



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:28 PM UTC

PDB ID : 6TF9 / pdb_00006tf9
EMDB ID : EMD-10491
Title : Structure of the vertebrate gamma-Tubulin Ring Complex
Authors : Zupa, E.; Pfeffer, S.
Deposited on : 2019-11-13
Resolution : 4.80 Å(reported)
Based on initial model : 3RIP

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

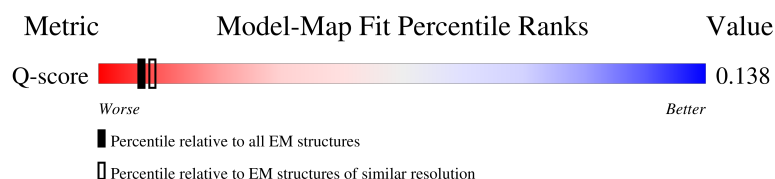
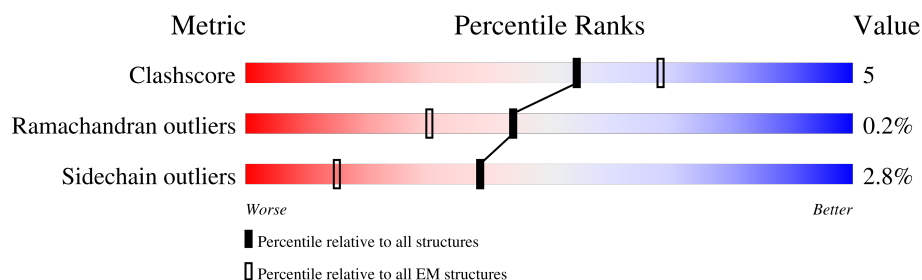
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.80 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	1575 (4.30 - 5.30)

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	AP1	29	100%
2	CP1	13	100%
2	HP1	13	100%
2	IP1	13	100%

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Mol	Chain	Length	Quality of chain
2	XP1	13	100%
3	DP1	31	100%
4	EP1	23	100%
5	FP1	18	100%
6	GP1	15	13% 100%
6	LP1	15	100%
6	NP1	15	100%
7	JP1	14	7% 100%
7	vP1	14	100%
8	KP1	16	100%
8	OP1	16	100%
8	PP1	16	100%
8	uP1	16	12% 94% 6%
9	MP1	17	6% 100%
10	QP1	906	15% 56% 10% 31%
10	cP1	906	17% 61% 8% 31%
10	dP1	906	15% 58% 11% 31%
10	eP1	906	12% 59% 9% 31%
10	fP1	906	16% 58% 10% 31%
11	RP1	896	10% 49% 12% 38%
11	YP1	896	11% 50% 11% 38%
11	ZP1	896	9% 52% 8% 39%
11	aP1	896	9% 53% 8% 39%
11	bP1	896	11% 54% 8% 38%
12	SP1	1625	8% 29% 6% 65%

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Mol	Chain	Length	Quality of chain
13	TP1	451	
13	hP1	451	
13	iP1	451	
13	kP1	451	
13	lP1	451	
13	mP1	451	
13	nP1	451	
13	oP1	451	
13	pP1	451	
13	qP1	451	
13	rP1	451	
13	sP1	451	
13	tP1	451	
13	wP1	451	
14	UP1	1019	
15	VP1	666	
15	WP1	666	
16	gP1	19	
17	jP1	375	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 120053 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 Helix 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	AP1	29	Total	C	N	O	0	0
			146	87	29	30		

- Molecule 2 is a protein called Belt helices 1,2,3,4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	CP1	13	Total	C	N	O	0	0
			66	39	13	14		
2	HP1	13	Total	C	N	O	0	0
			66	39	13	14		
2	IP1	13	Total	C	N	O	0	0
			66	39	13	14		
2	XP1	13	Total	C	N	O	0	0
			66	39	13	14		

- Molecule 3 is a protein called Belt helix 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	DP1	31	Total	C	N	O	0	0
			156	93	31	32		

- Molecule 4 is a protein called Belt helix 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	EP1	23	Total	C	N	O	0	0
			116	69	23	24		

- Molecule 5 is a protein called Belt helix 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	FP1	18	Total	C	N	O	0	0
			91	54	18	19		

- Molecule 6 is a protein called Belt helices 8,9,10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	GP1	15	Total	C	N	O	0	0
			76	45	15	16		
6	LP1	15	Total	C	N	O	0	0
			76	45	15	16		
6	NP1	15	Total	C	N	O	0	0
			76	45	15	16		

- Molecule 7 is a protein called Belt helices 11,12.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	JP1	14	Total	C	N	O	0	0
			71	42	14	15		
7	vP1	14	Total	C	N	O	0	0
			71	42	14	15		

- Molecule 8 is a protein called Belt helices 13,14,15 and Helix 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	KP1	16	Total	C	N	O	0	0
			81	48	16	17		
8	OP1	16	Total	C	N	O	0	0
			81	48	16	17		
8	PP1	16	Total	C	N	O	0	0
			81	48	16	17		
8	uP1	16	Total	C	N	O	0	0
			81	48	16	17		

- Molecule 9 is a protein called Belt helix 16.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	MP1	17	Total	C	N	O	0	0
			86	51	17	18		

- Molecule 10 is a protein called Gamma-tubulin complex component 3 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	QP1	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
10	cP1	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	dP1	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
10	eP1	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
10	fP1	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		

- Molecule 11 is a protein called Gamma-tubulin complex component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	RP1	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
11	YP1	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
11	ZP1	551	Total	C	N	O	S	0	0
			4508	2898	740	838	32		
11	aP1	551	Total	C	N	O	S	0	0
			4503	2894	739	838	32		
11	bP1	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		

- Molecule 12 is a protein called Gamma tubulin ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SP1	576	Total	C	N	O	S	0	0
			4699	3068	765	843	23		

- Molecule 13 is a protein called Tubulin gamma-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	TP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	hP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	iP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	kP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	lP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	mP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	nP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	oP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	pP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	qP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	rP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	sP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	tP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		
13	wP1	436	Total	C	N	O	S	0	0
			3479	2188	615	662	14		

- Molecule 14 is a protein called Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UP1	569	Total	C	N	O	S	0	0
			4679	3041	787	825	26		

- Molecule 15 is a protein called Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	VP1	571	Total	C	N	O	S	0	0
			4635	2993	790	831	21		
15	WP1	571	Total	C	N	O	S	0	0
			4635	2993	790	831	21		

- Molecule 16 is a protein called Belt helix 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	gP1	19	Total	C	N	O	0	0
			96	57	19	20		

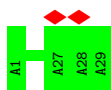
- Molecule 17 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	jP1	371	Total	C	N	O	S	0	0
			2892	1828	486	557	21		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Helix 1

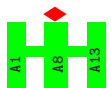


- Molecule 2: Belt helices 1,2,3,4



There are no outlier residues recorded for this chain.

- Molecule 2: Belt helices 1,2,3,4



- Molecule 2: Belt helices 1,2,3,4



- Molecule 2: Belt helices 1,2,3,4



There are no outlier residues recorded for this chain.

- Molecule 3: Belt helix 5



There are no outlier residues recorded for this chain.

- Molecule 4: Belt helix 6

Chain EP1:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: Belt helix 7

Chain FP1:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: Belt helices 8,9,10

Chain GP1:  13% 100%



- Molecule 6: Belt helices 8,9,10

Chain LP1:  100%

There are no outlier residues recorded for this chain.

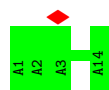
- Molecule 6: Belt helices 8,9,10

Chain NP1:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: Belt helices 11,12

Chain JP1:  7% 100%



- Molecule 7: Belt helices 11,12

Chain vP1:  100%

There are no outlier residues recorded for this chain.

- Molecule 8: Belt helices 13,14,15 and Helix 2

Chain KP1:  100%

There are no outlier residues recorded for this chain.

- Molecule 8: Belt helices 13,14,15 and Helix 2

Chain OP1:  100%

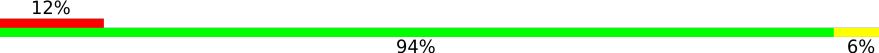
There are no outlier residues recorded for this chain.

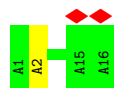
- Molecule 8: Belt helices 13,14,15 and Helix 2

Chain PP1:  100%

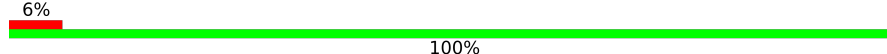
There are no outlier residues recorded for this chain.

- Molecule 8: Belt helices 13,14,15 and Helix 2

Chain uP1:  12% 94% 6%



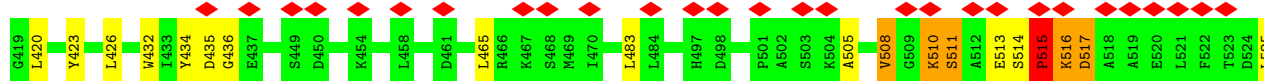
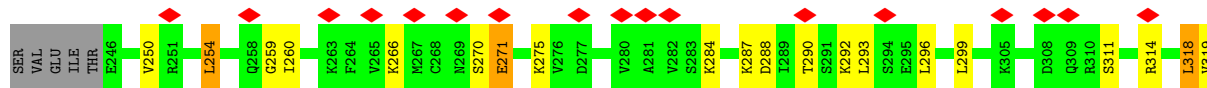
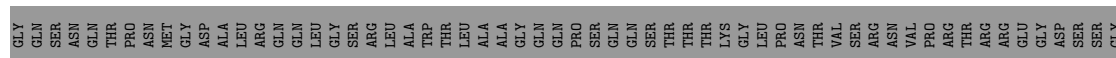
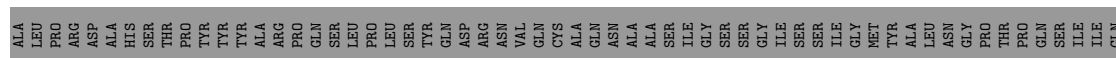
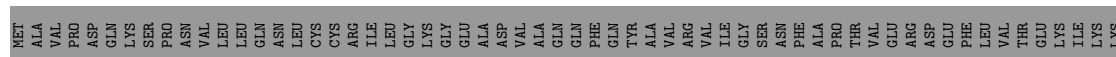
- Molecule 9: Belt helix 16

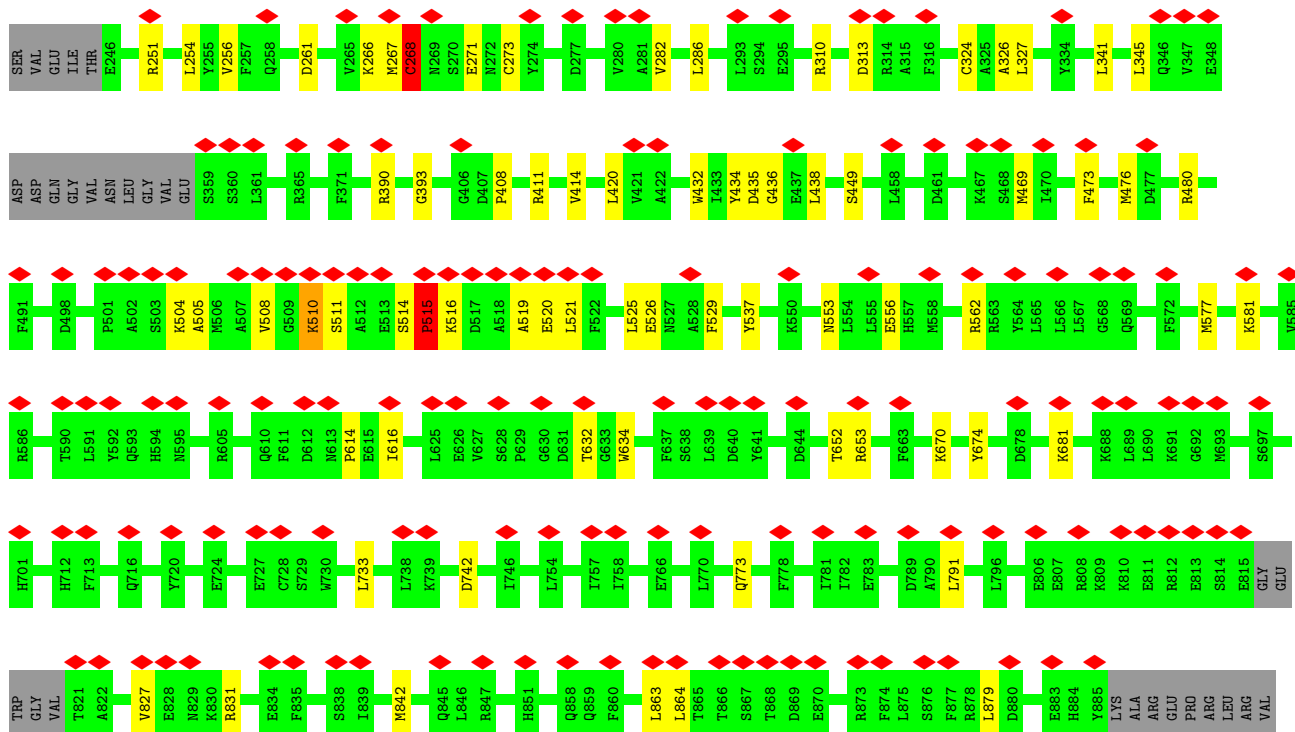
Chain MP1:  6% 100%



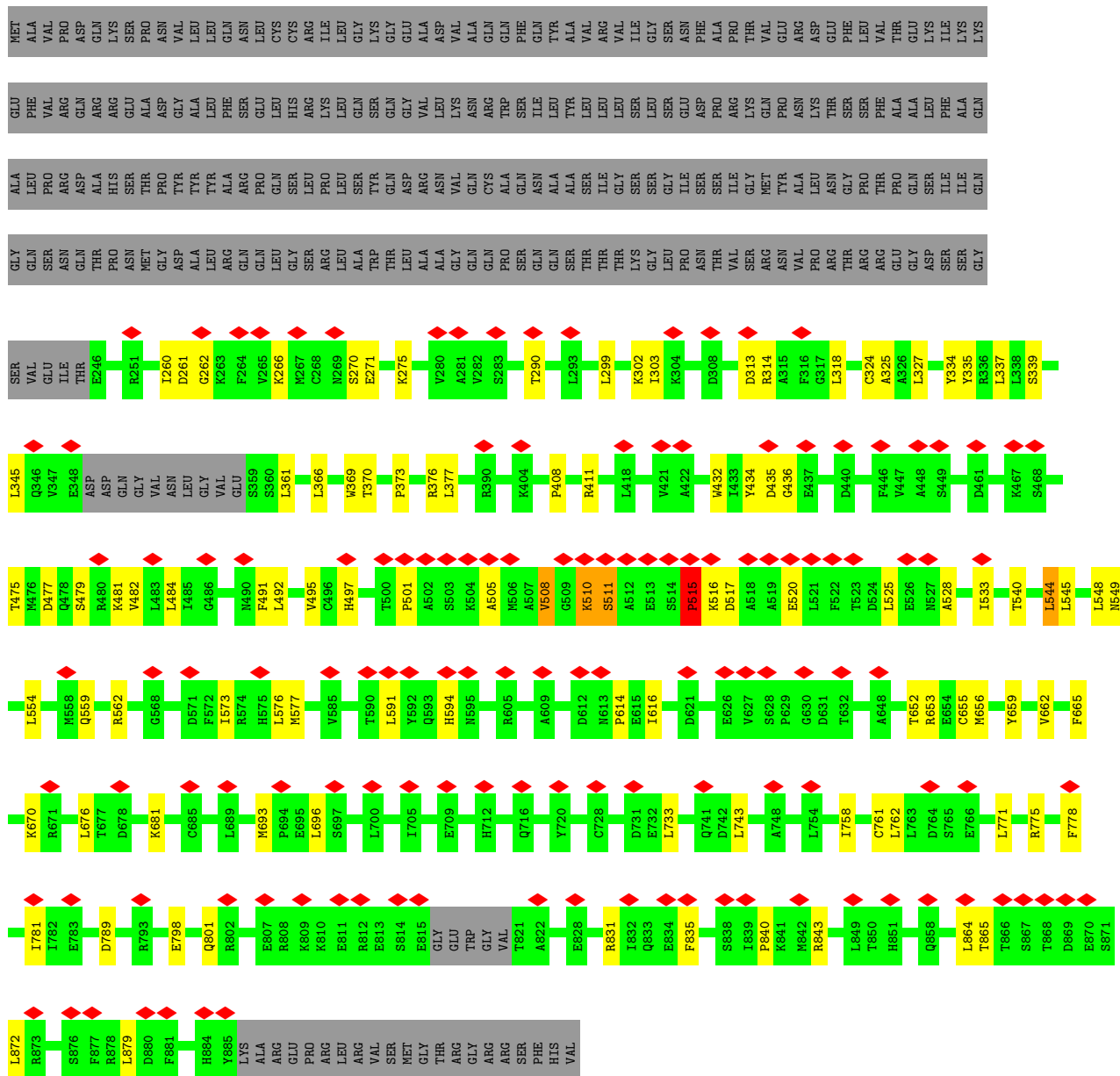
- Molecule 10: Gamma-tubulin complex component 3 homolog

Chain QP1:  15% 56% 10% 31%

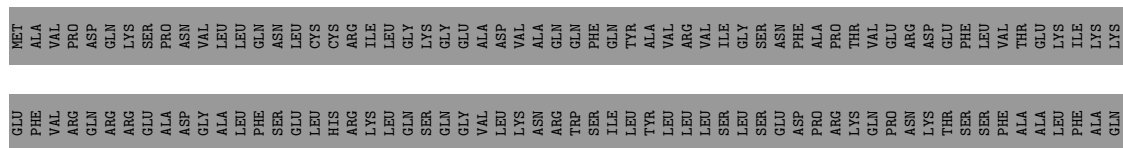


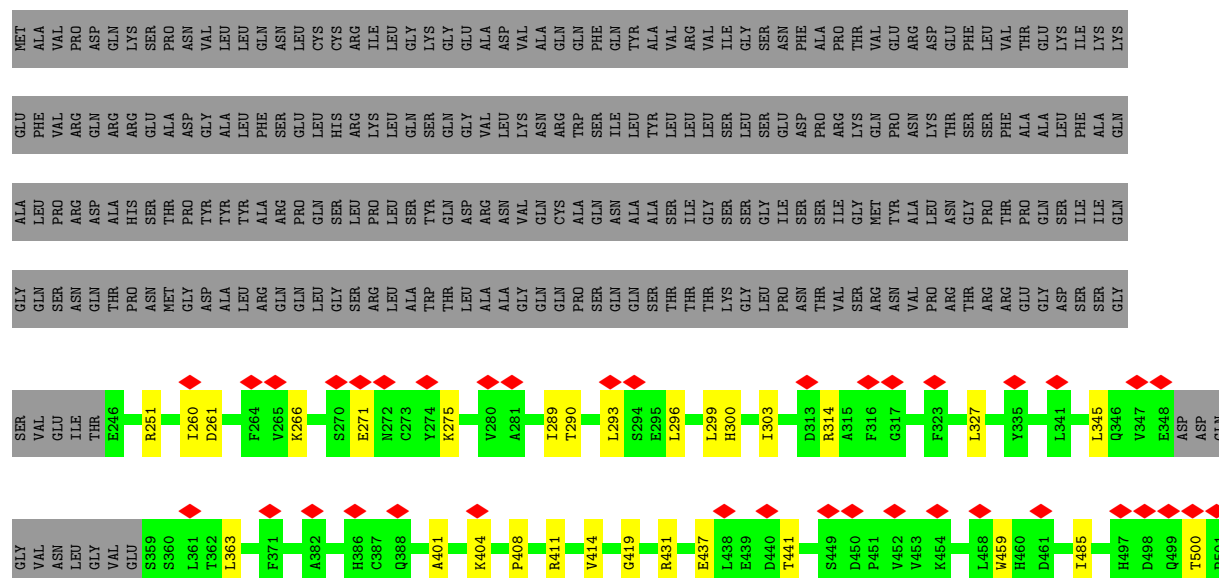


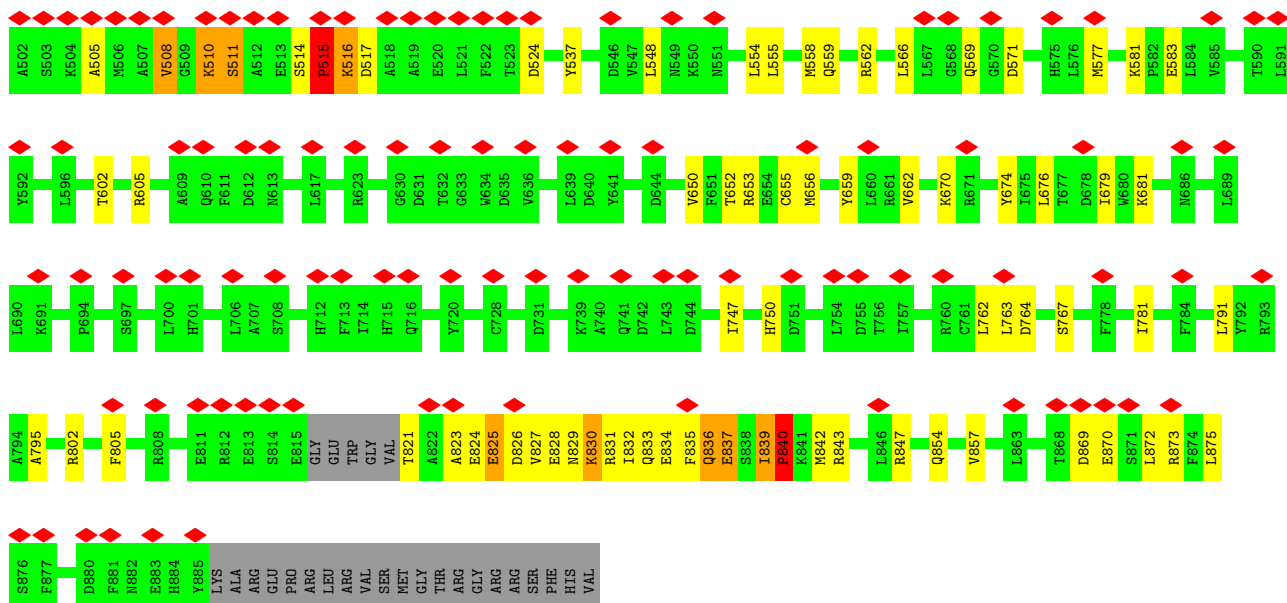
Chain dP1:



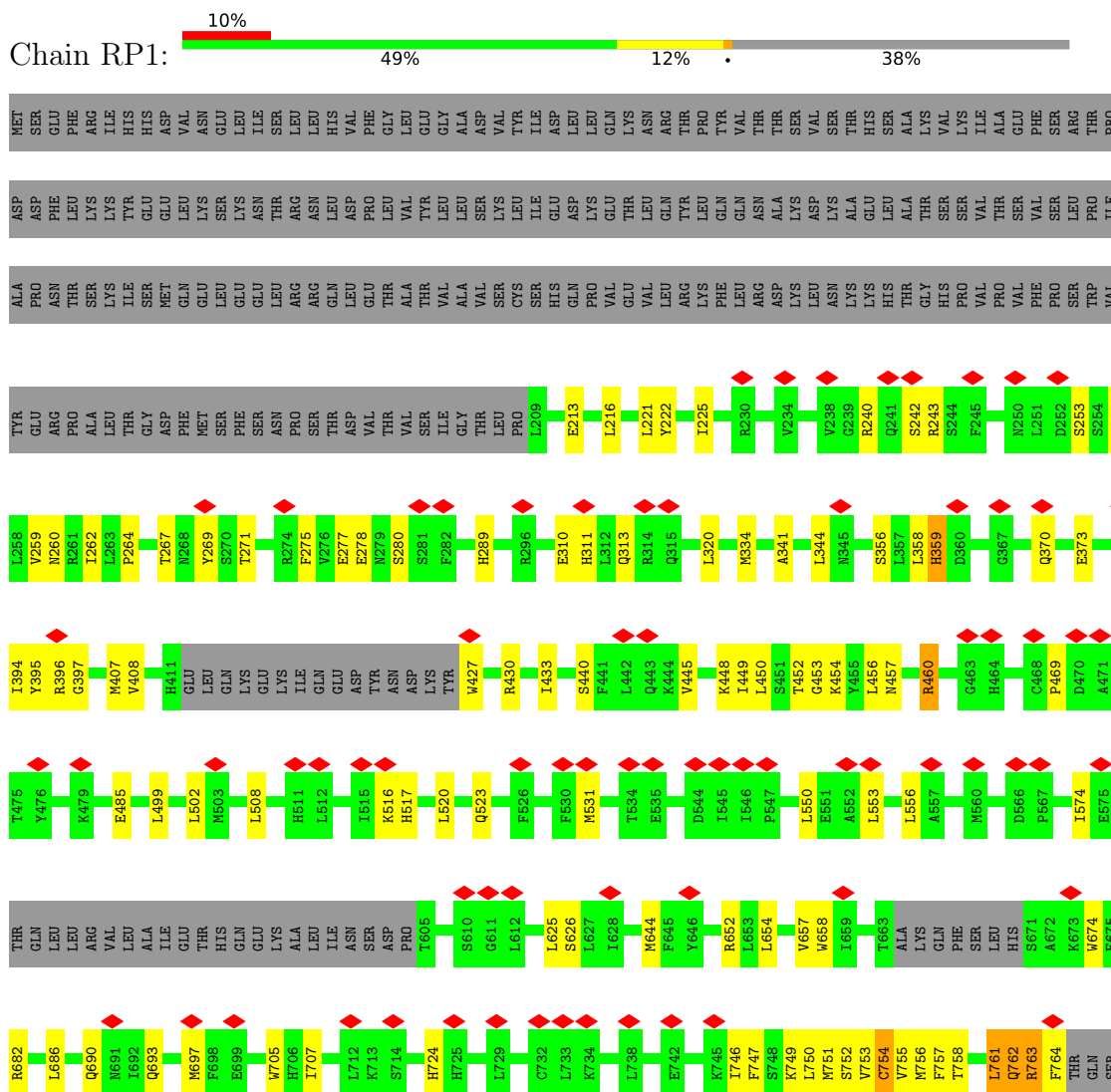
Chain eP1:

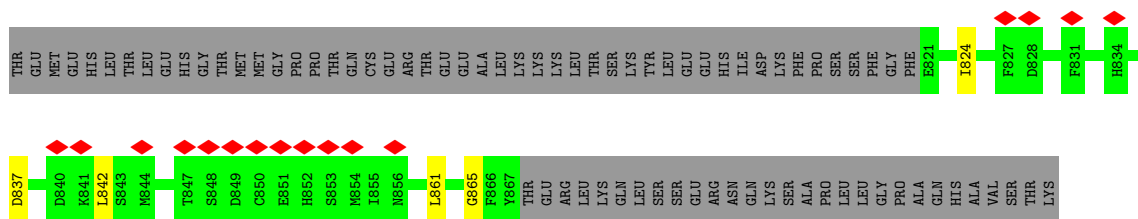




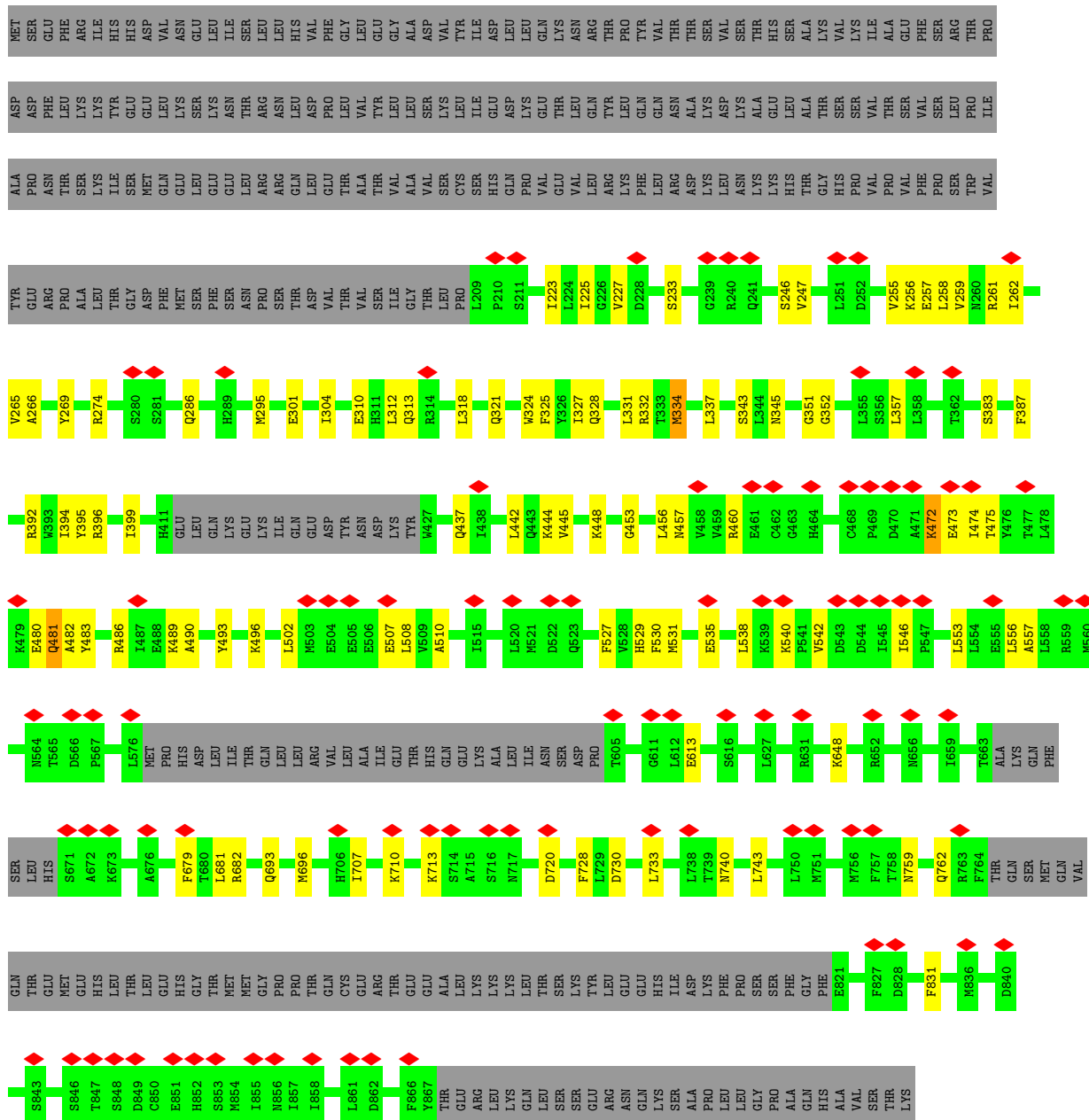


• Molecule 11: Gamma-tubulin complex component 2

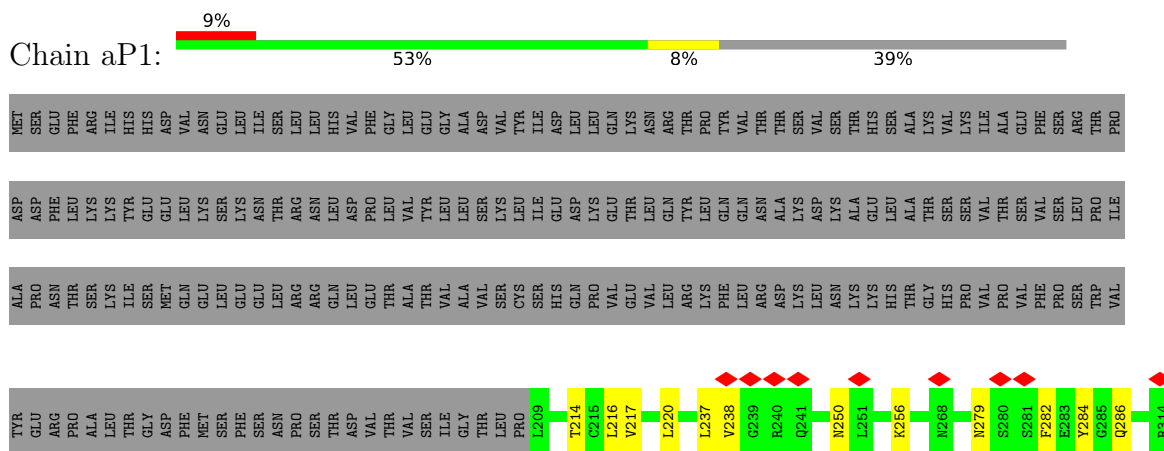


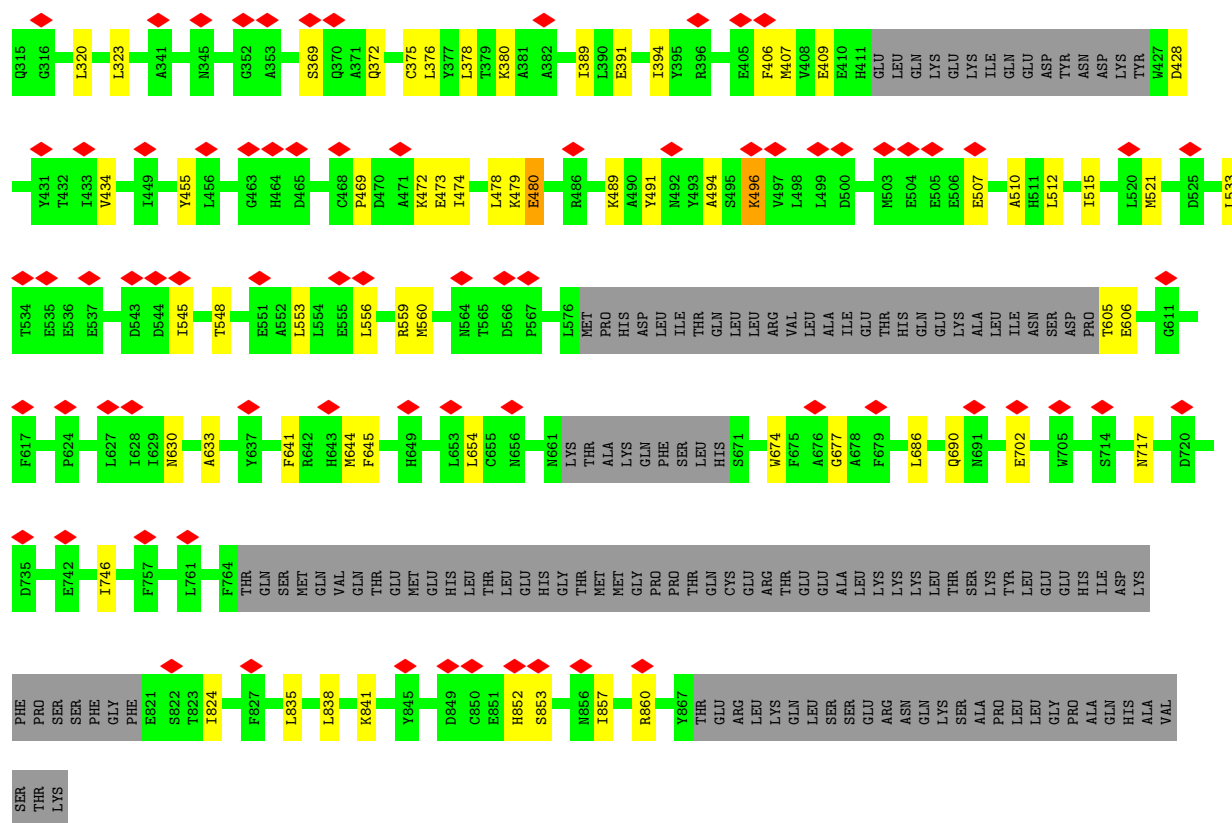


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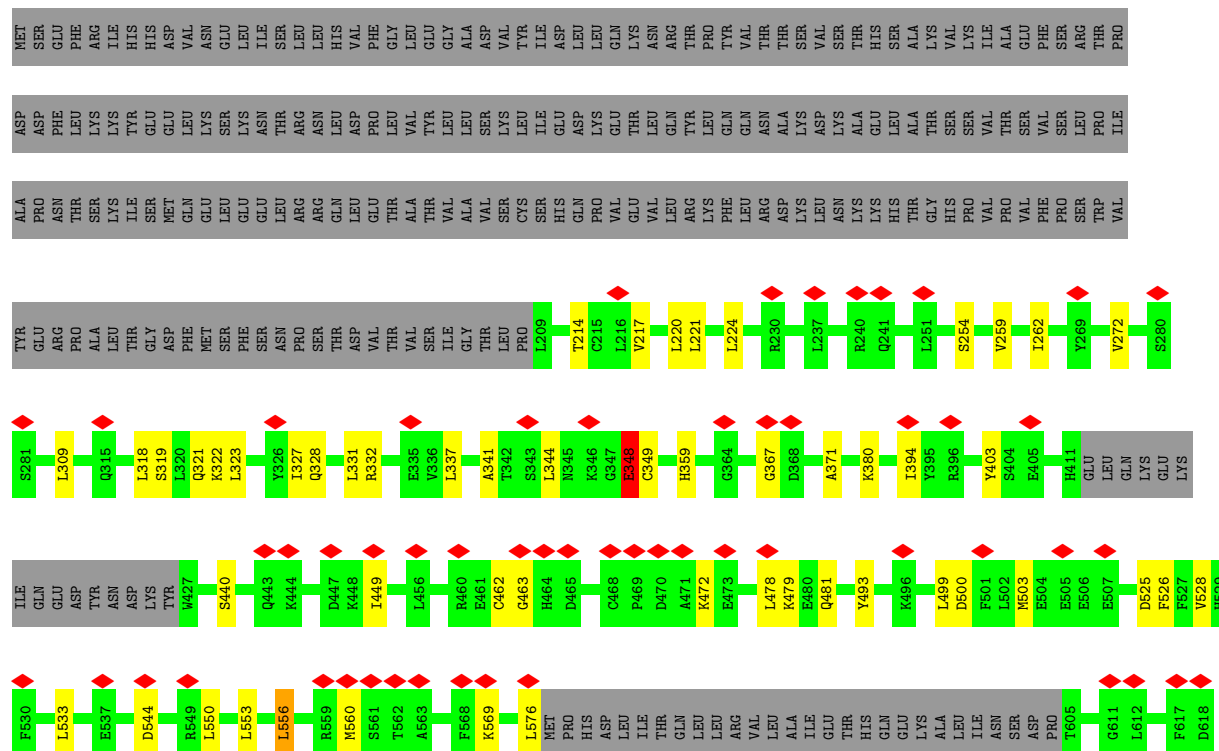


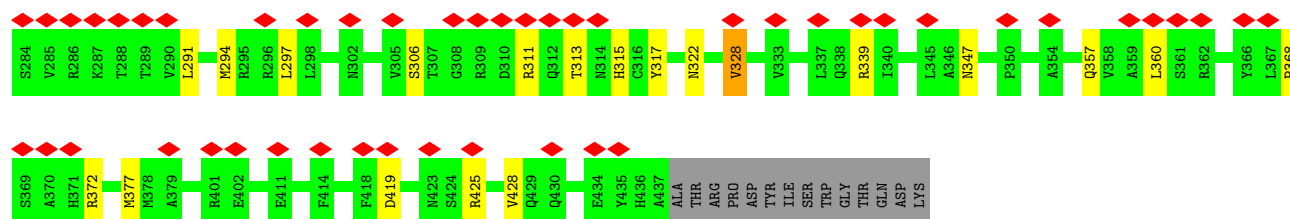
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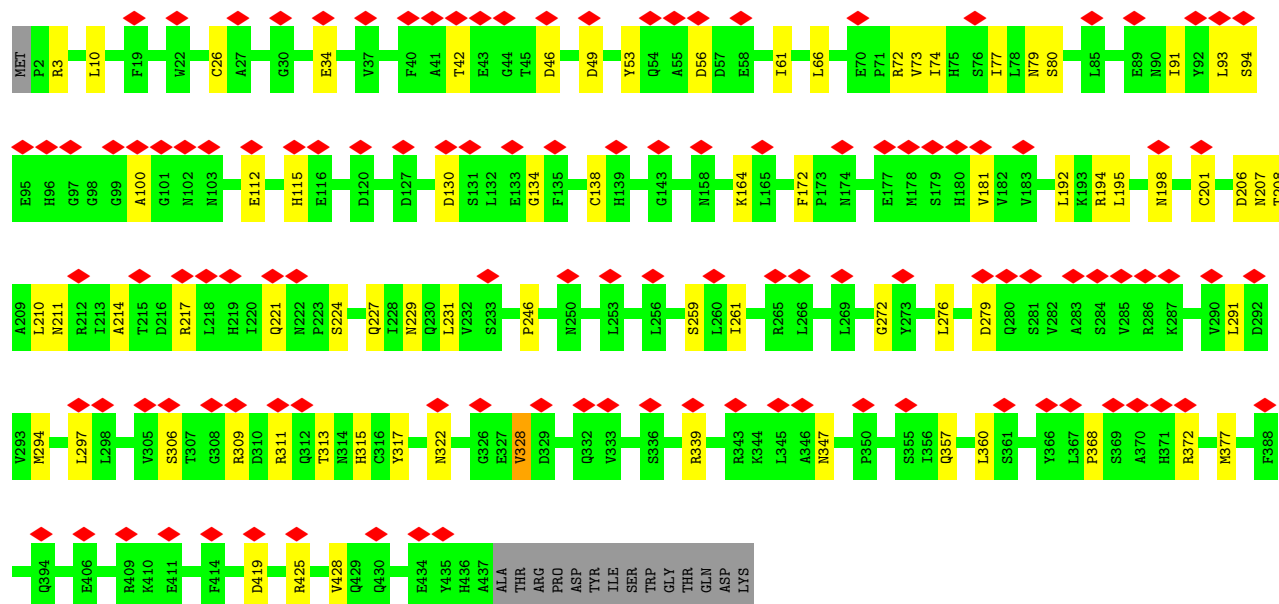
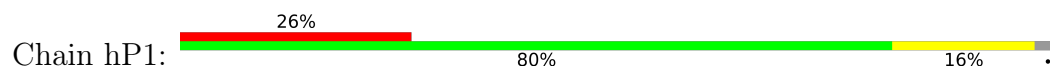


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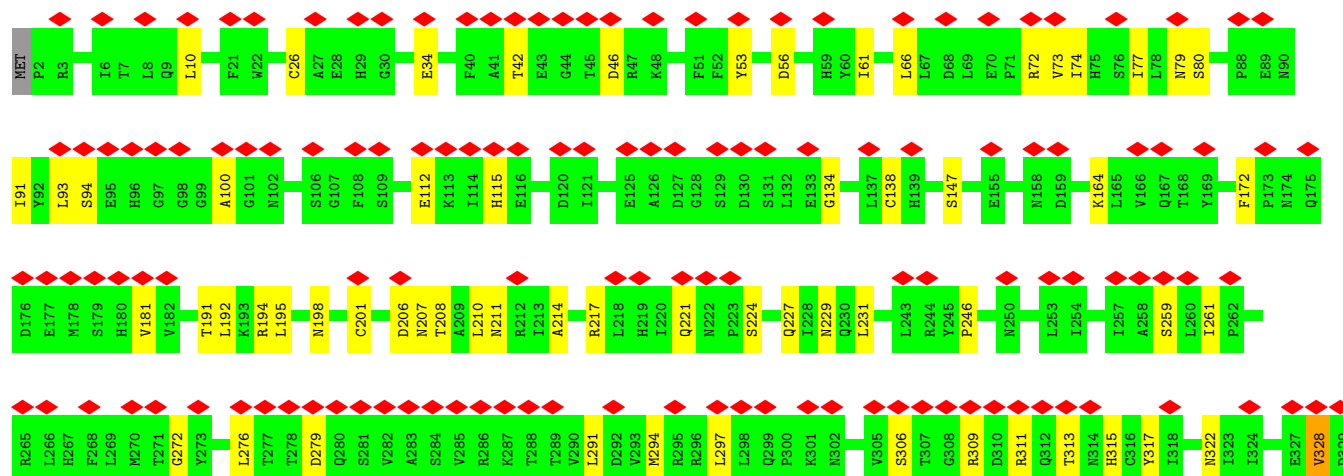
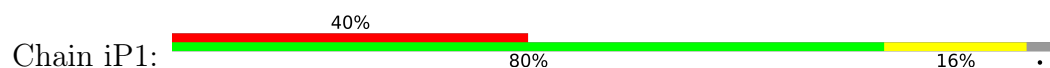


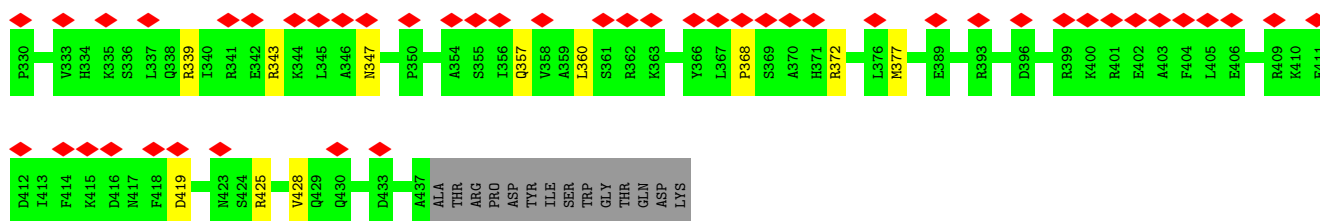


• Molecule 13: Tubulin gamma-1 chain

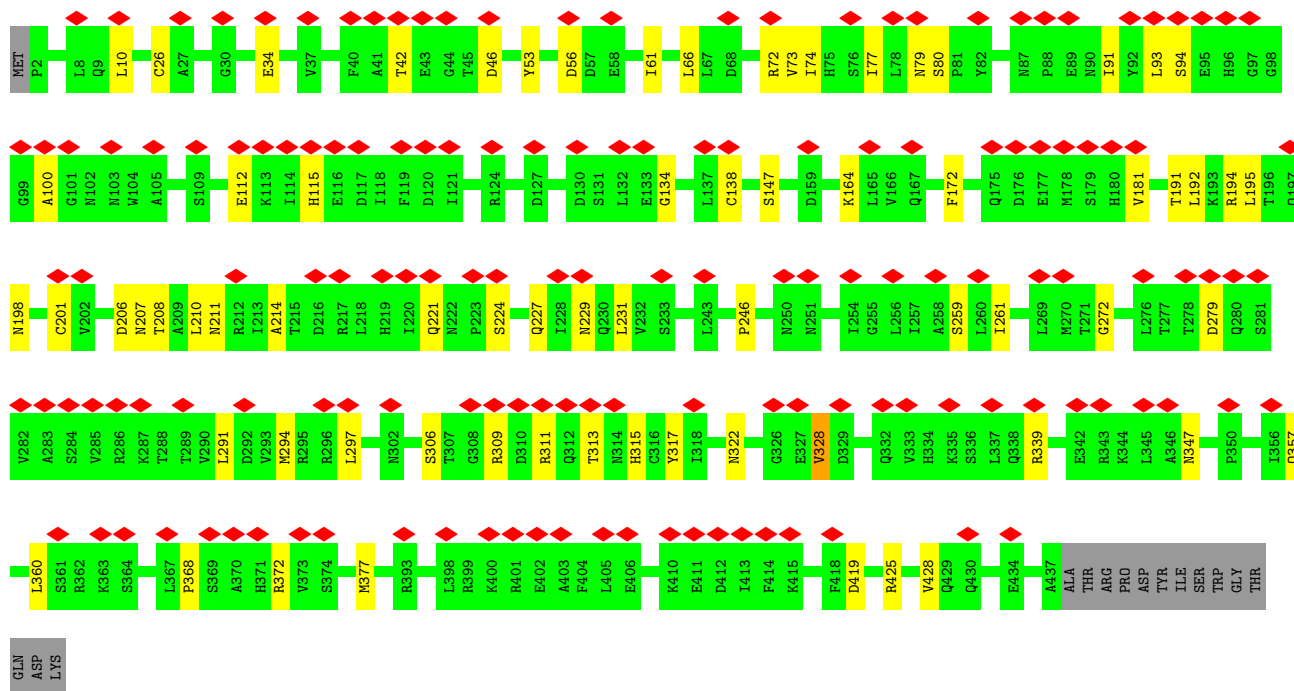
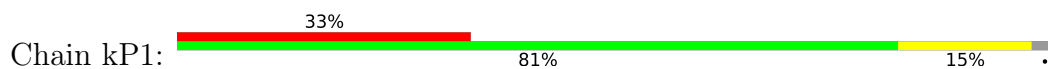


