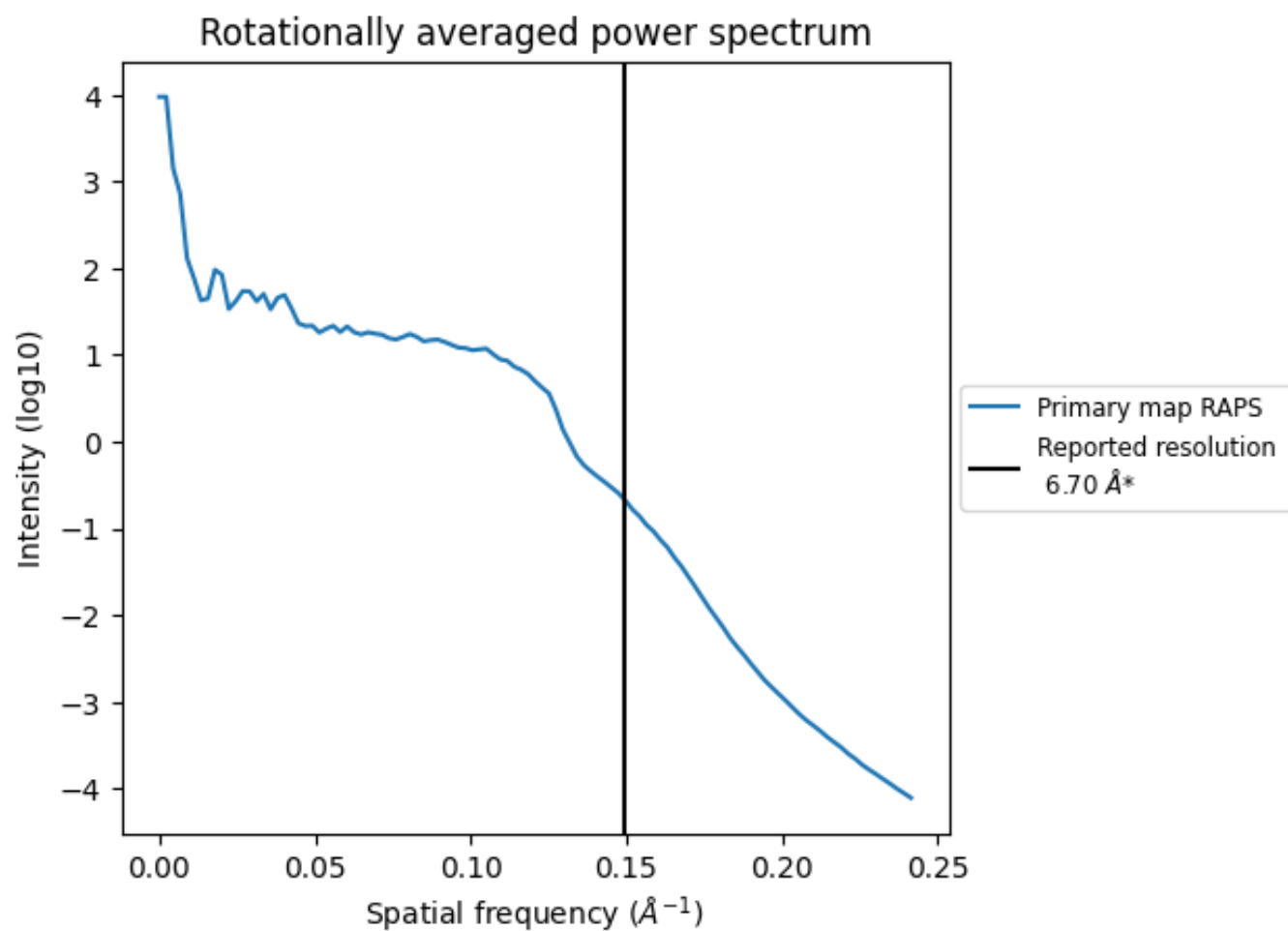
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2760 nm³; this corresponds to an approximate mass of 2494 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 0.149 Å⁻¹

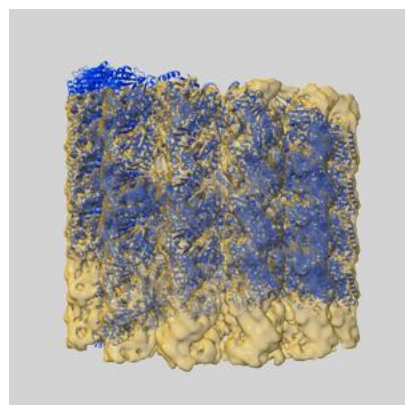
8 Fourier-Shell correlation

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

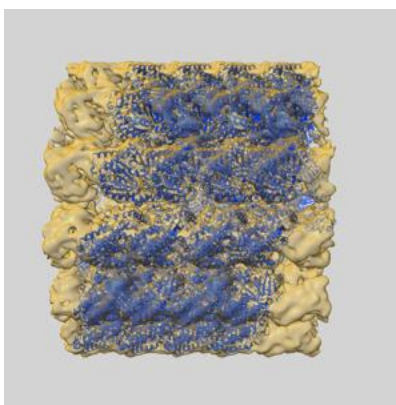
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26019 and PDB model 7TNS. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

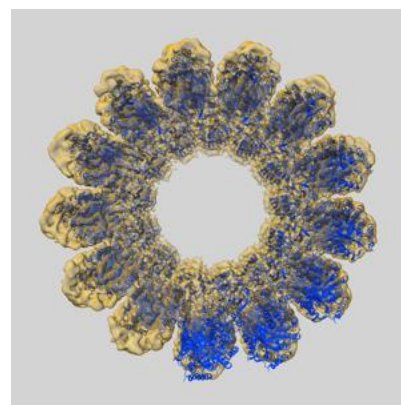
9.1 Map-model overlay [i](#)



X



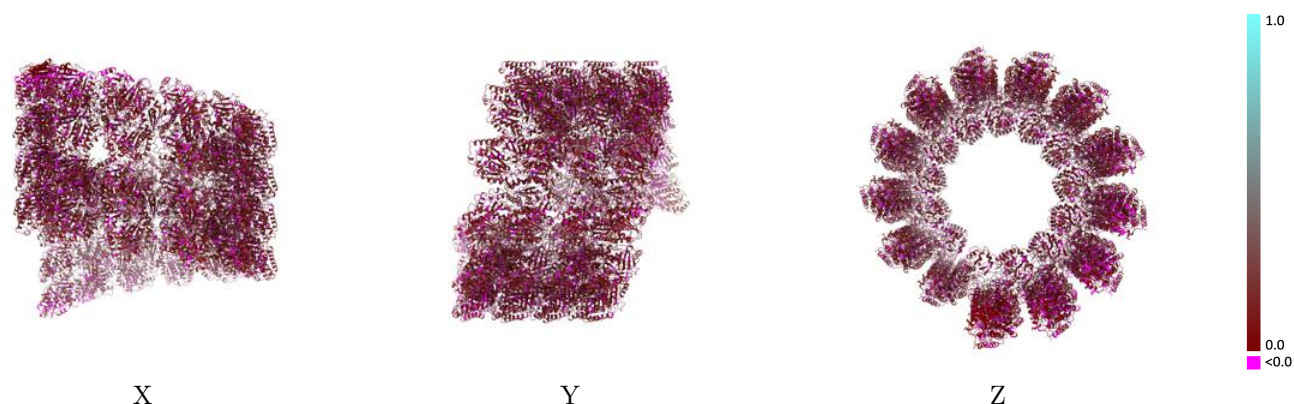
Y



Z

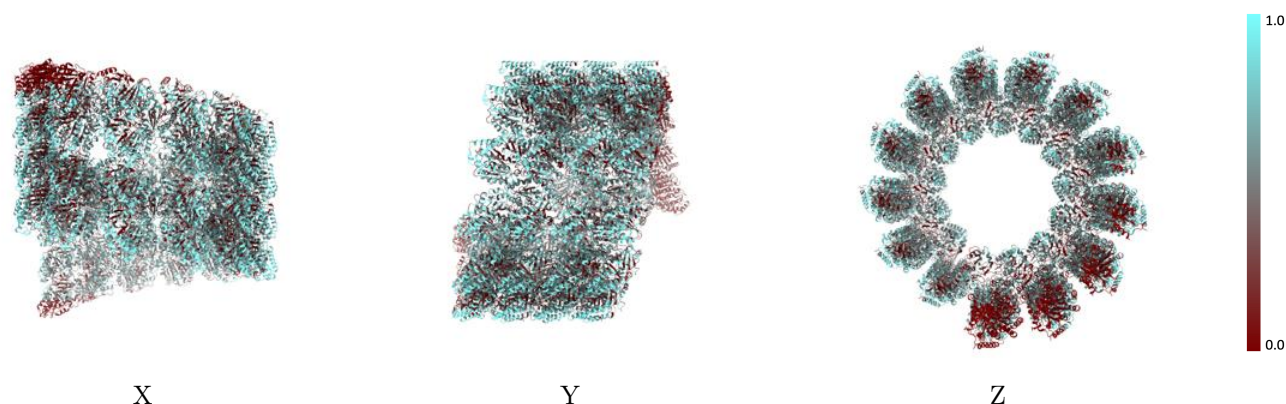
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