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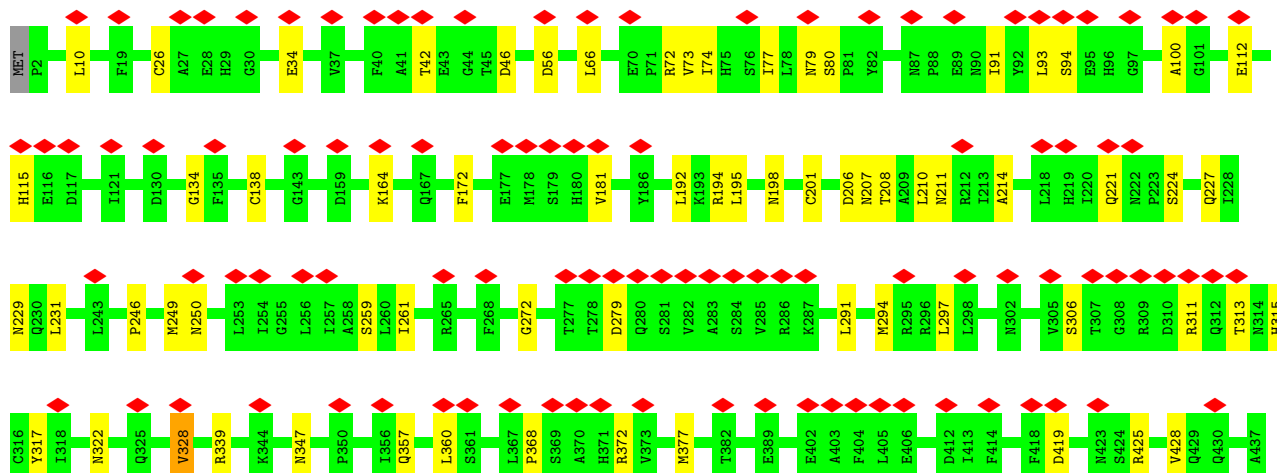
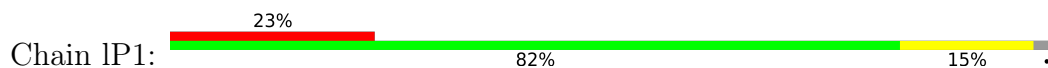




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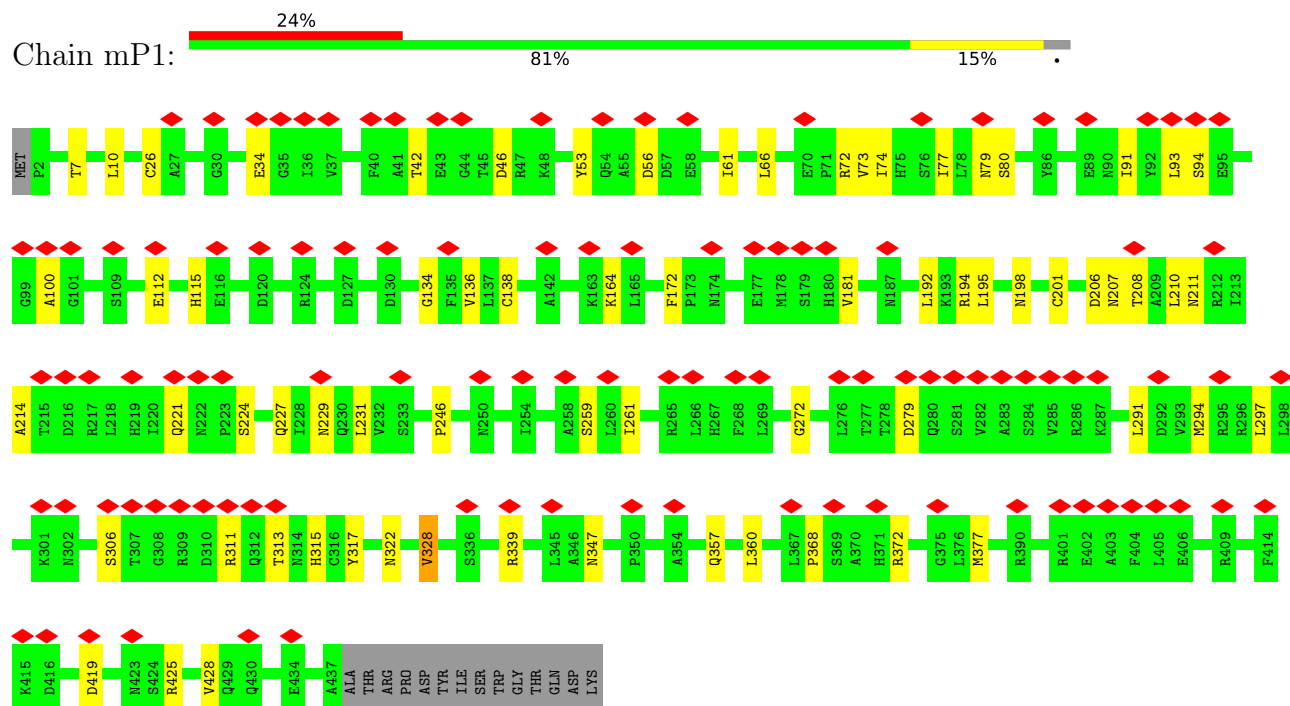


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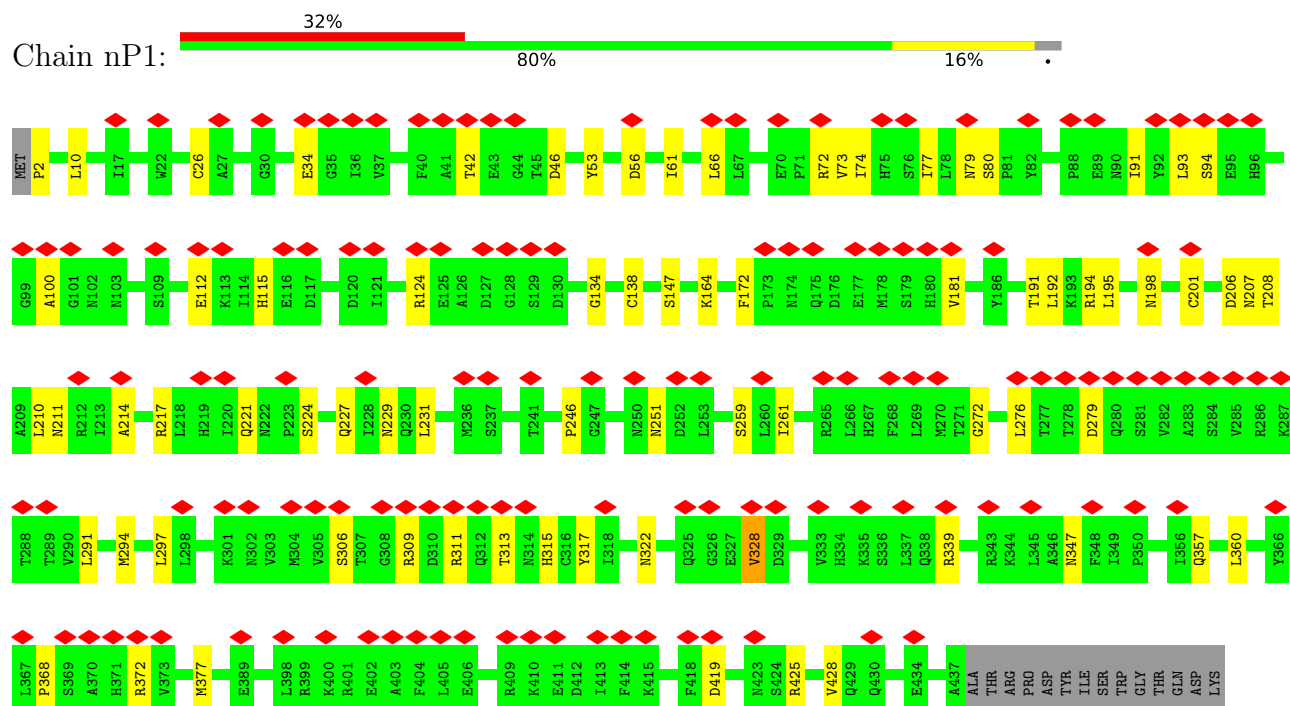


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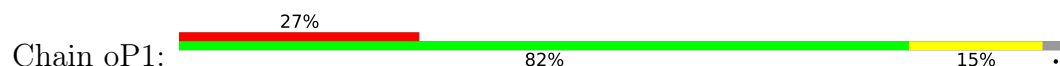
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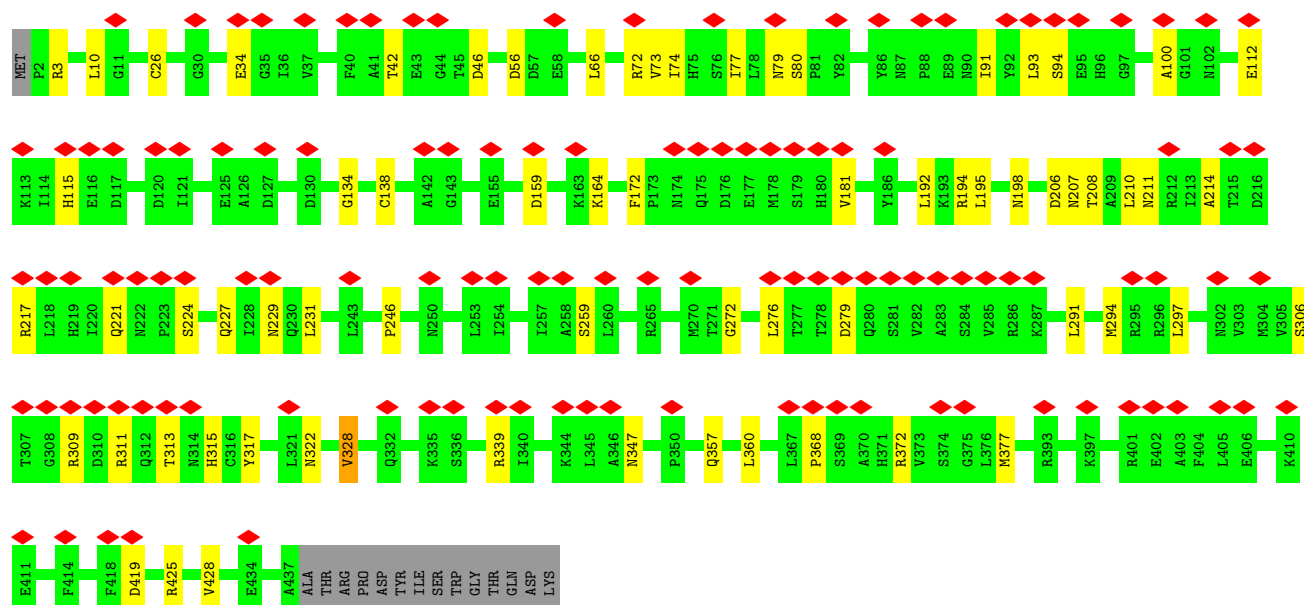


• Molecule 13: Tubulin gamma-1 chain

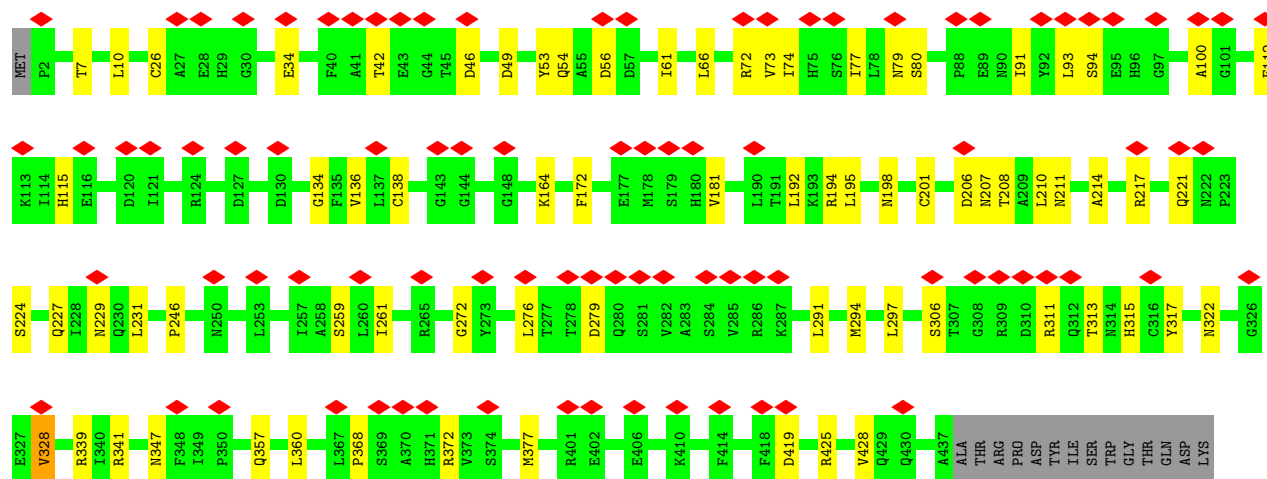
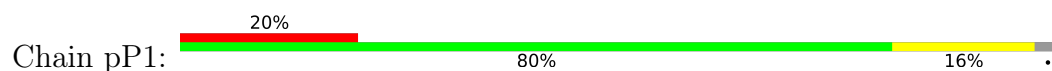


• Molecule 13: Tubulin gamma-1 chain

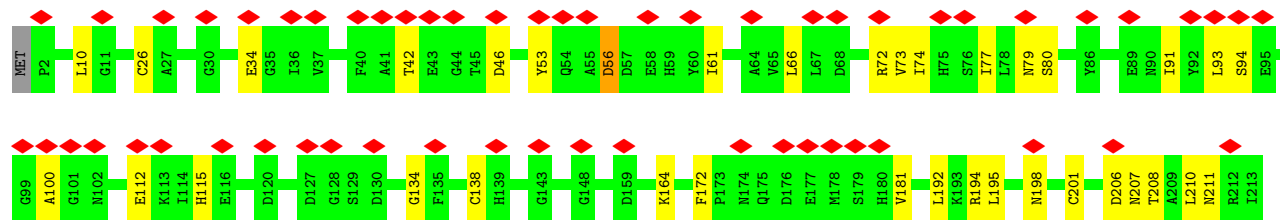
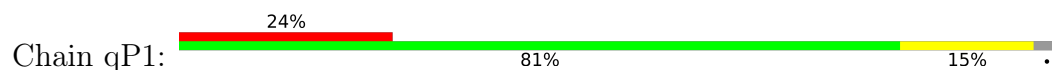


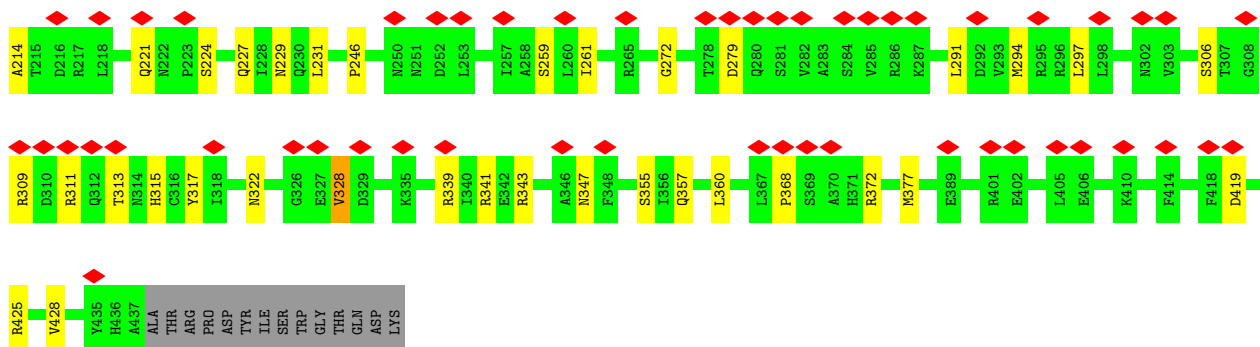


• Molecule 13: Tubulin gamma-1 chain



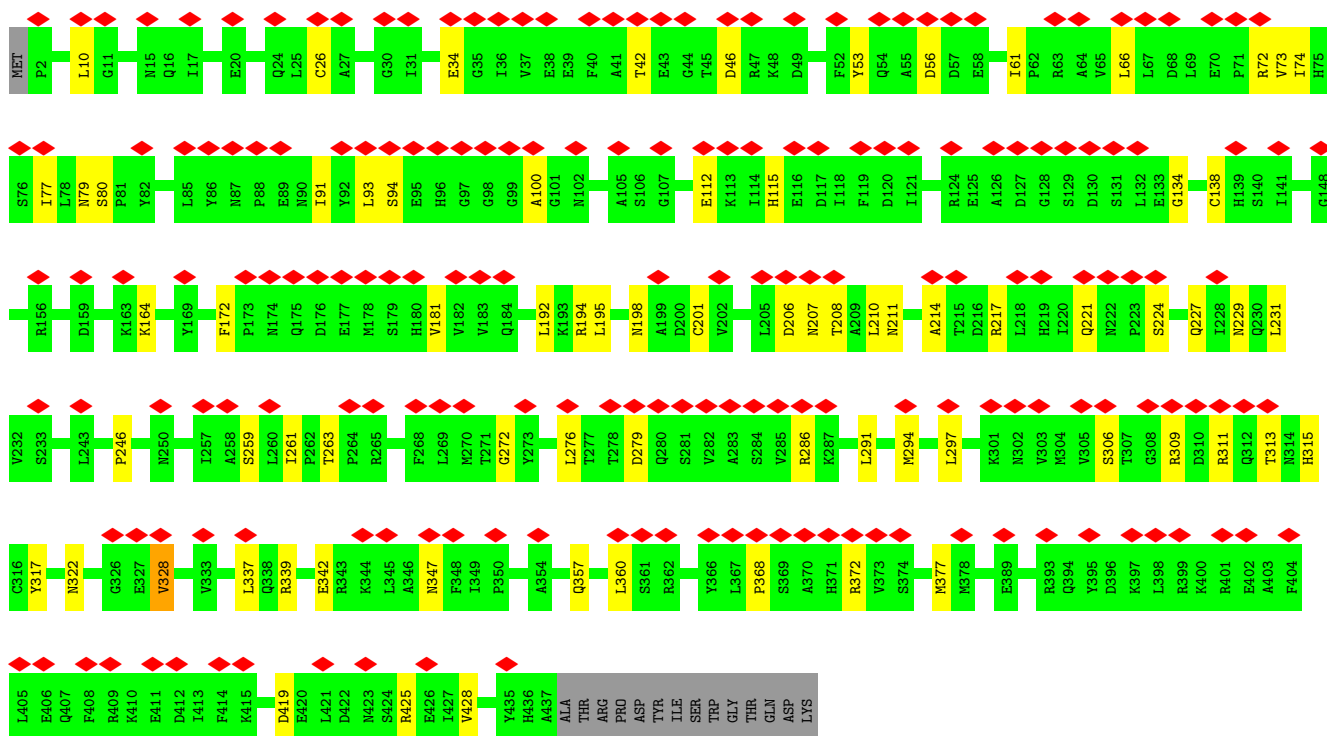
• Molecule 13: Tubulin gamma-1 chain





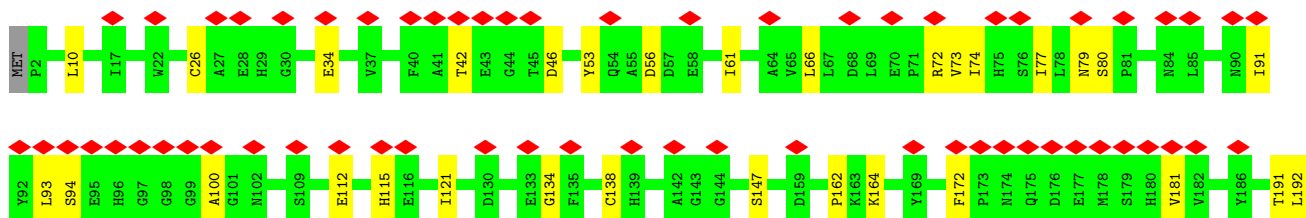
• Molecule 13: Tubulin gamma-1 chain

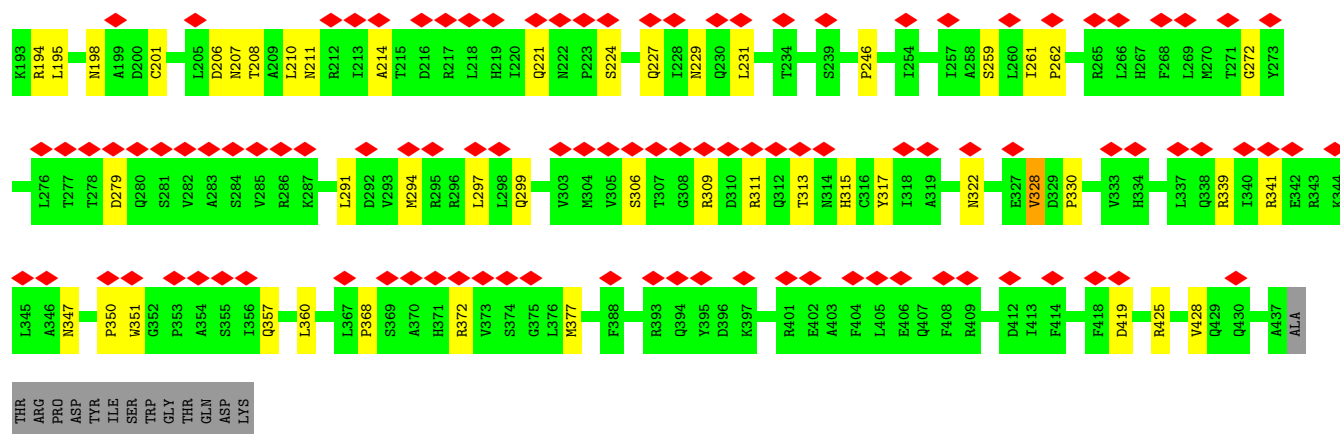
Chain rP1: 42% 80% 16%



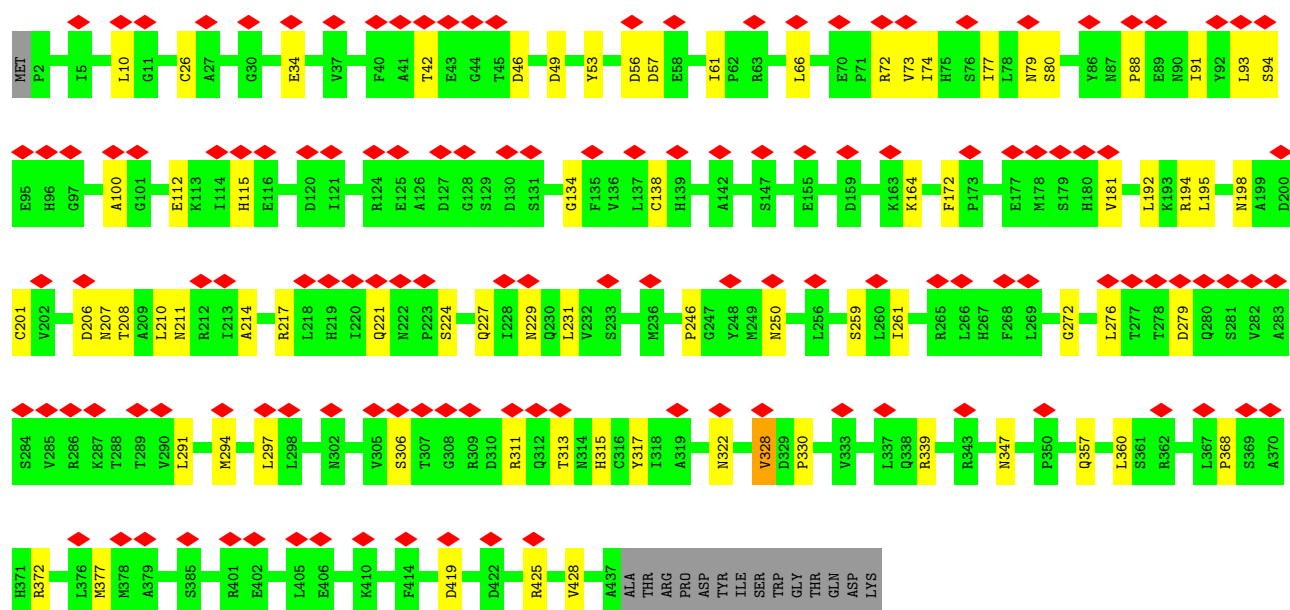
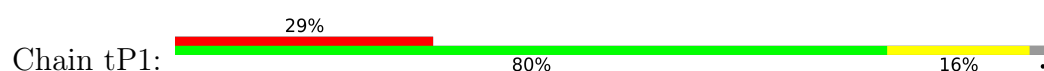
• Molecule 13: Tubulin gamma-1 chain

Chain sP1: 36% 79% 17%

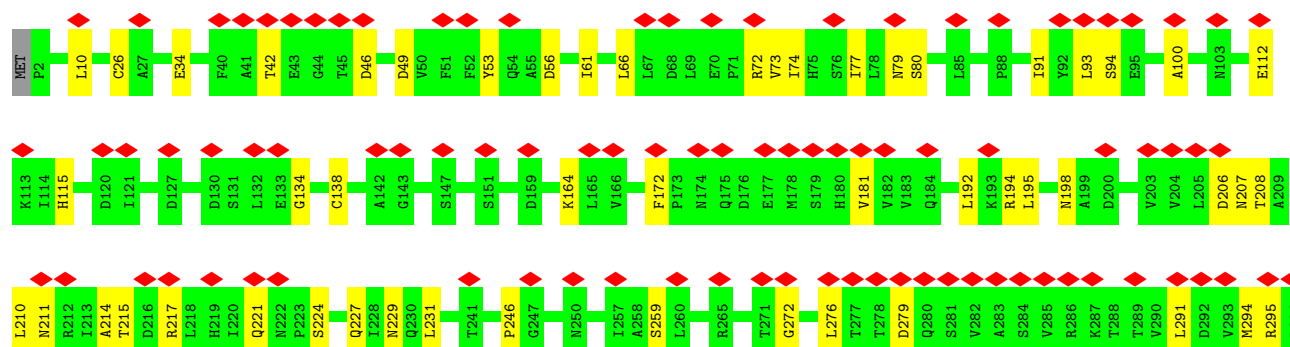
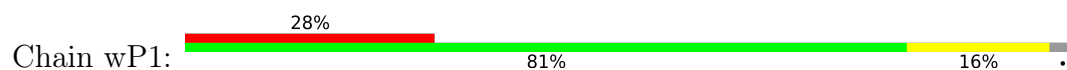


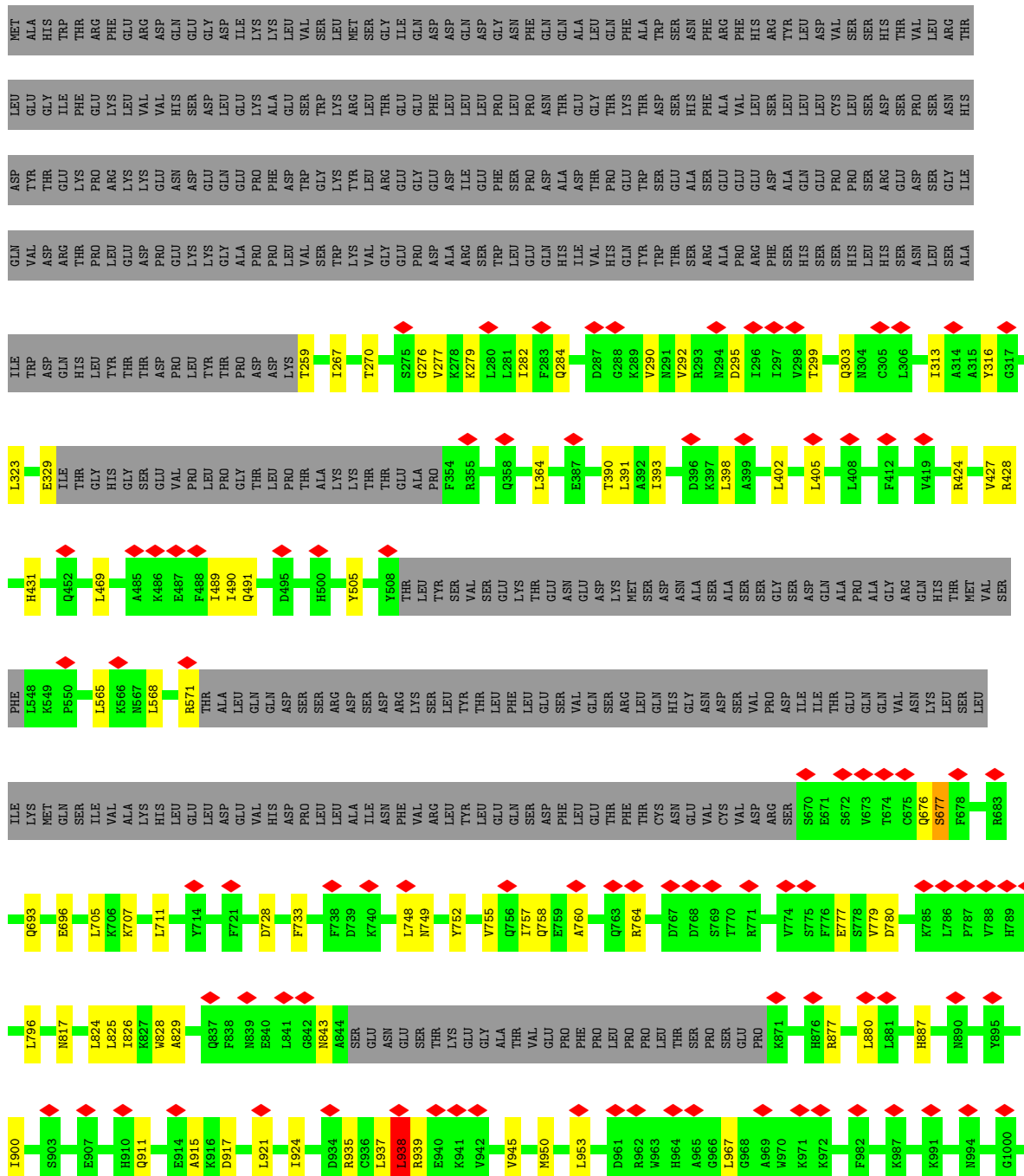


• Molecule 13: Tubulin gamma-1 chain



• Molecule 13: Tubulin gamma-1 chain









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46096	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	42000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.247	Depositor
Minimum map value	-0.079	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	537.6, 537.6, 537.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.1, 2.1, 2.1	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	AP1	0.05	0/145	0.16	0/200
2	CP1	0.06	0/65	0.15	0/88
2	HP1	0.05	0/65	0.15	0/88
2	IP1	0.05	0/65	0.13	0/88
2	XP1	0.04	0/65	0.14	0/88
3	DP1	0.10	0/155	0.23	0/214
4	EP1	0.05	0/115	0.19	0/158
5	FP1	0.06	0/90	0.18	0/123
6	GP1	0.06	0/75	0.23	0/102
6	LP1	0.06	0/75	0.16	0/102
6	NP1	0.05	0/75	0.17	0/102
7	JP1	0.05	0/70	0.21	0/95
7	vP1	0.04	0/70	0.19	0/95
8	KP1	0.05	0/80	0.15	0/109
8	OP1	0.06	0/80	0.17	0/109
8	PP1	0.06	0/80	0.18	0/109
8	uP1	0.07	0/80	0.22	0/109
9	MP1	0.06	0/85	0.15	0/116
10	QP1	0.31	0/5227	0.67	7/7060 (0.1%)
10	cP1	0.27	0/5227	0.63	4/7060 (0.1%)
10	dP1	0.27	0/5227	0.63	6/7060 (0.1%)
10	eP1	0.25	0/5227	0.61	5/7060 (0.1%)
10	fP1	0.28	0/5227	0.63	2/7060 (0.0%)
11	RP1	0.32	0/4614	0.69	3/6236 (0.0%)
11	YP1	0.27	0/4614	0.67	1/6236 (0.0%)
11	ZP1	0.27	0/4603	0.65	2/6221 (0.0%)
11	aP1	0.23	0/4598	0.61	7/6215 (0.1%)
11	bP1	0.23	0/4614	0.60	7/6236 (0.1%)
12	SP1	0.30	0/4812	0.76	12/6525 (0.2%)
13	TP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	hP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	iP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	kP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	lP1	0.20	0/3551	0.51	2/4815 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	mP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	nP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	oP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	pP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	qP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	rP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	sP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	tP1	0.20	0/3551	0.51	2/4815 (0.0%)
13	wP1	0.20	0/3551	0.51	2/4815 (0.0%)
14	UP1	0.26	0/4778	0.69	5/6459 (0.1%)
15	VP1	0.29	0/4738	0.69	0/6416
15	WP1	0.28	0/4738	0.68	0/6416
16	gP1	0.06	0/95	0.15	0/130
17	jP1	0.17	0/2954	0.43	0/4003
All	All	0.24	0/122542	0.59	89/165898 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	QP1	0	3
10	cP1	0	2
10	dP1	0	2
10	eP1	0	4
10	fP1	0	3
11	RP1	0	1
11	YP1	0	2
11	ZP1	0	5
11	aP1	0	3
11	bP1	0	2
12	SP1	0	11
14	UP1	0	5
15	VP1	0	3
15	WP1	0	3
All	All	0	49

There are no bond length outliers.

All (89) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	RP1	277	GLU	CB-CG-CD	7.04	124.57	112.60
11	aP1	469	PRO	CA-C-N	6.91	134.13	121.70
11	aP1	469	PRO	C-N-CA	6.91	134.13	121.70
14	UP1	748	LEU	CA-C-N	6.78	133.90	121.70
14	UP1	748	LEU	C-N-CA	6.78	133.90	121.70
11	bP1	348	GLU	N-CA-C	-6.62	97.55	108.07
10	cP1	273	CYS	CA-C-N	6.55	134.06	121.54
10	cP1	273	CYS	C-N-CA	6.55	134.06	121.54
12	SP1	513	VAL	N-CA-C	6.49	122.85	109.34
11	ZP1	433	ILE	CA-C-N	6.29	133.29	121.97
11	ZP1	433	ILE	C-N-CA	6.29	133.29	121.97
12	SP1	1459	LEU	CA-C-N	6.26	133.24	121.97
12	SP1	1459	LEU	C-N-CA	6.26	133.24	121.97
11	RP1	359	HIS	CA-CB-CG	6.17	119.97	113.80
12	SP1	1457	THR	CA-C-N	6.14	132.76	121.70
12	SP1	1457	THR	C-N-CA	6.14	132.76	121.70
10	dP1	515	PRO	CA-N-CD	-6.06	103.52	112.00
10	eP1	515	PRO	CA-N-CD	-6.01	103.59	112.00
10	fP1	515	PRO	CA-N-CD	-5.93	103.69	112.00
10	QP1	515	PRO	CA-N-CD	-5.87	103.78	112.00
11	aP1	480	GLU	CA-C-N	5.78	132.58	121.54
11	aP1	480	GLU	C-N-CA	5.78	132.58	121.54
10	cP1	515	PRO	CA-N-CD	-5.74	103.96	112.00
10	fP1	840	PRO	CA-N-CD	-5.74	103.96	112.00
11	aP1	496	LYS	CB-CG-CD	5.71	124.42	111.30
10	eP1	270	SER	CA-C-N	5.58	132.19	121.54
10	eP1	270	SER	C-N-CA	5.58	132.19	121.54
10	QP1	271	GLU	CA-C-N	5.57	132.19	121.54
10	QP1	271	GLU	C-N-CA	5.57	132.19	121.54
10	eP1	271	GLU	CA-C-N	5.57	132.17	121.54
10	eP1	271	GLU	C-N-CA	5.57	132.17	121.54
13	TP1	100	ALA	CA-C-N	5.55	131.69	121.70
13	TP1	100	ALA	C-N-CA	5.55	131.69	121.70
13	tP1	100	ALA	CA-C-N	5.55	131.68	121.70
13	tP1	100	ALA	C-N-CA	5.55	131.68	121.70
13	iP1	100	ALA	CA-C-N	5.54	131.68	121.70
13	iP1	100	ALA	C-N-CA	5.54	131.68	121.70
13	hP1	100	ALA	CA-C-N	5.53	131.66	121.70
13	hP1	100	ALA	C-N-CA	5.53	131.66	121.70
13	sP1	100	ALA	CA-C-N	5.53	131.66	121.70
13	sP1	100	ALA	C-N-CA	5.53	131.66	121.70
13	qP1	100	ALA	CA-C-N	5.53	131.66	121.70
13	qP1	100	ALA	C-N-CA	5.53	131.66	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	nP1	100	ALA	CA-C-N	5.53	131.66	121.70
13	nP1	100	ALA	C-N-CA	5.53	131.66	121.70
13	pP1	100	ALA	CA-C-N	5.53	131.65	121.70
13	pP1	100	ALA	C-N-CA	5.53	131.65	121.70
13	wP1	100	ALA	CA-C-N	5.53	131.65	121.70
13	wP1	100	ALA	C-N-CA	5.53	131.65	121.70
13	lP1	100	ALA	CA-C-N	5.53	131.65	121.70
13	lP1	100	ALA	C-N-CA	5.53	131.65	121.70
13	kP1	100	ALA	CA-C-N	5.52	131.64	121.70
13	kP1	100	ALA	C-N-CA	5.52	131.64	121.70
13	mP1	100	ALA	CA-C-N	5.52	131.64	121.70
13	mP1	100	ALA	C-N-CA	5.52	131.64	121.70
13	oP1	100	ALA	CA-C-N	5.52	131.64	121.70
13	oP1	100	ALA	C-N-CA	5.52	131.64	121.70
13	rP1	100	ALA	CA-C-N	5.52	131.63	121.70
13	rP1	100	ALA	C-N-CA	5.52	131.63	121.70
10	QP1	270	SER	CA-C-N	5.51	132.07	121.54
10	QP1	270	SER	C-N-CA	5.51	132.07	121.54
14	UP1	676	GLN	CA-C-N	5.48	131.57	121.70
14	UP1	676	GLN	C-N-CA	5.48	131.57	121.70
10	dP1	544	LEU	CB-CG-CD2	-5.41	94.47	110.70
10	QP1	866	THR	N-CA-C	5.36	117.46	109.59
12	SP1	1531	LEU	CA-C-N	5.36	131.77	121.54
12	SP1	1531	LEU	C-N-CA	5.36	131.77	121.54
12	SP1	1460	VAL	N-CA-C	5.33	120.44	109.34
11	aP1	545	ILE	CA-C-N	5.32	123.59	120.24
11	aP1	545	ILE	C-N-CA	5.32	123.59	120.24
11	bP1	348	GLU	CB-CA-C	5.28	119.11	110.03
11	bP1	348	GLU	CA-C-N	5.25	131.15	121.70
11	bP1	348	GLU	C-N-CA	5.25	131.15	121.70
11	YP1	334	MET	CB-CG-SD	5.25	128.44	112.70
11	bP1	556	LEU	CA-CB-CG	5.23	134.62	116.30
10	dP1	270	SER	CA-C-N	5.21	131.50	121.54
10	dP1	270	SER	C-N-CA	5.21	131.50	121.54
14	UP1	791	LEU	CA-CB-CG	5.20	134.49	116.30
11	bP1	348	GLU	CA-CB-CG	5.18	124.47	114.10
12	SP1	1469	TYR	N-CA-C	-5.18	107.98	114.56
12	SP1	1460	VAL	CA-C-N	5.17	131.41	121.54
12	SP1	1460	VAL	C-N-CA	5.17	131.41	121.54
11	bP1	348	GLU	O-C-N	-5.12	118.80	123.41
10	QP1	865	THR	CA-C-O	-5.05	115.51	120.82
10	dP1	501	PRO	CA-C-N	5.05	131.19	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	dP1	501	PRO	C-N-CA	5.05	131.19	121.54
12	SP1	513	VAL	N-CA-CB	-5.05	102.90	111.23
11	RP1	460	ARG	NE-CZ-NH2	5.04	123.73	119.20
10	cP1	268	CYS	CA-CB-SG	5.01	125.92	114.40

There are no chirality outliers.

All (49) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	QP1	271	GLU	Peptide
10	QP1	311	SER	Peptide
10	QP1	318	LEU	Peptide
11	RP1	485	GLU	Sidechain
12	SP1	1456	ARG	Peptide
12	SP1	1460	VAL	Peptide
12	SP1	1466	SER	Peptide
12	SP1	1467	VAL	Peptide
12	SP1	1600	LEU	Peptide
12	SP1	1601	VAL	Peptide
12	SP1	312	TYR	Peptide
12	SP1	439	ASN	Peptide
12	SP1	502	LEU	Peptide
12	SP1	509	ASP	Peptide
12	SP1	512	PRO	Peptide
14	UP1	276	GLY	Peptide
14	UP1	277	VAL	Peptide
14	UP1	424	ARG	Peptide
14	UP1	677	SER	Peptide
14	UP1	938	LEU	Peptide
15	VP1	460	TRP	Peptide
15	VP1	572	PHE	Peptide
15	VP1	635	HIS	Peptide
15	WP1	460	TRP	Peptide
15	WP1	572	PHE	Peptide
15	WP1	635	HIS	Peptide
11	YP1	472	LYS	Peptide
11	YP1	480	GLU	Peptide
11	ZP1	282	PHE	Peptide
11	ZP1	432	THR	Peptide
11	ZP1	433	ILE	Peptide
11	ZP1	515	ILE	Peptide
11	ZP1	520	LEU	Peptide

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Mol	Chain	Res	Type	Group
11	aP1	428	ASP	Peptide
11	aP1	473	GLU	Peptide
11	aP1	479	LYS	Peptide
11	bP1	348	GLU	Peptide
11	bP1	403	TYR	Peptide
10	cP1	266	LYS	Peptide
10	cP1	313	ASP	Peptide
10	dP1	271	GLU	Peptide
10	dP1	313	ASP	Peptide
10	eP1	271	GLU	Peptide
10	eP1	313	ASP	Peptide
10	eP1	522	PHE	Peptide
10	eP1	523	THR	Peptide
10	fP1	271	GLU	Peptide
10	fP1	500	THR	Peptide
10	fP1	839	ILE	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	AP1	146	0	147	0	0
2	CP1	66	0	67	0	0
2	HP1	66	0	67	0	0
2	IP1	66	0	67	0	0
2	XP1	66	0	67	0	0
3	DP1	156	0	157	0	0
4	EP1	116	0	117	0	0
5	FP1	91	0	92	0	0
6	GP1	76	0	77	0	0
6	LP1	76	0	77	0	0
6	NP1	76	0	77	0	0
7	JP1	71	0	72	0	0
7	vP1	71	0	72	0	0
8	KP1	81	0	82	0	0
8	OP1	81	0	82	0	0
8	PP1	81	0	82	0	0
8	uP1	81	0	82	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	MP1	86	0	87	0	0
10	QP1	5118	0	5103	101	0
10	cP1	5118	0	5103	42	0
10	dP1	5118	0	5103	61	0
10	eP1	5118	0	5103	57	0
10	fP1	5118	0	5103	77	0
11	RP1	4519	0	4476	81	0
11	YP1	4519	0	4476	62	0
11	ZP1	4508	0	4466	51	0
11	aP1	4503	0	4456	39	0
11	bP1	4519	0	4476	49	0
12	SP1	4699	0	4724	70	0
13	TP1	3479	0	3428	26	0
13	hP1	3479	0	3428	30	0
13	iP1	3479	0	3428	30	0
13	kP1	3479	0	3428	28	0
13	lP1	3479	0	3428	27	0
13	mP1	3479	0	3428	26	0
13	nP1	3479	0	3428	32	0
13	oP1	3479	0	3428	29	0
13	pP1	3479	0	3428	31	0
13	qP1	3479	0	3428	30	0
13	rP1	3479	0	3428	34	0
13	sP1	3479	0	3428	37	0
13	tP1	3479	0	3428	32	0
13	wP1	3479	0	3428	32	0
14	UP1	4679	0	4788	48	0
15	VP1	4635	0	4670	58	0
15	WP1	4635	0	4670	56	0
16	gP1	96	0	97	0	0
17	jP1	2892	0	2854	11	0
All	All	120053	0	119231	1216	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 5.