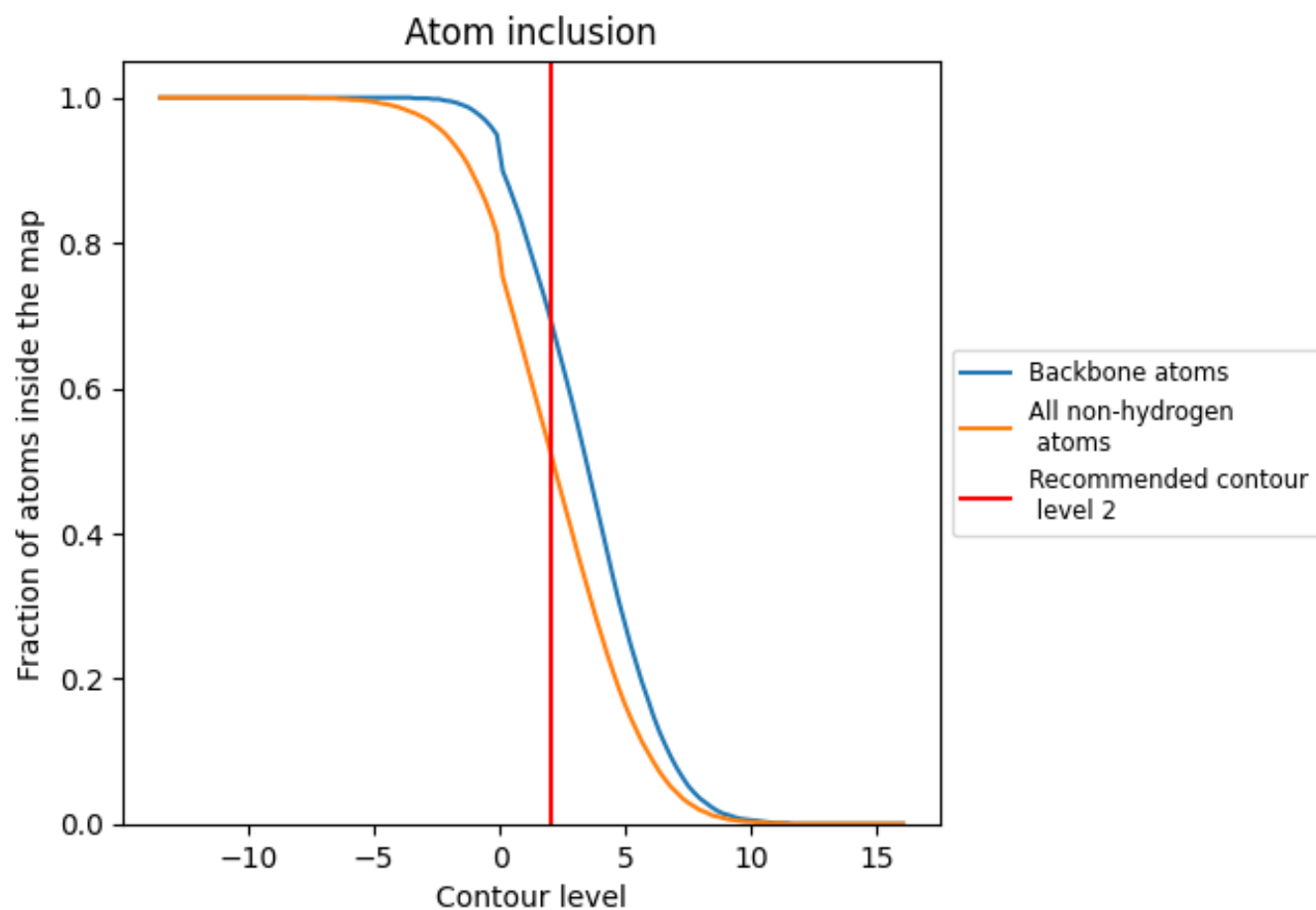
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 52% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5150	 0.1180
0	 0.2880	 0.1450
1	 0.3000	 0.1410
10	 0.3880	 0.1250
11	 0.3770	 0.1420
12	 0.3710	 0.1570
13	 0.3470	 0.1610
14	 0.2770	 0.1400
15	 0.3350	 0.1650
16	 0.2120	 0.1180
17	 0.3000	 0.1450
18	 0.0470	 0.0790
19	 0.1000	 0.0800
2	 0.3240	 0.1350
20	 0.0000	 0.0610
21	 0.1710	 0.0210
22	 0.3650	 0.1020
23	 0.3590	 0.1330
3	 0.3410	 0.1590
4	 0.3350	 0.1460
5	 0.3880	 0.1640
6	 0.3710	 0.1390
7	 0.3180	 0.1220
8	 0.3470	 0.1410
9	 0.3180	 0.1130
A0	 0.5410	 0.1270
A1	 0.5410	 0.1220
A2	 0.5450	 0.1240
A3	 0.3160	 0.0720
A4	 0.5640	 0.1300
A5	 0.5420	 0.1250
A6	 0.5610	 0.1270
A7	 0.4440	 0.0970
A8	 0.5680	 0.1290
A9	 0.5510	 0.1270