All (1216) 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)
10:QP1:366:LEU:HD22	10:QP1:366:LEU:H	1.08	1.14
10:QP1:364:ARG:HD3	11:RP1:225:ILE:HD13	1.23	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:QP1:364:ARG:HA	10:QP1:367:LEU:HB2	1.45	0.97
11:RP1:763:ARG:CZ	11:RP1:763:ARG:HA	1.96	0.96
10:cP1:511:SER:O	10:cP1:515:PRO:HD2	1.68	0.93
10:dP1:511:SER:O	10:dP1:515:PRO:HD2	1.69	0.92
10:fP1:830:LYS:HE2	10:fP1:830:LYS:HA	1.50	0.92
10:fP1:511:SER:O	10:fP1:515:PRO:HD2	1.70	0.91
10:eP1:511:SER:O	10:eP1:515:PRO:HD2	1.70	0.91
10:QP1:511:SER:O	10:QP1:515:PRO:HD2	1.69	0.90
10:QP1:364:ARG:HD3	11:RP1:225:ILE:HG21	1.54	0.89
10:QP1:364:ARG:CD	11:RP1:225:ILE:HD13	2.03	0.89
10:QP1:366:LEU:HD22	10:QP1:366:LEU:N	1.91	0.86
10:QP1:366:LEU:H	10:QP1:366:LEU:CD2	1.88	0.83
10:cP1:434:TYR:CD2	10:cP1:510:LYS:HB2	2.14	0.81
10:fP1:836:GLN:O	10:fP1:840:PRO:HD2	1.79	0.81
15:WP1:313:ARG:HG3	15:WP1:313:ARG:HH11	1.46	0.81
10:fP1:516:LYS:NZ	10:fP1:516:LYS:HA	2.00	0.77
10:QP1:510:LYS:HE2	10:QP1:510:LYS:O	1.89	0.73
11:RP1:763:ARG:HA	11:RP1:763:ARG:NH1	2.02	0.73
11:RP1:763:ARG:HA	11:RP1:763:ARG:NE	1.98	0.73
12:SP1:513:VAL:HG11	12:SP1:518:VAL:HB	1.69	0.73
15:WP1:184:TYR:CE1	15:WP1:314:LEU:HB3	2.25	0.72
13:qP1:56:ASP:O	13:rP1:286:ARG:NE	2.22	0.72
15:WP1:313:ARG:HG3	15:WP1:313:ARG:NH1	2.04	0.72
10:dP1:337:LEU:HG	10:dP1:373:PRO:HG3	1.70	0.72
12:SP1:1505:LYS:NZ	12:SP1:1505:LYS:HB3	2.04	0.72
10:QP1:364:ARG:CD	11:RP1:225:ILE:HG21	2.19	0.72
10:eP1:310:ARG:HD2	10:eP1:321:GLN:HE21	1.55	0.72
10:eP1:510:LYS:O	10:eP1:510:LYS:NZ	2.19	0.71
13:hP1:130:ASP:OD2	13:iP1:343:ARG:NH1	2.23	0.71
13:pP1:54:GLN:OE1	13:qP1:343:ARG:NH2	2.21	0.71
15:VP1:87:ARG:HH21	15:VP1:91:ARG:HH22	1.39	0.70
10:fP1:833:GLN:HA	10:fP1:833:GLN:NE2	2.06	0.70
12:SP1:1509:VAL:HG12	12:SP1:1509:VAL:O	1.91	0.70
10:QP1:839:ILE:HG13	10:QP1:840:PRO:HD3	1.74	0.69
15:WP1:87:ARG:HH21	15:WP1:91:ARG:HH22	1.39	0.69
11:YP1:352:GLY:H	11:YP1:437:GLN:HB3	1.58	0.69
10:QP1:514:SER:OG	10:QP1:515:PRO:HD2	1.92	0.69
10:cP1:514:SER:OG	10:cP1:515:PRO:HD2	1.94	0.68
15:WP1:313:ARG:HH12	15:WP1:328:VAL:HG11	1.59	0.68
11:RP1:747:PHE:HA	11:RP1:750:LEU:HD12	1.74	0.67
11:YP1:274:ARG:HH21	11:YP1:345:ASN:HB3	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:dP1:505:ALA:HA	10:dP1:508:VAL:HG13	1.76	0.67
14:UP1:267:ILE:HD12	14:UP1:391:LEU:HD12	1.76	0.67
10:fP1:516:LYS:HA	10:fP1:516:LYS:CE	2.24	0.67
10:eP1:514:SER:OG	10:eP1:515:PRO:HD2	1.96	0.66
10:fP1:296:LEU:HA	10:fP1:299:LEU:HD12	1.78	0.66
12:SP1:1457:THR:H	12:SP1:1458:ALA:HA	1.59	0.66
10:QP1:762:LEU:HB3	10:QP1:763:LEU:HD12	1.77	0.66
10:dP1:324:CYS:SG	10:dP1:325:ALA:N	2.69	0.65
10:eP1:299:LEU:HD12	10:eP1:302:LYS:HZ1	1.61	0.65
15:VP1:313:ARG:HH11	15:VP1:313:ARG:HB2	1.62	0.65
15:WP1:184:TYR:OH	15:WP1:311:LEU:HA	1.97	0.65
10:dP1:573:ILE:HD12	10:dP1:576:LEU:HD12	1.79	0.64
10:QP1:364:ARG:HH22	11:RP1:221:LEU:CB	2.10	0.64
10:fP1:514:SER:OG	10:fP1:515:PRO:HD2	1.98	0.63
15:VP1:313:ARG:HH11	15:VP1:313:ARG:CB	2.11	0.63
15:VP1:19:TRP:HE1	15:VP1:22:ARG:H	1.46	0.63
15:WP1:19:TRP:HE1	15:WP1:22:ARG:H	1.46	0.63
11:ZP1:533:LEU:HD13	11:ZP1:553:LEU:HD22	1.81	0.63
10:fP1:505:ALA:HA	10:fP1:508:VAL:HG13	1.81	0.63
10:QP1:525:LEU:HG	10:QP1:529:PHE:HB2	1.81	0.63
10:QP1:863:LEU:HD23	10:QP1:863:LEU:N	2.13	0.63
12:SP1:1505:LYS:O	12:SP1:1509:VAL:HG23	1.99	0.63
11:bP1:696:MET:HA	11:bP1:860:ARG:HH22	1.63	0.63
11:bP1:867:TYR:OH	13:nP1:357:GLN:NE2	2.30	0.62
11:bP1:528:VAL:HG11	13:nP1:251:ASN:HD21	1.64	0.62
10:cP1:256:VAL:HG22	10:cP1:261:ASP:HA	1.82	0.62
10:eP1:251:ARG:HG2	10:eP1:345:LEU:HD21	1.82	0.62
10:QP1:601:GLU:HB3	10:QP1:605:ARG:HH12	1.65	0.62
10:eP1:510:LYS:HZ1	10:eP1:514:SER:HB3	1.64	0.62
10:fP1:832:ILE:HA	10:fP1:835:PHE:CD2	2.33	0.62
10:QP1:266:LYS:HG3	10:QP1:275:LYS:HA	1.80	0.62
10:dP1:762:LEU:HD11	10:dP1:771:LEU:HD13	1.81	0.62
10:QP1:364:ARG:HH22	11:RP1:221:LEU:HB2	1.65	0.61
10:fP1:830:LYS:HA	10:fP1:830:LYS:CE	2.28	0.61
14:UP1:938:LEU:HB3	14:UP1:939:ARG:HG2	1.80	0.61
14:UP1:937:LEU:HD12	14:UP1:945:VAL:HG13	1.81	0.61
10:QP1:299:LEU:HG	10:QP1:377:LEU:HB3	1.82	0.61
10:QP1:364:ARG:HD3	11:RP1:225:ILE:CD1	2.15	0.61
10:cP1:514:SER:OG	10:cP1:515:PRO:CD	2.49	0.60
10:fP1:762:LEU:HB3	10:fP1:763:LEU:HD12	1.83	0.60
12:SP1:513:VAL:HG13	12:SP1:515:LEU:H	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SP1:1364:LEU:HD13	12:SP1:1367:ILE:HD11	1.83	0.60
15:WP1:296:THR:HB	15:WP1:307:PHE:HE2	1.66	0.60
15:WP1:380:LEU:HD22	15:WP1:448:GLY:HA3	1.83	0.60
14:UP1:316:TYR:HD1	14:UP1:405:LEU:HD11	1.66	0.60
10:fP1:821:THR:O	10:fP1:824:GLU:HG2	2.02	0.60
10:QP1:369:TRP:HA	10:QP1:369:TRP:CE3	2.37	0.60
13:rP1:53:TYR:OH	13:sP1:299:GLN:NE2	2.23	0.60
11:ZP1:656:ASN:O	11:ZP1:659:ILE:HG12	2.01	0.60
11:RP1:445:VAL:HA	11:RP1:448:LYS:HE2	1.83	0.60
10:fP1:791:LEU:HD22	10:fP1:842:MET:HB2	1.83	0.60
10:QP1:514:SER:OG	10:QP1:515:PRO:CD	2.49	0.59
11:RP1:657:VAL:HG13	11:RP1:761:LEU:HD12	1.84	0.59
10:cP1:827:VAL:HG12	10:cP1:831:ARG:HE	1.66	0.59
10:fP1:823:ALA:O	10:fP1:827:VAL:HG13	2.02	0.59
10:eP1:275:LYS:HD2	10:eP1:290:THR:HB	1.85	0.59
10:QP1:275:LYS:HB3	10:QP1:290:THR:HB	1.84	0.59
14:UP1:299:THR:HA	14:UP1:303:GLN:HE22	1.66	0.59
10:fP1:516:LYS:HA	10:fP1:516:LYS:HZ1	1.66	0.59
15:VP1:313:ARG:HB2	15:VP1:313:ARG:NH1	2.17	0.59
15:VP1:380:LEU:HD22	15:VP1:448:GLY:HA3	1.83	0.59
11:ZP1:861:LEU:HD13	11:ZP1:864:ASN:HD22	1.68	0.59
13:tP1:57:ASP:HB3	13:wP1:217:ARG:HH21	1.66	0.59
10:eP1:314:ARG:HE	10:eP1:318:LEU:HA	1.67	0.59
11:ZP1:657:VAL:HG22	11:ZP1:761:LEU:HD11	1.84	0.58
10:fP1:824:GLU:O	10:fP1:827:VAL:HG22	2.03	0.58
10:QP1:505:ALA:HA	10:QP1:508:VAL:HG13	1.85	0.58
11:ZP1:504:GLU:HG3	11:ZP1:505:GLU:HG2	1.84	0.58
11:ZP1:695:TYR:HB3	11:ZP1:860:ARG:HD2	1.85	0.58
14:UP1:491:GLN:HB3	14:UP1:505:TYR:HB2	1.86	0.58
11:bP1:332:ARG:HH12	11:bP1:371:ALA:HB2	1.69	0.58
11:bP1:321:GLN:HB3	10:dP1:339:SER:HB3	1.85	0.58
11:bP1:656:ASN:HA	11:bP1:659:ILE:HD12	1.84	0.58
10:dP1:303:ILE:HD12	10:dP1:327:LEU:HD11	1.86	0.58
10:fP1:510:LYS:HD2	10:fP1:510:LYS:O	2.03	0.58
10:fP1:825:GLU:OE1	10:fP1:825:GLU:HA	2.03	0.58
12:SP1:1310:VAL:HG23	12:SP1:1512:LEU:HB2	1.85	0.58
15:WP1:56:THR:HA	15:WP1:59:ILE:HD12	1.85	0.58
10:eP1:708:SER:HA	10:eP1:711:VAL:HG12	1.86	0.58
12:SP1:1509:VAL:O	12:SP1:1511:ASN:N	2.37	0.57
11:YP1:693:GLN:HA	11:YP1:696:MET:HG2	1.86	0.57
11:ZP1:241:GLN:HG3	11:ZP1:274:ARG:HD2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:dP1:481:LYS:HG2	10:dP1:533:ILE:HG13	1.86	0.57
15:VP1:56:THR:HA	15:VP1:59:ILE:HD12	1.85	0.57
15:WP1:516:LEU:HD11	15:WP1:615:VAL:HG12	1.87	0.57
11:YP1:256:LYS:HA	11:YP1:259:VAL:HG12	1.85	0.57
10:cP1:324:CYS:HA	10:cP1:327:LEU:HB2	1.86	0.57
10:dP1:314:ARG:HE	10:dP1:318:LEU:HA	1.70	0.57
11:RP1:658:TRP:HB2	11:RP1:682:ARG:HH21	1.68	0.57
10:dP1:840:PRO:HA	10:dP1:843:ARG:HB2	1.86	0.57
12:SP1:1503:ARG:HD3	12:SP1:1504:ASN:H	1.69	0.57
11:bP1:658:TRP:HA	11:bP1:682:ARG:HH22	1.70	0.56
10:cP1:254:LEU:HD11	10:cP1:341:LEU:HD22	1.87	0.56
10:QP1:366:LEU:HA	10:QP1:369:TRP:HB2	1.86	0.56
13:pP1:328:VAL:HG21	13:pP1:360:LEU:HD22	1.88	0.56
11:bP1:341:ALA:HA	11:bP1:344:LEU:HD12	1.87	0.56
13:hP1:328:VAL:HG21	13:hP1:360:LEU:HD22	1.88	0.56
13:iP1:328:VAL:HG21	13:iP1:360:LEU:HD22	1.87	0.56
17:jP1:50:LYS:HG3	17:jP1:52:SER:H	1.70	0.56
13:lP1:328:VAL:HG21	13:lP1:360:LEU:HD22	1.87	0.56
13:mP1:328:VAL:HG21	13:mP1:360:LEU:HD22	1.88	0.56
13:wP1:328:VAL:HG21	13:wP1:360:LEU:HD22	1.87	0.56
15:WP1:2:ILE:HD12	15:WP1:111:PHE:HB3	1.88	0.56
10:QP1:344:GLN:HE22	10:QP1:366:LEU:HD21	1.71	0.56
14:UP1:796:LEU:O	14:UP1:817:ASN:ND2	2.38	0.56
15:VP1:516:LEU:HD11	15:VP1:615:VAL:HG12	1.87	0.56
11:ZP1:486:ARG:HA	11:ZP1:489:LYS:HG2	1.88	0.56
13:qP1:328:VAL:HG21	13:qP1:360:LEU:HD22	1.87	0.56
13:kP1:328:VAL:HG21	13:kP1:360:LEU:HD22	1.87	0.56
11:bP1:328:GLN:HA	11:bP1:331:LEU:HG	1.87	0.56
10:eP1:505:ALA:HA	10:eP1:508:VAL:HG23	1.88	0.56
13:tP1:328:VAL:HG21	13:tP1:360:LEU:HD22	1.88	0.56
15:VP1:274:GLU:HA	15:VP1:277:LEU:HB3	1.88	0.56
11:YP1:255:VAL:HA	11:YP1:258:LEU:HD12	1.88	0.56
11:aP1:560:MET:HA	13:wP1:295:ARG:HH12	1.71	0.56
13:nP1:328:VAL:HG21	13:nP1:360:LEU:HD22	1.88	0.56
13:rP1:328:VAL:HG21	13:rP1:360:LEU:HD22	1.87	0.56
15:VP1:308:ALA:HA	15:VP1:311:LEU:HD12	1.87	0.56
11:YP1:472:LYS:H	11:YP1:474:ILE:HG12	1.71	0.56
13:rP1:291:LEU:O	13:rP1:339:ARG:NH1	2.39	0.56
11:YP1:223:ILE:HG22	11:YP1:265:VAL:HG21	1.86	0.55
11:YP1:312:LEU:HB3	11:YP1:318:LEU:HD21	1.88	0.55
10:QP1:861:LEU:O	10:QP1:865:THR:HG23	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:UP1:733:PHE:HB2	14:UP1:760:ALA:HB2	1.88	0.55
14:UP1:758:GLN:HG3	14:UP1:779:VAL:HG11	1.89	0.55
15:WP1:274:GLU:HA	15:WP1:277:LEU:HB3	1.88	0.55
11:ZP1:445:VAL:HA	11:ZP1:448:LYS:HE2	1.87	0.55
10:eP1:864:LEU:HD13	10:eP1:879:LEU:HD13	1.88	0.55
10:QP1:369:TRP:HA	10:QP1:369:TRP:HE3	1.69	0.55
10:dP1:516:LYS:HE2	10:dP1:520:GLU:HB2	1.88	0.55
13:kP1:291:LEU:O	13:kP1:339:ARG:NH1	2.39	0.55
13:mP1:291:LEU:O	13:mP1:339:ARG:NH1	2.39	0.55
13:nP1:291:LEU:O	13:nP1:339:ARG:NH1	2.39	0.55
10:QP1:434:TYR:CD2	10:QP1:510:LYS:HB2	2.41	0.55
12:SP1:1501:GLU:O	12:SP1:1505:LYS:HB2	2.06	0.55
13:TP1:291:LEU:O	13:TP1:339:ARG:NH1	2.39	0.55
10:dP1:432:TRP:HD1	10:dP1:436:GLY:HA2	1.71	0.55
10:dP1:434:TYR:HD2	10:dP1:510:LYS:HB2	1.72	0.55
10:dP1:665:PHE:HB2	10:dP1:762:LEU:HD22	1.88	0.55
13:iP1:291:LEU:O	13:iP1:339:ARG:NH1	2.39	0.55
13:lP1:291:LEU:O	13:lP1:339:ARG:NH1	2.39	0.55
13:tP1:291:LEU:O	13:tP1:339:ARG:NH1	2.39	0.55
12:SP1:1505:LYS:HE2	12:SP1:1505:LYS:HA	1.89	0.55
13:TP1:328:VAL:HG21	13:TP1:360:LEU:HD22	1.87	0.55
11:ZP1:407:MET:HB2	11:ZP1:434:VAL:HG22	1.88	0.55
11:bP1:553:LEU:HD23	11:bP1:556:LEU:HD23	1.87	0.55
10:cP1:268:CYS:HB2	10:cP1:271:GLU:HB3	1.88	0.55
13:oP1:328:VAL:HG21	13:oP1:360:LEU:HD22	1.88	0.55
13:pP1:291:LEU:O	13:pP1:339:ARG:NH1	2.39	0.55
14:UP1:728:ASP:H	14:UP1:764:ARG:HE	1.54	0.55
15:WP1:295:ARG:HG3	15:WP1:340:LEU:HB3	1.89	0.55
13:hP1:291:LEU:O	13:hP1:339:ARG:NH1	2.39	0.55
13:nP1:124:ARG:HG3	13:oP1:309:ARG:HE	1.72	0.55
11:RP1:391:GLU:HA	11:RP1:394:ILE:HG22	1.89	0.55
10:dP1:299:LEU:HD23	10:dP1:377:LEU:HG	1.89	0.55
10:QP1:366:LEU:O	10:QP1:370:THR:HG23	2.07	0.55
14:UP1:755:VAL:HG11	13:rP1:342:GLU:HG3	1.88	0.55
15:VP1:365:ARG:HD3	15:VP1:368:LEU:HD22	1.88	0.55
11:aP1:237:LEU:HD23	11:aP1:238:VAL:HG13	1.87	0.55
10:fP1:303:ILE:HD11	10:fP1:327:LEU:HB3	1.89	0.55
13:oP1:291:LEU:O	13:oP1:339:ARG:NH1	2.39	0.55
13:qP1:291:LEU:O	13:qP1:339:ARG:NH1	2.39	0.55
15:WP1:313:ARG:HH11	15:WP1:313:ARG:CG	2.18	0.54
11:ZP1:457:ASN:HD21	11:ZP1:460:ARG:HH21	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:eP1:514:SER:OG	10:eP1:515:PRO:CD	2.55	0.54
13:sP1:328:VAL:HG21	13:sP1:360:LEU:HD22	1.87	0.54
13:wP1:291:LEU:O	13:wP1:339:ARG:NH1	2.40	0.54
14:UP1:279:LYS:HE3	15:VP1:37:GLY:HA2	1.88	0.54
10:dP1:676:LEU:HD21	10:dP1:781:ILE:HG12	1.89	0.54
13:sP1:291:LEU:O	13:sP1:339:ARG:NH1	2.39	0.54
15:VP1:295:ARG:HG3	15:VP1:340:LEU:HB3	1.89	0.54
11:bP1:220:LEU:HD12	11:bP1:259:VAL:HG13	1.88	0.54
11:RP1:450:LEU:HD11	11:RP1:454:LYS:HE2	1.88	0.54
12:SP1:1478:GLU:HA	12:SP1:1481:HIS:HB2	1.89	0.54
11:YP1:396:ARG:O	11:YP1:460:ARG:NH2	2.40	0.54
10:dP1:370:THR:HA	10:dP1:373:PRO:HG2	1.89	0.54
11:RP1:763:ARG:NE	11:RP1:763:ARG:CA	2.70	0.54
12:SP1:1614:LEU:HD23	13:sP1:341:ARG:HD3	1.90	0.54
15:VP1:2:ILE:HD12	15:VP1:111:PHE:HB3	1.88	0.54
15:WP1:365:ARG:HD3	15:WP1:368:LEU:HD22	1.88	0.54
11:bP1:533:LEU:HB3	11:bP1:553:LEU:HD13	1.89	0.54
12:SP1:480:MET:HB3	12:SP1:501:VAL:HB	1.89	0.54
12:SP1:521:GLU:HA	12:SP1:524:ILE:HG12	1.89	0.54
10:dP1:545:LEU:O	10:dP1:549:ASN:ND2	2.41	0.54
10:eP1:434:TYR:CD2	10:eP1:510:LYS:HB2	2.42	0.54
13:qP1:311:ARG:O	13:qP1:315:HIS:ND1	2.41	0.54
15:VP1:484:VAL:HA	15:VP1:487:VAL:HG12	1.89	0.54
15:WP1:184:TYR:HE1	15:WP1:314:LEU:HB3	1.72	0.54
11:YP1:553:LEU:HD23	11:YP1:556:LEU:HD23	1.89	0.54
11:ZP1:689:VAL:O	11:ZP1:693:GLN:NE2	2.41	0.54
10:dP1:511:SER:O	10:dP1:515:PRO:CD	2.52	0.54
15:VP1:184:TYR:OH	15:VP1:311:LEU:O	2.26	0.54
11:ZP1:473:GLU:HG2	11:ZP1:486:ARG:HH22	1.72	0.54
13:wP1:311:ARG:O	13:wP1:315:HIS:ND1	2.41	0.54
14:UP1:267:ILE:HA	14:UP1:270:THR:HG22	1.89	0.53
10:fP1:431:ARG:NH1	10:fP1:437:GLU:O	2.41	0.53
13:oP1:311:ARG:O	13:oP1:315:HIS:ND1	2.41	0.53
13:pP1:311:ARG:O	13:pP1:315:HIS:ND1	2.41	0.53
13:wP1:207:ASN:HA	13:wP1:210:LEU:HD12	1.91	0.53
14:UP1:259:THR:N	14:UP1:295:ASP:OD2	2.41	0.53
11:YP1:286:GLN:HE22	11:YP1:351:GLY:H	1.55	0.53
13:tP1:207:ASN:HA	13:tP1:210:LEU:HD12	1.90	0.53
10:QP1:652:THR:OG1	10:QP1:653:ARG:N	2.42	0.53
11:RP1:754:CYS:O	11:RP1:758:THR:HG23	2.09	0.53
13:TP1:207:ASN:HA	13:TP1:210:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:aP1:556:LEU:HD13	13:wP1:339:ARG:HB3	1.89	0.53
13:iP1:207:ASN:HA	13:iP1:210:LEU:HD12	1.91	0.53
15:WP1:484:VAL:HA	15:WP1:487:VAL:HG12	1.89	0.53
11:YP1:445:VAL:HA	11:YP1:448:LYS:HE2	1.90	0.53
13:nP1:207:ASN:HA	13:nP1:210:LEU:HD12	1.90	0.53
13:oP1:207:ASN:HA	13:oP1:210:LEU:HD12	1.91	0.53
13:hP1:207:ASN:HA	13:hP1:210:LEU:HD12	1.90	0.53
12:SP1:1506:LEU:HG	12:SP1:1507:SER:N	2.24	0.53
13:iP1:311:ARG:O	13:iP1:315:HIS:ND1	2.41	0.53
13:kP1:207:ASN:HA	13:kP1:210:LEU:HD12	1.90	0.53
13:rP1:311:ARG:O	13:rP1:315:HIS:ND1	2.41	0.53
13:sP1:207:ASN:HA	13:sP1:210:LEU:HD12	1.90	0.53
15:WP1:290:ASN:HB3	15:WP1:293:MET:HG2	1.91	0.53
14:UP1:565:LEU:HD23	14:UP1:568:LEU:HD13	1.90	0.53
14:UP1:1012:LEU:HD11	13:qP1:341:ARG:HH11	1.72	0.53
13:mP1:311:ARG:O	13:mP1:315:HIS:ND1	2.41	0.53
13:qP1:207:ASN:HA	13:qP1:210:LEU:HD12	1.90	0.53
13:rP1:207:ASN:HA	13:rP1:210:LEU:HD12	1.90	0.53
13:tP1:311:ARG:O	13:tP1:315:HIS:ND1	2.41	0.53
15:VP1:290:ASN:HB3	15:VP1:293:MET:HG2	1.91	0.53
10:dP1:614:PRO:HB2	10:dP1:616:ILE:HG12	1.91	0.53
17:jP1:300:SER:HA	17:jP1:335:ARG:HB2	1.90	0.53
10:QP1:840:PRO:HA	10:QP1:843:ARG:HB2	1.91	0.52
14:UP1:921:LEU:HD13	14:UP1:924:ILE:HD11	1.91	0.52
11:ZP1:434:VAL:HG23	11:ZP1:437:GLN:H	1.73	0.52
10:fP1:839:ILE:O	10:fP1:843:ARG:HG2	2.09	0.52
13:hP1:311:ARG:O	13:hP1:315:HIS:ND1	2.41	0.52
11:bP1:319:SER:H	11:bP1:322:LYS:HB2	1.74	0.52
10:QP1:250:VAL:CG1	10:QP1:362:THR:OG1	2.58	0.52
12:SP1:500:TYR:HB3	12:SP1:503:ILE:HA	1.91	0.52
15:WP1:633:ARG:HE	10:eP1:592:TYR:HB3	1.72	0.52
11:YP1:740:ASN:H	11:YP1:743:LEU:HD13	1.75	0.52
11:bP1:699:GLU:HB2	11:bP1:860:ARG:HH21	1.74	0.52
13:nP1:311:ARG:O	13:nP1:315:HIS:ND1	2.41	0.52
10:QP1:364:ARG:CA	10:QP1:367:LEU:HB2	2.30	0.52
12:SP1:319:ASP:HB3	15:VP1:14:GLY:HA2	1.92	0.52
11:ZP1:217:VAL:HG13	11:ZP1:323:LEU:HD22	1.91	0.52
11:ZP1:694:TYR:OH	13:lP1:250:ASN:ND2	2.43	0.52
13:kP1:311:ARG:O	13:kP1:315:HIS:ND1	2.41	0.52
15:WP1:397:GLN:HG2	15:WP1:411:LEU:HD21	1.92	0.52
11:aP1:284:TYR:HB2	11:aP1:286:GLN:HE21	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:mP1:207:ASN:HA	13:mP1:210:LEU:HD12	1.91	0.52
13:sP1:311:ARG:O	13:sP1:315:HIS:ND1	2.41	0.52
10:QP1:293:LEU:HA	10:QP1:296:LEU:HD12	1.92	0.52
12:SP1:1459:LEU:O	12:SP1:1461:ASN:N	2.41	0.52
15:VP1:27:VAL:O	15:VP1:29:GLN:NE2	2.41	0.52
11:YP1:507:GLU:HB3	11:YP1:510:ALA:HB3	1.91	0.52
11:aP1:409:GLU:HG2	11:aP1:434:VAL:HB	1.92	0.52
10:eP1:511:SER:O	10:eP1:515:PRO:CD	2.52	0.52
13:pP1:207:ASN:HA	13:pP1:210:LEU:HD12	1.90	0.52
13:TP1:311:ARG:O	13:TP1:315:HIS:ND1	2.41	0.52
15:VP1:397:GLN:HG2	15:VP1:411:LEU:HD21	1.92	0.52
11:RP1:427:TRP:N	11:RP1:626:SER:O	2.43	0.52
11:bP1:550:LEU:HD11	11:bP1:576:LEU:HD22	1.91	0.52
10:dP1:655:CYS:SG	10:dP1:656:MET:N	2.83	0.52
13:lP1:207:ASN:HA	13:lP1:210:LEU:HD12	1.90	0.52
13:lP1:311:ARG:O	13:lP1:315:HIS:ND1	2.41	0.52
13:nP1:147:SER:HG	13:nP1:191:THR:HG1	1.57	0.52
10:QP1:250:VAL:HG13	10:QP1:362:THR:OG1	2.08	0.52
10:dP1:434:TYR:CD2	10:dP1:510:LYS:HB2	2.44	0.52
13:mP1:194:ARG:HD2	13:mP1:198:ASN:HD22	1.75	0.52
11:aP1:369:SER:HA	11:aP1:372:GLN:HG2	1.91	0.52
10:eP1:430:TYR:HE1	10:eP1:510:LYS:HZ3	1.58	0.52
13:kP1:194:ARG:HD2	13:kP1:198:ASN:HD22	1.76	0.52
13:sP1:194:ARG:HD2	13:sP1:198:ASN:HD22	1.75	0.52
11:YP1:233:SER:HB2	11:YP1:246:SER:HB3	1.91	0.51
17:jP1:136:ILE:HG22	17:jP1:138:ALA:H	1.75	0.51
13:oP1:194:ARG:HD2	13:oP1:198:ASN:HD22	1.75	0.51
13:rP1:194:ARG:HD2	13:rP1:198:ASN:HD22	1.75	0.51
12:SP1:1543:ILE:HD12	12:SP1:1546:ILE:HD11	1.92	0.51
13:iP1:194:ARG:HD2	13:iP1:198:ASN:HD22	1.75	0.51
11:RP1:553:LEU:HA	11:RP1:556:LEU:HG	1.93	0.51
12:SP1:320:ASN:ND2	15:VP1:7:LEU:HB3	2.26	0.51
12:SP1:1394:PRO:HB2	12:SP1:1397:PHE:HA	1.92	0.51
12:SP1:426:VAL:H	12:SP1:478:GLU:HG2	1.75	0.51
15:WP1:408:ASP:OD1	15:WP1:408:ASP:N	2.44	0.51
11:bP1:272:VAL:HG11	11:bP1:337:LEU:HB3	1.92	0.51
11:bP1:654:LEU:HD13	11:bP1:686:LEU:HA	1.92	0.51
10:eP1:434:TYR:HD2	10:eP1:510:LYS:HB2	1.75	0.51
13:nP1:194:ARG:HD2	13:nP1:198:ASN:HD22	1.75	0.51
12:SP1:508:GLU:HB3	12:SP1:515:LEU:HB3	1.93	0.51
15:VP1:35:HIS:HB2	15:VP1:38:GLU:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:YP1:527:PHE:HA	11:YP1:530:PHE:HB2	1.92	0.51
11:ZP1:661:ASN:HB3	11:ZP1:679:PHE:CE1	2.46	0.51
13:pP1:194:ARG:HD2	13:pP1:198:ASN:HD22	1.75	0.51
11:RP1:397:GLY:CA	11:RP1:460:ARG:HH21	2.24	0.51
13:hP1:194:ARG:HD2	13:hP1:198:ASN:HD22	1.75	0.51
10:eP1:525:LEU:HD22	10:eP1:528:ALA:HB3	1.91	0.51
10:fP1:275:LYS:HD2	10:fP1:290:THR:HB	1.92	0.51
13:wP1:194:ARG:HD2	13:wP1:198:ASN:HD22	1.75	0.51
13:TP1:194:ARG:HD2	13:TP1:198:ASN:HD22	1.75	0.51
15:VP1:90:CYS:HA	15:VP1:93:LEU:HG	1.92	0.51
11:aP1:702:GLU:HB3	13:tP1:330:PRO:HB2	1.93	0.51
10:cP1:525:LEU:O	10:cP1:529:PHE:N	2.40	0.51
10:fP1:514:SER:OG	10:fP1:515:PRO:CD	2.59	0.51
17:jP1:291:LYS:HE3	17:jP1:326:LYS:H	1.75	0.51
11:RP1:752:SER:O	11:RP1:755:VAL:HG22	2.10	0.51
15:VP1:293:MET:HG3	15:VP1:460:TRP:HH2	1.76	0.51
10:cP1:562:ARG:HH21	10:cP1:733:LEU:HD23	1.76	0.51
11:RP1:761:LEU:O	11:RP1:764:PHE:HB3	2.11	0.51
13:TP1:259:SER:OG	13:TP1:357:GLN:NE2	2.45	0.51
11:ZP1:562:THR:OG1	13:lP1:46:ASP:O	2.28	0.51
11:aP1:512:LEU:HA	11:aP1:515:ILE:HB	1.93	0.51
10:cP1:434:TYR:CE2	10:cP1:510:LYS:HB2	2.46	0.51
10:dP1:495:VAL:HG23	10:dP1:497:HIS:H	1.76	0.51
13:iP1:259:SER:OG	13:iP1:357:GLN:NE2	2.44	0.51
13:lP1:194:ARG:HD2	13:lP1:198:ASN:HD22	1.75	0.51
13:mP1:259:SER:OG	13:mP1:357:GLN:NE2	2.45	0.51
11:ZP1:531:MET:HE3	11:ZP1:652:ARG:HH11	1.76	0.50
11:aP1:376:LEU:HD21	11:aP1:478:LEU:HD13	1.92	0.50
10:QP1:513:GLU:HA	10:QP1:516:LYS:HD3	1.94	0.50
15:WP1:293:MET:HG3	15:WP1:460:TRP:HH2	1.76	0.50
11:YP1:258:LEU:HD22	11:YP1:261:ARG:HH21	1.76	0.50
10:cP1:251:ARG:HG2	10:cP1:345:LEU:HD21	1.93	0.50
10:cP1:505:ALA:HA	10:cP1:508:VAL:HG23	1.91	0.50
13:sP1:259:SER:OG	13:sP1:357:GLN:NE2	2.45	0.50
15:VP1:184:TYR:OH	15:VP1:311:LEU:HA	2.12	0.50
15:WP1:35:HIS:HB2	15:WP1:38:GLU:HG3	1.92	0.50
13:iP1:294:MET:HA	13:iP1:297:LEU:HG	1.94	0.50
13:lP1:259:SER:OG	13:lP1:357:GLN:NE2	2.44	0.50
12:SP1:1426:CYS:HB2	12:SP1:1523:LEU:HD13	1.92	0.50
15:VP1:405:LEU:HD21	15:VP1:410:LEU:HD22	1.94	0.50
15:VP1:491:LEU:HD21	15:VP1:589:CYS:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:WP1:27:VAL:O	15:WP1:29:GLN:NE2	2.41	0.50
15:WP1:405:LEU:HD21	15:WP1:410:LEU:HD22	1.94	0.50
11:YP1:331:LEU:HA	11:YP1:334:MET:SD	2.51	0.50
11:ZP1:655:CYS:O	11:ZP1:659:ILE:HG23	2.11	0.50
13:mP1:294:MET:HA	13:mP1:297:LEU:HG	1.94	0.50
13:nP1:259:SER:OG	13:nP1:357:GLN:NE2	2.44	0.50
13:pP1:294:MET:HA	13:pP1:297:LEU:HG	1.94	0.50
13:tP1:294:MET:HA	13:tP1:297:LEU:HG	1.94	0.50
14:UP1:777:GLU:HB2	14:UP1:779:VAL:HG23	1.93	0.50
11:YP1:679:PHE:HA	11:YP1:682:ARG:HH11	1.76	0.50
13:tP1:194:ARG:HD2	13:tP1:198:ASN:HD22	1.75	0.50
11:RP1:469:PRO:HB3	11:RP1:472:LYS:HB3	1.94	0.50
12:SP1:1502:PHE:HB2	12:SP1:1522:TYR:CE1	2.46	0.50
14:UP1:915:ALA:HB1	14:UP1:921:LEU:HD21	1.92	0.50
10:dP1:475:THR:OG1	10:dP1:477:ASP:OD1	2.30	0.50
13:hP1:259:SER:OG	13:hP1:357:GLN:NE2	2.44	0.50
13:mP1:211:ASN:HA	13:mP1:214:ALA:HB3	1.94	0.50
15:WP1:577:PRO:O	15:WP1:581:CYS:N	2.42	0.50
13:TP1:294:MET:HA	13:TP1:297:LEU:HG	1.94	0.50
11:ZP1:483:TYR:HA	11:ZP1:486:ARG:HG2	1.93	0.50
13:hP1:294:MET:HA	13:hP1:297:LEU:HG	1.94	0.50
13:pP1:211:ASN:HA	13:pP1:214:ALA:HB3	1.94	0.50
13:qP1:259:SER:OG	13:qP1:357:GLN:NE2	2.44	0.50
13:tP1:259:SER:OG	13:tP1:357:GLN:NE2	2.45	0.50
13:wP1:294:MET:HA	13:wP1:297:LEU:HG	1.94	0.50
10:QP1:511:SER:O	10:QP1:515:PRO:CD	2.52	0.50
13:hP1:211:ASN:HA	13:hP1:214:ALA:HB3	1.94	0.50
13:kP1:259:SER:OG	13:kP1:357:GLN:NE2	2.45	0.50
13:qP1:211:ASN:HA	13:qP1:214:ALA:HB3	1.94	0.50
11:RP1:264:PRO:HA	11:RP1:267:THR:HB	1.94	0.49
13:TP1:211:ASN:HA	13:TP1:214:ALA:HB3	1.94	0.49
13:TP1:272:GLY:HA3	13:TP1:377:MET:HE2	1.94	0.49
10:dP1:299:LEU:HA	10:dP1:302:LYS:HZ3	1.76	0.49
10:eP1:562:ARG:HH21	10:eP1:733:LEU:HD23	1.78	0.49
13:oP1:211:ASN:HA	13:oP1:214:ALA:HB3	1.94	0.49
13:oP1:259:SER:OG	13:oP1:357:GLN:NE2	2.45	0.49
13:qP1:194:ARG:HD2	13:qP1:198:ASN:HD22	1.75	0.49
13:rP1:259:SER:OG	13:rP1:357:GLN:NE2	2.45	0.49
13:sP1:211:ASN:HA	13:sP1:214:ALA:HB3	1.94	0.49
13:tP1:272:GLY:HA3	13:tP1:377:MET:HE2	1.94	0.49
10:dP1:525:LEU:HD12	10:dP1:528:ALA:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:lP1:211:ASN:HA	13:lP1:214:ALA:HB3	1.94	0.49
13:pP1:272:GLY:HA3	13:pP1:377:MET:HE2	1.94	0.49
13:sP1:272:GLY:HA3	13:sP1:377:MET:HE2	1.94	0.49
13:tP1:211:ASN:HA	13:tP1:214:ALA:HB3	1.94	0.49
13:lP1:66:LEU:H	13:lP1:91:ILE:HG21	1.78	0.49
13:wP1:66:LEU:H	13:wP1:91:ILE:HG21	1.78	0.49
13:wP1:259:SER:OG	13:wP1:357:GLN:NE2	2.45	0.49
10:QP1:326:ALA:HB2	10:QP1:420:LEU:HD23	1.95	0.49
11:RP1:242:SER:HB3	11:RP1:267:THR:HG22	1.94	0.49
11:bP1:262:ILE:HG23	11:bP1:327:ILE:HG21	1.94	0.49
10:cP1:473:PHE:HB2	10:cP1:526:GLU:HG2	1.94	0.49
13:nP1:211:ASN:HA	13:nP1:214:ALA:HB3	1.94	0.49
14:UP1:825:LEU:HD21	14:UP1:953:LEU:HD21	1.94	0.49
15:WP1:90:CYS:HA	15:WP1:93:LEU:HG	1.92	0.49
10:cP1:434:TYR:HD2	10:cP1:510:LYS:HB2	1.76	0.49
13:kP1:211:ASN:HA	13:kP1:214:ALA:HB3	1.94	0.49
13:nP1:272:GLY:HA3	13:nP1:377:MET:HE2	1.94	0.49
13:oP1:272:GLY:HA3	13:oP1:377:MET:HE2	1.94	0.49
13:oP1:294:MET:HA	13:oP1:297:LEU:HG	1.94	0.49
13:rP1:211:ASN:HA	13:rP1:214:ALA:HB3	1.94	0.49
10:QP1:259:GLY:HA3	11:YP1:256:LYS:NZ	2.27	0.49
10:QP1:318:LEU:O	10:QP1:320:GLY:N	2.45	0.49
10:QP1:365:ARG:O	10:QP1:368:VAL:HG22	2.12	0.49
10:cP1:326:ALA:HB2	10:cP1:420:LEU:HD23	1.93	0.49
13:wP1:211:ASN:HA	13:wP1:214:ALA:HB3	1.94	0.49
11:RP1:690:GLN:O	11:RP1:693:GLN:NE2	2.45	0.49
15:WP1:491:LEU:HD21	15:WP1:589:CYS:HB2	1.93	0.49
10:fP1:411:ARG:HA	10:fP1:414:VAL:HG22	1.93	0.49
13:kP1:294:MET:HA	13:kP1:297:LEU:HG	1.94	0.49
13:rP1:294:MET:HA	13:rP1:297:LEU:HG	1.94	0.49
11:bP1:380:LYS:HB3	11:bP1:478:LEU:HD12	1.95	0.49
11:RP1:751:MET:O	11:RP1:755:VAL:HG13	2.13	0.49
11:YP1:472:LYS:HE3	11:YP1:490:ALA:HB2	1.95	0.49
11:aP1:605:THR:OG1	11:aP1:606:GLU:N	2.46	0.49
11:aP1:835:LEU:HD23	11:aP1:838:LEU:HD21	1.93	0.49
10:dP1:345:LEU:HA	10:dP1:361:LEU:HD21	1.93	0.49
13:nP1:294:MET:HA	13:nP1:297:LEU:HG	1.94	0.49
13:qP1:294:MET:HA	13:qP1:297:LEU:HG	1.94	0.49
12:SP1:1533:THR:HG23	12:SP1:1535:LYS:HA	1.94	0.49
11:YP1:442:LEU:HD23	11:YP1:444:LYS:H	1.78	0.49
13:lP1:294:MET:HA	13:lP1:297:LEU:HG	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:pP1:259:SER:OG	13:pP1:357:GLN:NE2	2.45	0.49
11:ZP1:396:ARG:NH2	11:ZP1:466:VAL:O	2.46	0.48
10:fP1:516:LYS:HD2	10:fP1:516:LYS:N	2.28	0.48
13:hP1:66:LEU:H	13:hP1:91:ILE:HG21	1.78	0.48
13:pP1:66:LEU:H	13:pP1:91:ILE:HG21	1.78	0.48
13:sP1:294:MET:HA	13:sP1:297:LEU:HG	1.94	0.48
10:QP1:259:GLY:HA3	11:YP1:256:LYS:HZ1	1.77	0.48
11:ZP1:646:TYR:OH	11:ZP1:751:MET:SD	2.61	0.48
13:iP1:211:ASN:HA	13:iP1:214:ALA:HB3	1.94	0.48
13:kP1:272:GLY:HA3	13:kP1:377:MET:HE2	1.94	0.48
13:tP1:206:ASP:OD2	13:tP1:208:THR:OG1	2.31	0.48
11:RP1:240:ARG:HH11	11:RP1:243:ARG:HD3	1.78	0.48
11:RP1:508:LEU:HD13	11:RP1:625:LEU:HD22	1.95	0.48
14:UP1:826:ILE:HA	14:UP1:829:ALA:HB3	1.96	0.48
11:YP1:395:TYR:OH	11:YP1:475:THR:O	2.28	0.48
11:aP1:507:GLU:HB2	11:aP1:510:ALA:HB3	1.95	0.48
11:aP1:690:GLN:NE2	13:tP1:250:ASN:HD21	2.11	0.48
10:fP1:266:LYS:HG3	10:fP1:275:LYS:HA	1.95	0.48
10:fP1:511:SER:O	10:fP1:515:PRO:CD	2.52	0.48
13:nP1:206:ASP:OD2	13:nP1:208:THR:OG1	2.31	0.48
13:qP1:66:LEU:H	13:qP1:91:ILE:HG21	1.78	0.48
13:rP1:272:GLY:HA3	13:rP1:377:MET:HE2	1.94	0.48
11:RP1:654:LEU:HB3	11:RP1:686:LEU:HD12	1.96	0.48
11:YP1:321:GLN:HA	11:YP1:324:TRP:HB3	1.96	0.48
10:fP1:828:GLU:HG2	10:fP1:831:ARG:NH2	2.29	0.48
13:qP1:224:SER:OG	13:qP1:227:GLN:NE2	2.46	0.48
12:SP1:1499:TRP:O	12:SP1:1503:ARG:HD2	2.12	0.48
13:TP1:66:LEU:H	13:TP1:91:ILE:HG21	1.78	0.48
14:UP1:427:VAL:O	14:UP1:431:HIS:ND1	2.46	0.48
11:YP1:343:SER:HB2	11:YP1:357:LEU:HD11	1.95	0.48
11:bP1:321:GLN:HG3	10:dP1:335:TYR:HB3	1.94	0.48
11:bP1:861:LEU:HD12	11:bP1:864:ASN:HD22	1.78	0.48
10:fP1:602:THR:HG22	10:fP1:605:ARG:HH22	1.78	0.48
13:iP1:66:LEU:H	13:iP1:91:ILE:HG21	1.78	0.48
13:iP1:272:GLY:HA3	13:iP1:377:MET:HE2	1.95	0.48
13:lP1:206:ASP:OD2	13:lP1:208:THR:OG1	2.31	0.48
13:lP1:272:GLY:HA3	13:lP1:377:MET:HE2	1.94	0.48
10:QP1:706:LEU:HD13	10:QP1:850:THR:HG21	1.93	0.48
15:VP1:408:ASP:N	15:VP1:408:ASP:OD1	2.44	0.48
10:cP1:553:ASN:HB3	10:cP1:556:GLU:HB2	1.96	0.48
10:dP1:577:MET:HE1	10:dP1:670:LYS:HE2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:eP1:598:GLY:HA3	13:pP1:341:ARG:HH21	1.79	0.48
10:fP1:676:LEU:HD12	10:fP1:781:ILE:HD11	1.96	0.48
17:jP1:61:LYS:HB3	17:jP1:64:ILE:HB	1.94	0.48
13:kP1:224:SER:OG	13:kP1:227:GLN:NE2	2.46	0.48
13:oP1:172:PHE:HB2	13:oP1:206:ASP:HA	1.96	0.48
13:tP1:66:LEU:H	13:tP1:91:ILE:HG21	1.78	0.48
14:UP1:749:ASN:HD21	14:UP1:752:TYR:HB3	1.79	0.48
14:UP1:824:LEU:O	14:UP1:828:TRP:N	2.47	0.48
11:ZP1:531:MET:HE3	11:ZP1:652:ARG:HD2	1.96	0.48
11:aP1:559:ARG:O	13:wP1:295:ARG:NH1	2.46	0.48
10:cP1:476:MET:SD	10:cP1:480:ARG:NH1	2.87	0.48
13:kP1:206:ASP:OD2	13:kP1:208:THR:OG1	2.31	0.48
13:mP1:66:LEU:H	13:mP1:91:ILE:HG21	1.78	0.48
13:mP1:272:GLY:HA3	13:mP1:377:MET:HE2	1.94	0.48
13:oP1:66:LEU:H	13:oP1:91:ILE:HG21	1.78	0.48
13:sP1:172:PHE:HB2	13:sP1:206:ASP:HA	1.96	0.48
10:QP1:344:GLN:CD	10:QP1:362:THR:HG22	2.39	0.48
10:QP1:860:PHE:O	10:QP1:864:LEU:HB3	2.13	0.48
11:RP1:761:LEU:HD23	11:RP1:761:LEU:N	2.29	0.48
10:QP1:344:GLN:HE22	10:QP1:366:LEU:CG	2.27	0.48
14:UP1:911:GLN:HB3	14:UP1:924:ILE:HD12	1.96	0.48
11:YP1:266:ALA:HA	11:YP1:269:TYR:CE2	2.49	0.48
13:hP1:272:GLY:HA3	13:hP1:377:MET:HE2	1.94	0.48
17:jP1:156:GLY:HA2	17:jP1:302:GLY:H	1.77	0.48
13:rP1:66:LEU:H	13:rP1:91:ILE:HG21	1.78	0.48
13:tP1:224:SER:OG	13:tP1:227:GLN:NE2	2.46	0.48
10:QP1:254:LEU:HD11	10:QP1:345:LEU:HD22	1.95	0.48
10:QP1:299:LEU:HD11	10:QP1:381:ALA:HB2	1.96	0.48
10:QP1:364:ARG:NH1	11:RP1:221:LEU:O	2.47	0.48
11:bP1:394:ILE:HD12	11:bP1:449:ILE:HG22	1.95	0.48
10:dP1:266:LYS:HE2	10:dP1:275:LYS:HG3	1.96	0.48
13:nP1:172:PHE:HB2	13:nP1:206:ASP:HA	1.96	0.48
13:qP1:272:GLY:HA3	13:qP1:377:MET:HE2	1.94	0.48
13:sP1:66:LEU:H	13:sP1:91:ILE:HG21	1.78	0.48
13:wP1:272:GLY:HA3	13:wP1:377:MET:HE2	1.95	0.48
11:YP1:481:GLN:O	11:YP1:483:TYR:N	2.34	0.47
11:ZP1:485:GLU:HA	11:ZP1:488:GLU:HG2	1.96	0.47
11:aP1:491:TYR:OH	11:aP1:717:ASN:ND2	2.42	0.47
11:bP1:367:GLY:HA3	10:dP1:314:ARG:HH12	1.79	0.47
10:fP1:837:GLU:OE1	10:fP1:837:GLU:HA	2.14	0.47
13:iP1:172:PHE:HB2	13:iP1:206:ASP:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SP1:1461:ASN:HB3	12:SP1:1462:GLN:H	1.46	0.47
11:YP1:542:VAL:HG13	11:YP1:546:ILE:HB	1.96	0.47
10:cP1:310:ARG:HA	10:cP1:390:ARG:HH12	1.78	0.47
10:fP1:747:ILE:HA	10:fP1:750:HIS:HB3	1.96	0.47
13:kP1:66:LEU:H	13:kP1:91:ILE:HG21	1.78	0.47
13:kP1:172:PHE:HB2	13:kP1:206:ASP:HA	1.96	0.47
13:nP1:66:LEU:H	13:nP1:91:ILE:HG21	1.78	0.47
12:SP1:1505:LYS:HB3	12:SP1:1505:LYS:HZ3	1.77	0.47
12:SP1:1509:VAL:O	12:SP1:1509:VAL:CG1	2.61	0.47
15:VP1:384:PRO:HD2	15:VP1:444:ALA:HA	1.96	0.47
11:bP1:220:LEU:HD21	11:bP1:262:ILE:HG21	1.96	0.47
13:pP1:172:PHE:HB2	13:pP1:206:ASP:HA	1.96	0.47
13:qP1:206:ASP:OD2	13:qP1:208:THR:OG1	2.31	0.47
12:SP1:1342:SER:HA	12:SP1:1345:LEU:HD12	1.96	0.47
13:TP1:224:SER:OG	13:TP1:227:GLN:NE2	2.46	0.47
10:cP1:581:LYS:HD2	10:cP1:674:TYR:HE2	1.80	0.47
13:hP1:172:PHE:HB2	13:hP1:206:ASP:HA	1.96	0.47
13:oP1:224:SER:OG	13:oP1:227:GLN:NE2	2.46	0.47