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Chain	Atom inclusion	Q-score
B0	 0.5640	 0.1260
B1	 0.4770	 0.0940
B2	 0.5620	 0.1280
B3	 0.5590	 0.1210
B4	 0.5620	 0.1260
B5	 0.5190	 0.1020
B6	 0.5520	 0.1200
B7	 0.5630	 0.1200
B8	 0.5570	 0.1190
B9	 0.5680	 0.1170
C0	 0.5670	 0.1310
C1	 0.5730	 0.1230
C2	 0.5620	 0.1300
C3	 0.5730	 0.1200
C4	 0.5620	 0.1310
C5	 0.5810	 0.1280
C6	 0.5520	 0.1250
C7	 0.5840	 0.1230
C8	 0.5470	 0.1270
C9	 0.5890	 0.1300
D0	 0.5540	 0.1270
D1	 0.5910	 0.1260
D2	 0.5270	 0.1210
D3	 0.5800	 0.1270
D4	 0.5520	 0.1280
D5	 0.5880	 0.1260
D6	 0.4660	 0.1050
D7	 0.5750	 0.1290
D8	 0.5500	 0.1300
D9	 0.5760	 0.1250
E0	 0.3190	 0.0770
E1	 0.5510	 0.1200
E2	 0.5540	 0.1280
E3	 0.5630	 0.1200
E4	 0.1930	 0.0440
E5	 0.5400	 0.1200
E6	 0.5510	 0.1250
E7	 0.5400	 0.1200
E8	 0.0500	 0.0060
E9	 0.5170	 0.1160
F0	 0.5540	 0.1250
F1	 0.5370	 0.1200

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Chain	Atom inclusion	Q-score
a	 0.4960	 0.1230
b	 0.4710	 0.1120
c	 0.4990	 0.1250
d	 0.5070	 0.1220
e	 0.5110	 0.1290
f	 0.5110	 0.1280
g	 0.5130	 0.1210
h	 0.5280	 0.1240
i	 0.5250	 0.1290
j	 0.5190	 0.1320
k	 0.5070	 0.1260
l	 0.5190	 0.1290
m	 0.5110	 0.1300
n	 0.5060	 0.1300
o	 0.4990	 0.1310
p	 0.4990	 0.1290
q	 0.4920	 0.1250
r	 0.4930	 0.1310
s	 0.4880	 0.1280
t	 0.4650	 0.1220
u	 0.4320	 0.1110
v	 0.4830	 0.1240
w	 0.3220	 0.0780
x	 0.4590	 0.1250
y	 0.3440	 0.1120