10:QP1:562:ARG:HH21	10:QP1:733:LEU:HD23	1.79	0.47
11:RP1:516:LYS:HZ2	11:RP1:705:TRP:HB2	1.79	0.47
13:pP1:206:ASP:OD2	13:pP1:208:THR:OG1	2.31	0.47
13:wP1:224:SER:OG	13:wP1:227:GLN:NE2	2.46	0.47
12:SP1:1549:LEU:O	12:SP1:1553:PHE:N	2.47	0.47
13:TP1:172:PHE:HB2	13:TP1:206:ASP:HA	1.96	0.47
14:UP1:428:ARG:HA	14:UP1:431:HIS:CE1	2.49	0.47
15:VP1:550:THR:HB	15:VP1:556:ILE:HD11	1.96	0.47
11:ZP1:661:ASN:HB3	11:ZP1:679:PHE:CZ	2.50	0.47
11:aP1:548:THR:HG23	10:fP1:873:ARG:HH21	1.80	0.47
10:fP1:802:ARG:HH22	10:fP1:828:GLU:HB3	1.78	0.47
10:fP1:830:LYS:HE2	10:fP1:830:LYS:CA	2.35	0.47
13:iP1:224:SER:OG	13:iP1:227:GLN:NE2	2.46	0.47
13:mP1:224:SER:OG	13:mP1:227:GLN:NE2	2.46	0.47
10:QP1:408:PRO:HA	10:QP1:411:ARG:HB3	1.97	0.47
11:RP1:356:SER:HA	11:RP1:440:SER:HB3	1.97	0.47
11:RP1:407:MET:HG3	11:RP1:408:VAL:HG13	1.95	0.47
12:SP1:437:LEU:HD23	12:SP1:1287:PRO:HG2	1.97	0.47
13:TP1:206:ASP:OD2	13:TP1:208:THR:OG1	2.31	0.47
15:WP1:550:THR:HB	15:WP1:556:ILE:HD11	1.96	0.47
11:ZP1:498:LEU:HD22	11:ZP1:718:ILE:HG13	1.95	0.47
11:aP1:250:ASN:HB3	11:aP1:256:LYS:HE2	1.96	0.47
11:aP1:407:MET:HB2	11:aP1:434:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:aP1:677:GLY:HA3	11:aP1:824:ILE:HD11	1.97	0.47
10:cP1:773:GLN:HG2	10:cP1:863:LEU:HD23	1.97	0.47
10:fP1:843:ARG:HD2	10:fP1:847:ARG:HH22	1.78	0.47
13:iP1:206:ASP:OD2	13:iP1:208:THR:OG1	2.31	0.47
13:mP1:172:PHE:HB2	13:mP1:206:ASP:HA	1.96	0.47
13:nP1:224:SER:OG	13:nP1:227:GLN:NE2	2.46	0.47
13:pP1:224:SER:OG	13:pP1:227:GLN:NE2	2.46	0.47
13:rP1:172:PHE:HB2	13:rP1:206:ASP:HA	1.96	0.47
13:wP1:172:PHE:HB2	13:wP1:206:ASP:HA	1.96	0.47
11:YP1:502:LEU:HB2	11:YP1:508:LEU:HD23	1.97	0.47
11:aP1:746:ILE:HG21	11:aP1:841:LYS:HD3	1.97	0.47
10:cP1:393:GLY:HA3	10:cP1:469:MET:HB2	1.97	0.47
13:iP1:147:SER:HG	13:iP1:191:THR:HG1	1.58	0.47
13:oP1:206:ASP:OD2	13:oP1:208:THR:OG1	2.31	0.47
10:QP1:368:VAL:O	10:QP1:369:TRP:C	2.57	0.47
12:SP1:1477:HIS:CD2	13:sP1:262:PRO:HA	2.50	0.47
14:UP1:282:ILE:HG23	14:UP1:292:VAL:HG22	1.96	0.47
11:YP1:256:LYS:HB3	11:YP1:256:LYS:HE3	1.72	0.47
10:cP1:519:ALA:HB3	10:cP1:520:GLU:OE1	2.13	0.47
10:eP1:432:TRP:HD1	10:eP1:436:GLY:HA2	1.80	0.47
10:eP1:610:GLN:O	10:eP1:613:ASN:ND2	2.48	0.47
13:hP1:224:SER:OG	13:hP1:227:GLN:NE2	2.46	0.47
10:QP1:324:CYS:HA	10:QP1:327:LEU:HB2	1.97	0.47
10:QP1:332:LYS:HD2	11:YP1:332:ARG:HH12	1.79	0.47
12:SP1:392:ARG:HG2	12:SP1:396:ARG:HH12	1.80	0.47
12:SP1:491:ARG:O	12:SP1:1419:ASN:ND2	2.47	0.47
12:SP1:1611:ASP:HA	12:SP1:1614:LEU:HD12	1.96	0.47
14:UP1:917:ASP:OD1	14:UP1:917:ASP:N	2.46	0.47
15:VP1:344:MET:HE2	15:VP1:350:LEU:HD21	1.97	0.47
11:YP1:324:TRP:HA	11:YP1:327:ILE:HG12	1.97	0.47
11:aP1:641:PHE:O	11:aP1:645:PHE:N	2.46	0.47
11:bP1:327:ILE:HG22	11:bP1:331:LEU:HD23	1.97	0.47
10:fP1:555:LEU:HA	10:fP1:558:MET:HG2	1.97	0.47
14:UP1:489:ILE:O	14:UP1:491:GLN:N	2.48	0.46
11:YP1:328:GLN:HA	11:YP1:331:LEU:HG	1.97	0.46
10:cP1:511:SER:O	10:cP1:515:PRO:CD	2.51	0.46
10:cP1:521:LEU:HD21	10:cP1:525:LEU:HB3	1.96	0.46
10:fP1:836:GLN:CD	10:fP1:836:GLN:C	2.83	0.46
13:rP1:224:SER:OG	13:rP1:227:GLN:NE2	2.46	0.46
13:sP1:206:ASP:OD2	13:sP1:208:THR:OG1	2.31	0.46
12:SP1:317:SER:HA	15:VP1:4:GLU:HG3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:IP1:172:PHE:HB2	13:IP1:206:ASP:HA	1.96	0.46
14:UP1:780:ASP:OD1	14:UP1:780:ASP:N	2.48	0.46
11:bP1:740:ASN:H	11:bP1:743:LEU:HD12	1.79	0.46
10:cP1:632:THR:HG23	10:cP1:634:TRP:H	1.79	0.46
10:fP1:408:PRO:HA	10:fP1:411:ARG:HB3	1.97	0.46
13:IP1:224:SER:OG	13:IP1:227:GLN:NE2	2.46	0.46
10:QP1:344:GLN:HE22	10:QP1:366:LEU:CD2	2.27	0.46
10:QP1:742:ASP:HB2	10:QP1:745:HIS:HB2	1.97	0.46
12:SP1:1509:VAL:O	12:SP1:1510:SER:C	2.58	0.46
15:VP1:315:LYS:C	15:VP1:317:GLN:H	2.23	0.46
15:WP1:120:SER:HB2	10:eP1:342:HIS:CE1	2.51	0.46
11:YP1:707:ILE:HG12	11:YP1:728:PHE:HB2	1.98	0.46
11:aP1:216:LEU:HD13	11:aP1:320:LEU:HD11	1.97	0.46
10:dP1:510:LYS:HE3	10:dP1:510:LYS:HB3	1.48	0.46
13:tP1:88:PRO:HG2	13:wP1:215:THR:HB	1.96	0.46
10:QP1:559:GLN:HA	10:QP1:562:ARG:HD2	1.96	0.46
11:RP1:449:ILE:O	11:RP1:452:THR:OG1	2.34	0.46
11:RP1:763:ARG:CZ	11:RP1:763:ARG:CA	2.82	0.46
12:SP1:1298:MET:HA	12:SP1:1301:HIS:CD2	2.51	0.46
14:UP1:571:ARG:HH21	14:UP1:707:LYS:HD2	1.81	0.46
15:WP1:384:PRO:HD2	15:WP1:444:ALA:HA	1.96	0.46
11:YP1:383:SER:O	11:YP1:387:PHE:N	2.40	0.46
10:cP1:408:PRO:HA	10:cP1:411:ARG:HB3	1.97	0.46
10:eP1:408:PRO:HA	10:eP1:411:ARG:HB3	1.97	0.46
10:fP1:562:ARG:HA	10:fP1:566:LEU:HB2	1.97	0.46
10:fP1:836:GLN:O	10:fP1:840:PRO:CD	2.56	0.46
13:oP1:192:LEU:HD23	13:oP1:195:LEU:HD12	1.98	0.46
13:tP1:172:PHE:HB2	13:tP1:206:ASP:HA	1.96	0.46
10:eP1:290:THR:HA	10:eP1:293:LEU:HD12	1.98	0.46
10:fP1:559:GLN:HA	10:fP1:562:ARG:HD2	1.98	0.46
10:fP1:870:GLU:H	10:fP1:872:LEU:HD23	1.81	0.46
13:qP1:172:PHE:HB2	13:qP1:206:ASP:HA	1.96	0.46
15:VP1:577:PRO:O	15:VP1:581:CYS:N	2.42	0.46
11:YP1:310:GLU:HA	11:YP1:313:GLN:HB3	1.98	0.46
11:ZP1:658:TRP:NE1	11:ZP1:682:ARG:HB3	2.29	0.46
10:eP1:314:ARG:NH2	10:eP1:321:GLN:HB2	2.30	0.46
13:mP1:46:ASP:HB2	13:mP1:246:PRO:HG3	1.98	0.46
10:QP1:866:THR:O	10:QP1:867:SER:HB3	2.16	0.46
12:SP1:1506:LEU:HG	12:SP1:1507:SER:H	1.81	0.46
15:VP1:514:TRP:HE1	13:rP1:263:THR:HA	1.81	0.46
10:fP1:251:ARG:HG2	10:fP1:345:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:hP1:206:ASP:OD2	13:hP1:208:THR:OG1	2.31	0.46
13:kP1:192:LEU:HD23	13:kP1:195:LEU:HD12	1.98	0.46
13:lP1:46:ASP:HB2	13:lP1:246:PRO:HG3	1.98	0.46
10:QP1:363:LEU:N	10:QP1:366:LEU:HD23	2.31	0.46
10:QP1:864:LEU:HD22	10:QP1:879:LEU:HG	1.97	0.46
11:RP1:344:LEU:HD11	11:RP1:358:LEU:HD21	1.96	0.46
15:VP1:300:LEU:HG	15:VP1:301:LYS:HG3	1.97	0.46
13:oP1:46:ASP:HB2	13:oP1:246:PRO:HG3	1.98	0.46
13:wP1:46:ASP:HB2	13:wP1:246:PRO:HG3	1.98	0.46
10:QP1:402:TYR:O	10:QP1:405:THR:OG1	2.34	0.46
12:SP1:1429:LYS:HB2	12:SP1:1523:LEU:HD21	1.98	0.46
14:UP1:284:GLN:HB3	14:UP1:290:VAL:HG13	1.97	0.46
11:RP1:359:HIS:CD2	11:RP1:440:SER:HB2	2.50	0.45
10:QP1:369:TRP:CE3	10:QP1:369:TRP:CA	2.99	0.45
11:RP1:502:LEU:HD22	11:RP1:508:LEU:HD22	1.97	0.45
12:SP1:1477:HIS:HE1	13:sP1:351:TRP:HH2	1.63	0.45
15:VP1:460:TRP:O	15:VP1:462:LEU:N	2.49	0.45
15:WP1:344:MET:HE2	15:WP1:350:LEU:HD21	1.97	0.45
10:cP1:681:LYS:HA	10:cP1:681:LYS:HD2	1.78	0.45
10:dP1:681:LYS:HA	10:dP1:681:LYS:HD2	1.83	0.45
10:eP1:773:GLN:HG2	10:eP1:863:LEU:HD23	1.98	0.45
13:tP1:192:LEU:HD23	13:tP1:195:LEU:HD12	1.98	0.45
10:QP1:365:ARG:HH22	11:RP1:311:HIS:HB2	1.81	0.45
11:RP1:657:VAL:CG1	11:RP1:761:LEU:HD12	2.46	0.45
14:UP1:469:LEU:HD22	8:uP1:2:ALA:HA	1.98	0.45
15:VP1:9:LEU:HD13	15:VP1:126:LEU:HD21	1.98	0.45
10:cP1:791:LEU:HD13	10:cP1:842:MET:HG2	1.99	0.45
10:dP1:408:PRO:HA	10:dP1:411:ARG:HB3	1.97	0.45
10:QP1:510:LYS:HE2	10:QP1:510:LYS:C	2.41	0.45
10:QP1:601:GLU:O	10:QP1:605:ARG:NH1	2.49	0.45
13:TP1:192:LEU:HD23	13:TP1:195:LEU:HD12	1.98	0.45
11:ZP1:710:LYS:HB3	11:ZP1:724:HIS:CE1	2.52	0.45
10:dP1:260:ILE:HG22	10:dP1:261:ASP:H	1.81	0.45
10:dP1:798:GLU:HB3	10:dP1:835:PHE:HE1	1.81	0.45
10:fP1:583:GLU:OE2	10:fP1:583:GLU:N	2.49	0.45
10:QP1:465:LEU:HB3	10:QP1:483:LEU:HD11	1.98	0.45
11:RP1:453:GLY:HA2	11:RP1:456:LEU:HB2	1.97	0.45
11:aP1:380:LYS:HE2	11:aP1:478:LEU:HA	1.99	0.45
11:aP1:389:ILE:HD12	11:aP1:406:PHE:HB2	1.98	0.45
10:dP1:275:LYS:HB2	10:dP1:290:THR:HB	1.97	0.45
10:dP1:548:LEU:HD22	10:dP1:554:LEU:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:fP1:401:ALA:HA	10:fP1:404:LYS:HE3	1.97	0.45
13:kP1:46:ASP:HB2	13:kP1:246:PRO:HG3	1.98	0.45
13:qP1:46:ASP:HB2	13:qP1:246:PRO:HG3	1.98	0.45
13:rP1:192:LEU:HD23	13:rP1:195:LEU:HD12	1.98	0.45
13:tP1:46:ASP:HB2	13:tP1:246:PRO:HG3	1.98	0.45
10:QP1:366:LEU:N	10:QP1:366:LEU:HD13	2.32	0.45
12:SP1:513:VAL:HG23	12:SP1:1295:THR:HG23	1.98	0.45
12:SP1:1351:SER:HA	12:SP1:1352:GLY:HA2	1.76	0.45
13:TP1:46:ASP:HB2	13:TP1:246:PRO:HG3	1.98	0.45
15:WP1:13:PRO:HB3	15:WP1:19:TRP:HB3	1.98	0.45
15:WP1:300:LEU:HG	15:WP1:301:LYS:HG3	1.97	0.45
15:WP1:304:GLU:HA	15:WP1:307:PHE:CD2	2.51	0.45
11:YP1:493:TYR:HA	11:YP1:496:LYS:HE3	1.98	0.45
11:bP1:319:SER:HB3	11:bP1:322:LYS:HG2	1.99	0.45
13:iP1:46:ASP:HB2	13:iP1:246:PRO:HG3	1.98	0.45
13:pP1:46:ASP:HB2	13:pP1:246:PRO:HG3	1.98	0.45
13:rP1:206:ASP:OD2	13:rP1:208:THR:OG1	2.31	0.45
13:wP1:192:LEU:HD23	13:wP1:195:LEU:HD12	1.98	0.45
11:RP1:216:LEU:HD11	11:RP1:320:LEU:HD11	1.98	0.45
11:aP1:630:ASN:HB3	11:aP1:633:ALA:H	1.82	0.45
10:cP1:577:MET:HE1	10:cP1:670:LYS:HE2	1.99	0.45
13:mP1:206:ASP:OD2	13:mP1:208:THR:OG1	2.31	0.45
11:RP1:240:ARG:HH11	11:RP1:243:ARG:HH11	1.65	0.45
12:SP1:1480:GLN:HB2	12:SP1:1484:LYS:NZ	2.31	0.45
12:SP1:1496:HIS:HB3	13:sP1:330:PRO:HB2	1.99	0.45
11:ZP1:531:MET:HE1	11:ZP1:648:LYS:HE2	1.98	0.45
10:eP1:652:THR:OG1	10:eP1:653:ARG:N	2.49	0.45
10:fP1:577:MET:HE1	10:fP1:670:LYS:HE2	1.98	0.45
13:qP1:192:LEU:HD23	13:qP1:195:LEU:HD12	1.98	0.45
10:QP1:553:ASN:HB3	10:QP1:556:GLU:HB2	1.99	0.45
15:WP1:9:LEU:HD13	15:WP1:126:LEU:HD21	1.99	0.45
10:cP1:864:LEU:HD12	10:cP1:879:LEU:HD13	1.99	0.45
13:nP1:192:LEU:HD23	13:nP1:195:LEU:HD12	1.98	0.45
11:RP1:370:GLN:HA	11:RP1:373:GLU:HG2	1.99	0.45
11:RP1:457:ASN:HA	11:RP1:460:ARG:HD2	1.99	0.45
14:UP1:900:ILE:HB	14:UP1:935:ARG:HB3	1.98	0.45
15:VP1:13:PRO:HB3	15:VP1:19:TRP:HB3	1.98	0.45
15:WP1:513:LYS:HG2	15:WP1:611:LEU:HD13	1.98	0.45
11:bP1:254:SER:HB3	10:dP1:262:GLY:HA2	1.98	0.45
10:cP1:411:ARG:HA	10:cP1:414:VAL:HG22	1.99	0.45
13:nP1:46:ASP:HB2	13:nP1:246:PRO:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:sP1:192:LEU:HD23	13:sP1:195:LEU:HD12	1.98	0.45
15:VP1:513:LYS:HG2	15:VP1:611:LEU:HD13	1.98	0.44
15:WP1:310:GLU:HA	15:WP1:313:ARG:CG	2.47	0.44
11:YP1:301:GLU:HA	11:YP1:304:ILE:HG12	1.98	0.44
10:eP1:644:ASP:OD1	10:eP1:644:ASP:N	2.48	0.44
13:kP1:112:GLU:HA	13:kP1:115:HIS:HB2	1.99	0.44
13:oP1:112:GLU:HA	13:oP1:115:HIS:HB2	2.00	0.44
13:pP1:192:LEU:HD23	13:pP1:195:LEU:HD12	1.98	0.44
13:wP1:49:ASP:OD1	13:wP1:49:ASP:N	2.46	0.44
11:ZP1:407:MET:HB3	11:ZP1:407:MET:HE2	1.71	0.44
11:ZP1:506:GLU:HB3	11:ZP1:625:LEU:HD21	1.99	0.44
10:dP1:544:LEU:HD21	10:dP1:743:LEU:HB3	1.99	0.44
10:eP1:254:LEU:HG	10:eP1:341:LEU:HD22	1.98	0.44
10:fP1:872:LEU:HD13	10:fP1:875:LEU:HD12	1.99	0.44
13:hP1:192:LEU:HD23	13:hP1:195:LEU:HD12	1.98	0.44
13:mP1:192:LEU:HD23	13:mP1:195:LEU:HD12	1.98	0.44
13:oP1:309:ARG:HA	13:oP1:309:ARG:HD3	1.84	0.44
13:pP1:49:ASP:OD1	13:pP1:49:ASP:N	2.46	0.44
10:QP1:596:LEU:HA	10:QP1:599:ILE:HG22	1.99	0.44
11:RP1:754:CYS:SG	11:RP1:755:VAL:N	2.89	0.44
11:RP1:762:GLN:HE21	11:RP1:763:ARG:HH11	1.65	0.44
12:SP1:280:LEU:HD21	12:SP1:313:ILE:HG21	1.99	0.44
10:eP1:827:VAL:HA	10:eP1:830:LYS:HE3	1.98	0.44
10:fP1:805:PHE:HZ	10:fP1:824:GLU:CG	2.30	0.44
13:hP1:46:ASP:HB2	13:hP1:246:PRO:HG3	1.98	0.44
15:VP1:310:GLU:HA	15:VP1:313:ARG:CZ	2.48	0.44
15:WP1:118:SER:HB3	10:eP1:342:HIS:CD2	2.52	0.44
11:bP1:220:LEU:HD11	11:bP1:262:ILE:HD12	2.00	0.44
10:dP1:479:SER:HA	10:dP1:482:VAL:HG22	1.98	0.44
10:dP1:652:THR:OG1	10:dP1:653:ARG:N	2.50	0.44
10:fP1:837:GLU:O	10:fP1:840:PRO:HB2	2.17	0.44
13:lP1:112:GLU:HA	13:lP1:115:HIS:HB2	1.99	0.44
11:RP1:746:ILE:HG23	11:RP1:837:ASP:HB3	2.00	0.44
14:UP1:877:ARG:HA	14:UP1:880:LEU:HG	1.99	0.44
11:aP1:690:GLN:HE22	13:tP1:250:ASN:HD21	1.65	0.44
10:cP1:537:TYR:OH	10:cP1:742:ASP:OD2	2.36	0.44
10:eP1:577:MET:HE1	10:eP1:670:LYS:HE2	2.00	0.44
10:eP1:791:LEU:HD13	10:eP1:842:MET:HA	2.00	0.44
13:kP1:147:SER:OG	13:kP1:191:THR:OG1	2.33	0.44
13:sP1:46:ASP:HB2	13:sP1:246:PRO:HG3	1.98	0.44
13:wP1:309:ARG:HA	13:wP1:309:ARG:HD3	1.84	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:QP1:798:GLU:HB3	10:QP1:835:PHE:HE1	1.82	0.44
11:RP1:750:LEU:O	11:RP1:753:VAL:HG22	2.17	0.44
11:bP1:679:PHE:HA	11:bP1:682:ARG:HD3	2.00	0.44
10:eP1:594:HIS:O	13:pP1:341:ARG:NH1	2.44	0.44
13:qP1:112:GLU:HA	13:qP1:115:HIS:HB2	1.99	0.44
13:rP1:46:ASP:HB2	13:rP1:246:PRO:HG3	1.98	0.44
13:sP1:224:SER:OG	13:sP1:227:GLN:NE2	2.46	0.44
11:RP1:259:VAL:HA	11:RP1:262:ILE:HG22	2.00	0.44
11:RP1:408:VAL:HG12	11:RP1:433:ILE:HG22	2.00	0.44
13:TP1:134:GLY:HA2	13:TP1:164:LYS:HB3	2.00	0.44
11:aP1:375:CYS:HA	11:aP1:378:LEU:HB2	2.00	0.44
11:bP1:855:ILE:HA	11:bP1:858:ILE:HG22	1.99	0.44
13:hP1:134:GLY:HA2	13:hP1:164:LYS:HB3	2.00	0.44
13:iP1:112:GLU:HA	13:iP1:115:HIS:HB2	2.00	0.44
13:kP1:309:ARG:HD3	13:kP1:309:ARG:HA	1.84	0.44
13:lP1:192:LEU:HD23	13:lP1:195:LEU:HD12	1.98	0.44
13:rP1:112:GLU:HA	13:rP1:115:HIS:HB2	1.99	0.44
13:rP1:134:GLY:HA2	13:rP1:164:LYS:HB3	2.00	0.44
10:QP1:659:TYR:HA	10:QP1:662:VAL:HG12	2.00	0.44
11:RP1:395:TYR:HA	11:RP1:469:PRO:HG2	2.00	0.44
11:RP1:842:LEU:HD13	11:RP1:861:LEU:HD22	1.99	0.44
15:VP1:5:LEU:HG	15:VP1:42:LEU:HD21	2.00	0.44
15:WP1:99:PRO:HA	15:WP1:102:GLN:HB3	2.00	0.44
11:aP1:852:HIS:CG	11:aP1:853:SER:H	2.35	0.44
13:iP1:192:LEU:HD23	13:iP1:195:LEU:HD12	1.98	0.44
13:kP1:134:GLY:HA2	13:kP1:164:LYS:HB3	2.00	0.44
13:lP1:368:PRO:HA	13:lP1:372:ARG:HH11	1.83	0.44
13:tP1:112:GLU:HA	13:tP1:115:HIS:HB2	2.00	0.44
15:WP1:393:ASN:ND2	15:WP1:415:ASN:HB2	2.33	0.44
11:bP1:217:VAL:HG22	11:bP1:323:LEU:HD21	2.00	0.44
10:eP1:289:ILE:HG21	10:eP1:363:LEU:HB3	1.99	0.44
13:kP1:368:PRO:HA	13:kP1:372:ARG:HH11	1.83	0.44
13:nP1:112:GLU:HA	13:nP1:115:HIS:HB2	1.99	0.44
13:qP1:72:ARG:HH21	13:qP1:73:VAL:HG12	1.83	0.44
13:qP1:134:GLY:HA2	13:qP1:164:LYS:HB3	2.00	0.44
13:rP1:309:ARG:HA	13:rP1:309:ARG:HD3	1.84	0.44
13:wP1:368:PRO:HA	13:wP1:372:ARG:HH11	1.83	0.44
13:TP1:368:PRO:HA	13:TP1:372:ARG:HH11	1.83	0.43
14:UP1:693:GLN:HA	14:UP1:696:GLU:HG2	2.00	0.43
15:VP1:393:ASN:ND2	15:VP1:415:ASN:HB2	2.33	0.43
11:YP1:394:ILE:O	11:YP1:472:LYS:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:YP1:538:LEU:HD13	11:YP1:613:GLU:HG3	2.00	0.43
11:YP1:681:LEU:HB2	11:YP1:831:PHE:HE2	1.83	0.43
11:aP1:521:MET:HB2	11:aP1:644:MET:HE2	2.00	0.43
11:bP1:499:LEU:HA	11:bP1:718:ILE:HD13	1.99	0.43
13:iP1:368:PRO:HA	13:iP1:372:ARG:HH11	1.83	0.43
13:pP1:112:GLU:HA	13:pP1:115:HIS:HB2	1.99	0.43
13:qP1:368:PRO:HA	13:qP1:372:ARG:HH11	1.83	0.43
13:wP1:112:GLU:HA	13:wP1:115:HIS:HB2	2.00	0.43
10:QP1:260:ILE:H	11:YP1:256:LYS:HE2	1.82	0.43
11:RP1:310:GLU:HA	11:RP1:313:GLN:HB2	1.99	0.43
11:RP1:517:HIS:CD2	11:RP1:523:GLN:HG2	2.52	0.43
12:SP1:328:VAL:HA	12:SP1:331:TYR:HB3	1.99	0.43
12:SP1:1612:PHE:HD1	12:SP1:1615:ARG:HH12	1.65	0.43
10:dP1:789:ASP:OD1	10:dP1:789:ASP:N	2.49	0.43
10:fP1:459:TRP:HE1	10:fP1:650:VAL:HA	1.83	0.43
10:fP1:869:ASP:H	10:fP1:872:LEU:HB2	1.83	0.43
17:jP1:304:THR:HB	17:jP1:335:ARG:HH11	1.83	0.43
13:oP1:368:PRO:HA	13:oP1:372:ARG:HH11	1.83	0.43
13:sP1:72:ARG:HH21	13:sP1:73:VAL:HG12	1.83	0.43
13:sP1:112:GLU:HA	13:sP1:115:HIS:HB2	1.99	0.43
11:ZP1:543:ASP:HB2	11:ZP1:546:ILE:HG12	1.99	0.43
11:ZP1:573:LYS:HD3	11:ZP1:620:ILE:HD11	2.00	0.43
10:dP1:864:LEU:HD13	10:dP1:879:LEU:HD13	2.00	0.43
10:fP1:676:LEU:HA	10:fP1:679:ILE:HG12	2.00	0.43
13:iP1:72:ARG:HH21	13:iP1:73:VAL:HG12	1.83	0.43
13:kP1:72:ARG:HH21	13:kP1:73:VAL:HG12	1.83	0.43
13:lP1:134:GLY:HA2	13:lP1:164:LYS:HB3	2.00	0.43
13:tP1:134:GLY:HA2	13:tP1:164:LYS:HB3	2.00	0.43
10:cP1:614:PRO:HB2	10:cP1:616:ILE:HG12	2.00	0.43
10:eP1:553:ASN:HB3	10:eP1:556:GLU:HB2	2.00	0.43
13:hP1:112:GLU:HA	13:hP1:115:HIS:HB2	1.99	0.43
12:SP1:1457:THR:HB	13:sP1:162:PRO:HB3	2.01	0.43
13:TP1:112:GLU:HA	13:TP1:115:HIS:HB2	1.99	0.43
15:VP1:99:PRO:HA	15:VP1:102:GLN:HB3	2.00	0.43
11:YP1:223:ILE:HD12	11:YP1:223:ILE:HG23	1.82	0.43
13:hP1:49:ASP:OD1	13:hP1:49:ASP:N	2.46	0.43
13:lP1:72:ARG:HH21	13:lP1:73:VAL:HG12	1.83	0.43
13:sP1:134:GLY:HA2	13:sP1:164:LYS:HB3	2.00	0.43
11:RP1:674:TRP:HB2	11:RP1:824:ILE:HB	1.99	0.43
15:WP1:5:LEU:HG	15:WP1:42:LEU:HD21	2.00	0.43
15:WP1:166:PRO:HD3	15:WP1:169:ARG:HH21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:WP1:460:TRP:O	15:WP1:462:LEU:N	2.49	0.43
11:bP1:359:HIS:CG	11:bP1:440:SER:HB2	2.53	0.43
11:bP1:479:LYS:HG3	11:bP1:481:GLN:H	1.84	0.43
10:cP1:438:LEU:HD13	10:cP1:449:SER:HB3	2.00	0.43
10:eP1:430:TYR:HE1	10:eP1:510:LYS:HG2	1.84	0.43
13:iP1:134:GLY:HA2	13:iP1:164:LYS:HB3	2.00	0.43
13:kP1:317:TYR:N	13:kP1:347:ASN:O	2.52	0.43
13:mP1:425:ARG:HH21	13:mP1:428:VAL:HG11	1.84	0.43
13:oP1:134:GLY:HA2	13:oP1:164:LYS:HB3	2.00	0.43
13:tP1:72:ARG:HH21	13:tP1:73:VAL:HG12	1.83	0.43
13:tP1:425:ARG:HH21	13:tP1:428:VAL:HG11	1.84	0.43
11:RP1:499:LEU:HD23	11:RP1:499:LEU:HA	1.86	0.43
15:VP1:383:PRO:HA	15:VP1:384:PRO:HD3	1.93	0.43
15:WP1:283:VAL:HG12	15:WP1:295:ARG:HB3	2.01	0.43
15:WP1:574:LEU:HG	15:WP1:577:PRO:HD2	2.01	0.43
11:YP1:486:ARG:HA	11:YP1:489:LYS:HE2	2.01	0.43
11:aP1:472:LYS:HG2	11:aP1:489:LYS:HD2	2.00	0.43
11:bP1:214:THR:HG23	11:bP1:318:LEU:HD21	2.01	0.43
11:bP1:348:GLU:CD	11:bP1:349:CYS:HA	2.44	0.43
11:bP1:544:ASP:O	10:eP1:873:ARG:NH2	2.52	0.43
10:eP1:324:CYS:HA	10:eP1:327:LEU:HD12	2.01	0.43
10:fP1:830:LYS:CE	10:fP1:830:LYS:CA	2.96	0.43
13:kP1:425:ARG:HH21	13:kP1:428:VAL:HG11	1.84	0.43
13:mP1:134:GLY:HA2	13:mP1:164:LYS:HB3	2.00	0.43
13:oP1:72:ARG:HH21	13:oP1:73:VAL:HG12	1.83	0.43
13:qP1:317:TYR:N	13:qP1:347:ASN:O	2.52	0.43
13:tP1:317:TYR:N	13:tP1:347:ASN:O	2.52	0.43
13:wP1:425:ARG:HH21	13:wP1:428:VAL:HG11	1.84	0.43
11:RP1:861:LEU:O	11:RP1:865:GLY:N	2.48	0.43
15:VP1:574:LEU:HG	15:VP1:577:PRO:HD2	2.01	0.43
11:bP1:560:MET:HE1	13:nP1:2:PRO:HG3	2.01	0.43
10:fP1:314:ARG:NH1	10:fP1:441:THR:OG1	2.48	0.43
10:fP1:827:VAL:HG23	10:fP1:831:ARG:HH21	1.83	0.43
17:jP1:250:ILE:HD12	17:jP1:254:ARG:HB2	2.00	0.43
13:mP1:74:ILE:HA	13:mP1:77:ILE:HD12	2.01	0.43
13:mP1:112:GLU:HA	13:mP1:115:HIS:HB2	1.99	0.43
13:nP1:134:GLY:HA2	13:nP1:164:LYS:HB3	2.00	0.43
13:nP1:425:ARG:HH21	13:nP1:428:VAL:HG11	1.84	0.43
13:pP1:368:PRO:HA	13:pP1:372:ARG:HH11	1.83	0.43
13:qP1:74:ILE:HA	13:qP1:77:ILE:HD12	2.01	0.43
13:rP1:72:ARG:HH21	13:rP1:73:VAL:HG12	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:rP1:368:PRO:HA	13:rP1:372:ARG:HH11	1.83	0.43
13:wP1:74:ILE:HA	13:wP1:77:ILE:HD12	2.01	0.43
13:wP1:134:GLY:HA2	13:wP1:164:LYS:HB3	2.00	0.43
12:SP1:512:PRO:HA	12:SP1:1291:LYS:HG3	1.99	0.43
14:UP1:390:THR:H	14:UP1:393:ILE:HG22	1.84	0.43
11:ZP1:527:PHE:O	11:ZP1:531:MET:N	2.52	0.43
10:cP1:432:TRP:HD1	10:cP1:436:GLY:HA2	1.84	0.43
10:cP1:504:LYS:HA	10:cP1:504:LYS:HD3	1.89	0.43
10:eP1:256:VAL:HG21	10:eP1:275:LYS:HE3	2.01	0.43
10:eP1:575:HIS:HE1	13:oP1:3:ARG:HG2	1.84	0.43
13:hP1:72:ARG:HH21	13:hP1:73:VAL:HG12	1.83	0.43
13:hP1:425:ARG:HH21	13:hP1:428:VAL:HG11	1.84	0.43
13:iP1:425:ARG:HH21	13:iP1:428:VAL:HG11	1.84	0.43
13:lP1:74:ILE:HA	13:lP1:77:ILE:HD12	2.01	0.43
13:pP1:74:ILE:HA	13:pP1:77:ILE:HD12	2.01	0.43
13:pP1:425:ARG:HH21	13:pP1:428:VAL:HG11	1.84	0.43
10:QP1:284:LYS:HD2	10:QP1:287:LYS:HE2	2.01	0.43
13:TP1:297:LEU:HD12	13:TP1:322:ASN:HD22	1.84	0.43
15:VP1:514:TRP:NE1	13:rP1:263:THR:HA	2.34	0.43
11:aP1:391:GLU:HA	11:aP1:394:ILE:HG22	1.99	0.43
10:eP1:541:SER:HB2	10:eP1:742:ASP:HA	2.01	0.43
10:eP1:581:LYS:HD2	10:eP1:674:TYR:HE2	1.84	0.43
10:fP1:260:ILE:HG22	10:fP1:261:ASP:H	1.83	0.43
13:lP1:297:LEU:HD12	13:lP1:322:ASN:HD22	1.84	0.43
13:lP1:425:ARG:HH21	13:lP1:428:VAL:HG11	1.84	0.43
13:mP1:297:LEU:HD12	13:mP1:322:ASN:HD22	1.84	0.43
13:nP1:74:ILE:HA	13:nP1:77:ILE:HD12	2.01	0.43
13:nP1:317:TYR:N	13:nP1:347:ASN:O	2.52	0.43
13:rP1:425:ARG:HH21	13:rP1:428:VAL:HG11	1.84	0.43
10:QP1:681:LYS:HD2	10:QP1:681:LYS:HA	1.81	0.42
13:TP1:72:ARG:HH21	13:TP1:73:VAL:HG12	1.84	0.42
14:UP1:843:ASN:HB3	14:UP1:967:LEU:H	1.84	0.42
14:UP1:950:MET:HA	14:UP1:953:LEU:HD22	2.00	0.42
15:WP1:277:LEU:O	15:WP1:281:GLU:N	2.49	0.42
11:bP1:526:PHE:CZ	11:bP1:569:LYS:HE2	2.54	0.42
10:dP1:266:LYS:HG3	10:dP1:275:LYS:HA	2.00	0.42
10:fP1:569:GLN:OE1	10:fP1:571:ASP:N	2.52	0.42
10:fP1:655:CYS:SG	10:fP1:656:MET:N	2.92	0.42
13:oP1:425:ARG:HH21	13:oP1:428:VAL:HG11	1.84	0.42
13:pP1:72:ARG:HH21	13:pP1:73:VAL:HG12	1.83	0.42
13:sP1:74:ILE:HA	13:sP1:77:ILE:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:tP1:74:ILE:HA	13:tP1:77:ILE:HD12	2.01	0.42
10:QP1:577:MET:HE1	10:QP1:670:LYS:HE2	2.01	0.42
11:RP1:213:GLU:HG2	11:RP1:255:VAL:HG21	2.01	0.42
11:ZP1:520:LEU:HG	11:ZP1:700:VAL:HG11	2.00	0.42
13:hP1:368:PRO:HA	13:hP1:372:ARG:HH11	1.83	0.42
13:nP1:72:ARG:HH21	13:nP1:73:VAL:HG12	1.84	0.42
13:oP1:317:TYR:N	13:oP1:347:ASN:O	2.52	0.42
13:pP1:134:GLY:HA2	13:pP1:164:LYS:HB3	2.00	0.42
13:pP1:297:LEU:HD12	13:pP1:322:ASN:HD22	1.84	0.42
13:rP1:74:ILE:HA	13:rP1:77:ILE:HD12	2.01	0.42
13:tP1:368:PRO:HA	13:tP1:372:ARG:HH11	1.83	0.42
10:QP1:516:LYS:HG2	10:QP1:517:ASP:N	2.34	0.42
15:VP1:96:ILE:HD12	15:VP1:96:ILE:HA	1.88	0.42
15:WP1:204:PHE:HA	15:WP1:260:ARG:HB3	2.01	0.42
11:ZP1:515:ILE:O	11:ZP1:519:PHE:N	2.52	0.42
11:aP1:654:LEU:HD12	11:aP1:686:LEU:HD12	2.01	0.42
11:bP1:221:LEU:HD21	11:bP1:309:LEU:HD22	2.01	0.42
10:dP1:865:THR:HA	10:dP1:872:LEU:HD21	2.01	0.42
10:eP1:706:LEU:HD13	10:eP1:850:THR:HG21	2.02	0.42
10:eP1:870:GLU:H	10:eP1:872:LEU:HD22	1.83	0.42
13:nP1:368:PRO:HA	13:nP1:372:ARG:HH11	1.83	0.42
13:qP1:297:LEU:HD12	13:qP1:322:ASN:HD22	1.84	0.42
13:sP1:297:LEU:HD12	13:sP1:322:ASN:HD22	1.84	0.42
13:wP1:206:ASP:OD2	13:wP1:208:THR:OG1	2.31	0.42
10:QP1:336:ARG:HA	11:YP1:325:PHE:CZ	2.54	0.42
10:QP1:575:HIS:HE1	13:hP1:3:ARG:HG2	1.84	0.42
10:QP1:676:LEU:HA	10:QP1:679:ILE:HG22	1.99	0.42
11:RP1:520:LEU:HA	11:RP1:644:MET:HE1	2.01	0.42
12:SP1:1477:HIS:CE1	13:sP1:351:TRP:HH2	2.37	0.42
12:SP1:1505:LYS:HE2	12:SP1:1505:LYS:CA	2.49	0.42
11:YP1:535:GLU:HA	11:YP1:538:LEU:HG	2.01	0.42
11:aP1:533:LEU:HD13	11:aP1:553:LEU:HD22	2.00	0.42
10:dP1:559:GLN:HA	10:dP1:562:ARG:HD2	2.02	0.42
13:kP1:297:LEU:HD12	13:kP1:322:ASN:HD22	1.84	0.42
13:mP1:368:PRO:HA	13:mP1:372:ARG:HH11	1.83	0.42
13:sP1:309:ARG:HA	13:sP1:309:ARG:HD3	1.84	0.42
10:QP1:328:HIS:CD2	11:YP1:328:GLN:HE21	2.36	0.42
10:QP1:374:LYS:HG3	10:QP1:378:LYS:NZ	2.34	0.42
14:UP1:757:ILE:HG23	14:UP1:779:VAL:HG13	2.01	0.42
15:VP1:512:ILE:HG23	15:VP1:611:LEU:HD21	2.01	0.42
10:dP1:492:LEU:HA	10:dP1:495:VAL:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:dP1:693:MET:HG2	10:dP1:696:LEU:H	1.84	0.42
10:dP1:758:ILE:HA	10:dP1:761:CYS:HB2	2.01	0.42
10:fP1:652:THR:OG1	10:fP1:653:ARG:N	2.52	0.42
10:fP1:681:LYS:HD2	10:fP1:681:LYS:HA	1.81	0.42
13:hP1:297:LEU:HD12	13:hP1:322:ASN:HD22	1.84	0.42
13:mP1:72:ARG:HH21	13:mP1:73:VAL:HG12	1.83	0.42
13:oP1:74:ILE:HA	13:oP1:77:ILE:HD12	2.01	0.42
13:oP1:297:LEU:HD12	13:oP1:322:ASN:HD22	1.84	0.42
13:rP1:317:TYR:N	13:rP1:347:ASN:O	2.52	0.42
13:wP1:297:LEU:HD12	13:wP1:322:ASN:HD22	1.84	0.42
10:QP1:862:VAL:HG13	10:QP1:863:LEU:HD23	2.00	0.42
12:SP1:1451:TRP:HE1	12:SP1:1480:GLN:HE22	1.67	0.42
11:YP1:453:GLY:HA2	11:YP1:456:LEU:HB2	2.02	0.42
11:ZP1:739:THR:HA	11:ZP1:743:LEU:HB2	2.01	0.42
11:bP1:462:CYS:SG	11:bP1:463:GLY:N	2.93	0.42
10:cP1:652:THR:OG1	10:cP1:653:ARG:N	2.52	0.42
13:iP1:317:TYR:N	13:iP1:347:ASN:O	2.52	0.42
13:sP1:368:PRO:HA	13:sP1:372:ARG:HH11	1.83	0.42
12:SP1:516:LYS:HA	12:SP1:516:LYS:HD3	1.88	0.42
14:UP1:677:SER:O	14:UP1:677:SER:OG	2.38	0.42
15:VP1:282:SER:OG	15:VP1:295:ARG:NH1	2.42	0.42
15:VP1:283:VAL:HG12	15:VP1:295:ARG:HB3	2.01	0.42
11:aP1:674:TRP:HD1	11:aP1:824:ILE:HB	1.84	0.42
10:fP1:764:ASP:HB2	10:fP1:767:SER:HB3	2.02	0.42
13:nP1:297:LEU:HD12	13:nP1:322:ASN:HD22	1.84	0.42
13:qP1:309:ARG:HD3	13:qP1:309:ARG:HA	1.84	0.42
13:wP1:317:TYR:N	13:wP1:347:ASN:O	2.52	0.42
11:RP1:757:PHE:CE1	11:RP1:761:LEU:HD21	2.55	0.42
12:SP1:464:TYR:HA	12:SP1:467:VAL:HG22	2.02	0.42
15:VP1:166:PRO:HD3	15:VP1:169:ARG:HH21	1.83	0.42
15:WP1:512:ILE:HG23	15:WP1:611:LEU:HD21	2.01	0.42
11:ZP1:658:TRP:CZ2	11:ZP1:683:GLN:HB2	2.54	0.42
11:ZP1:858:ILE:HD13	11:ZP1:858:ILE:HA	1.93	0.42
11:bP1:500:ASP:OD1	11:bP1:500:ASP:N	2.52	0.42
10:cP1:435:ASP:OD1	10:cP1:436:GLY:N	2.53	0.42
13:iP1:74:ILE:HA	13:iP1:77:ILE:HD12	2.01	0.42
13:pP1:317:TYR:N	13:pP1:347:ASN:O	2.52	0.42
10:QP1:288:ASP:O	10:QP1:292:LYS:HD2	2.20	0.42
11:YP1:531:MET:HE2	11:YP1:648:LYS:HG3	2.01	0.42
11:ZP1:319:SER:OG	11:ZP1:320:LEU:N	2.53	0.42
11:ZP1:396:ARG:HH22	11:ZP1:466:VAL:H	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:aP1:455:TYR:CZ	11:aP1:494:ALA:HA	2.55	0.42
11:bP1:838:LEU:HA	11:bP1:841:LYS:HB2	2.02	0.42
10:eP1:459:TRP:HE1	10:eP1:650:VAL:HA	1.85	0.42
10:eP1:559:GLN:HA	10:eP1:562:ARG:HD2	2.01	0.42
10:fP1:289:ILE:HG21	10:fP1:363:LEU:HB3	2.02	0.42
13:iP1:297:LEU:HD12	13:iP1:322:ASN:HD22	1.84	0.42
13:rP1:297:LEU:HD12	13:rP1:322:ASN:HD22	1.84	0.42
13:sP1:147:SER:OG	13:sP1:191:THR:OG1	2.33	0.42
10:QP1:541:SER:HB2	10:QP1:742:ASP:HA	2.02	0.42
10:QP1:652:THR:HG23	10:QP1:654:GLU:HG3	2.02	0.42
14:UP1:887:HIS:CE1	13:qP1:355:SER:HB3	2.55	0.42
11:YP1:453:GLY:O	11:YP1:457:ASN:ND2	2.44	0.42
10:dP1:775:ARG:HA	10:dP1:778:PHE:HB3	2.02	0.42
10:fP1:548:LEU:HD13	10:fP1:554:LEU:HB3	2.02	0.42
10:fP1:659:TYR:HA	10:fP1:662:VAL:HG12	2.02	0.42
13:iP1:147:SER:OG	13:iP1:191:THR:OG1	2.33	0.42
13:wP1:72:ARG:HH21	13:wP1:73:VAL:HG12	1.83	0.42
10:QP1:708:SER:HA	10:QP1:711:VAL:HB	2.02	0.41
13:TP1:317:TYR:N	13:TP1:347:ASN:O	2.52	0.41
15:VP1:204:PHE:HA	15:VP1:260:ARG:HB3	2.00	0.41
15:WP1:310:GLU:CD	15:WP1:310:GLU:C	2.88	0.41
11:ZP1:258:LEU:HD22	11:ZP1:261:ARG:HH21	1.84	0.41
11:aP1:214:THR:HA	11:aP1:217:VAL:HG22	2.02	0.41
10:fP1:802:ARG:NH2	10:fP1:828:GLU:HB3	2.34	0.41
10:fP1:830:LYS:NZ	10:fP1:834:GLU:HG3	2.34	0.41
13:hP1:317:TYR:N	13:hP1:347:ASN:O	2.52	0.41
13:lP1:317:TYR:N	13:lP1:347:ASN:O	2.52	0.41
13:pP1:53:TYR:HB3	13:pP1:61:ILE:HB	2.02	0.41
13:qP1:425:ARG:HH21	13:qP1:428:VAL:HG11	1.84	0.41
13:tP1:201:CYS:HB2	13:tP1:261:ILE:HD11	2.02	0.41
13:tP1:297:LEU:HD12	13:tP1:322:ASN:HD22	1.84	0.41
10:QP1:423:TYR:HA	10:QP1:426:LEU:HD23	2.02	0.41
10:QP1:432:TRP:HD1	10:QP1:436:GLY:HA2	1.85	0.41
12:SP1:512:PRO:C	12:SP1:514:PHE:H	2.27	0.41
12:SP1:1622:TYR:HB2	13:sP1:350:PRO:HA	2.02	0.41
13:TP1:53:TYR:HB3	13:TP1:61:ILE:HB	2.02	0.41
13:TP1:74:ILE:HA	13:TP1:77:ILE:HD12	2.01	0.41
13:TP1:425:ARG:HH21	13:TP1:428:VAL:HG11	1.84	0.41
11:YP1:529:HIS:HB3	11:YP1:557:ALA:HB1	2.01	0.41
11:ZP1:648:LYS:HD3	13:lP1:249:MET:HE1	2.02	0.41
10:cP1:282:VAL:HG21	10:cP1:286:LEU:HD22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:eP1:253:LEU:HB3	10:eP1:293:LEU:HD13	2.01	0.41
13:kP1:74:ILE:HA	13:kP1:77:ILE:HD12	2.01	0.41
13:sP1:53:TYR:HB3	13:sP1:61:ILE:HB	2.02	0.41
13:wP1:53:TYR:HB3	13:wP1:61:ILE:HB	2.03	0.41
10:QP1:364:ARG:HA	10:QP1:367:LEU:HD22	2.02	0.41
11:RP1:280:SER:OG	11:RP1:289:HIS:HA	2.20	0.41
15:VP1:309:ALA:O	15:VP1:313:ARG:HG3	2.20	0.41
15:WP1:282:SER:OG	15:WP1:295:ARG:NH1	2.42	0.41
11:YP1:759:ASN:HA	11:YP1:762:GLN:HE21	1.85	0.41
10:eP1:510:LYS:HZ3	10:eP1:510:LYS:HG2	1.43	0.41
10:fP1:825:GLU:OE1	10:fP1:825:GLU:CA	2.68	0.41
13:hP1:309:ARG:HD3	13:hP1:309:ARG:HA	1.84	0.41
13:kP1:201:CYS:HB2	13:kP1:261:ILE:HD11	2.03	0.41
13:nP1:201:CYS:HB2	13:nP1:261:ILE:HD11	2.03	0.41
13:sP1:201:CYS:HB2	13:sP1:261:ILE:HD11	2.03	0.41
13:sP1:425:ARG:HH21	13:sP1:428:VAL:HG11	1.84	0.41
10:QP1:368:VAL:C	10:QP1:370:THR:N	2.77	0.41
10:QP1:864:LEU:HG	10:QP1:865:THR:N	2.34	0.41
12:SP1:1479:MET:HE2	12:SP1:1550:ILE:HD13	2.02	0.41
13:hP1:53:TYR:HB3	13:hP1:61:ILE:HB	2.03	0.41
13:iP1:201:CYS:HB2	13:iP1:261:ILE:HD11	2.03	0.41
13:mP1:53:TYR:HB3	13:mP1:61:ILE:HB	2.02	0.41
13:mP1:317:TYR:N	13:mP1:347:ASN:O	2.52	0.41
13:rP1:53:TYR:HB3	13:rP1:61:ILE:HB	2.03	0.41
11:RP1:253:SER:HA	11:RP1:256:LYS:HD2	2.02	0.41
12:SP1:1551:LEU:HA	12:SP1:1554:ARG:HG2	2.03	0.41
13:TP1:201:CYS:HB2	13:TP1:261:ILE:HD11	2.02	0.41
14:UP1:316:TYR:CD1	14:UP1:405:LEU:HD11	2.51	0.41
14:UP1:323:LEU:HB3	14:UP1:364:LEU:HD21	2.03	0.41
11:bP1:472:LYS:HE2	11:bP1:493:TYR:HB3	2.02	0.41
10:dP1:591:LEU:HB2	10:dP1:594:HIS:CE1	2.55	0.41
13:hP1:74:ILE:HA	13:hP1:77:ILE:HD12	2.01	0.41
17:jP1:18:LYS:HG2	17:jP1:30:VAL:HG23	2.03	0.41
13:tP1:217:ARG:HH22	13:tP1:276:LEU:H	1.69	0.41
11:RP1:242:SER:HA	11:RP1:271:THR:HG21	2.03	0.41
11:RP1:275:PHE:CE1	11:RP1:341:ALA:HB1	2.55	0.41
12:SP1:1462:GLN:HE21	12:SP1:1466:SER:H	1.69	0.41
15:VP1:407:ASP:OD1	15:VP1:409:ASN:ND2	2.54	0.41
15:WP1:331:ARG:HD3	15:WP1:331:ARG:HA	1.95	0.41
10:dP1:334:TYR:HA	10:dP1:376:ARG:HH22	1.86	0.41
10:eP1:659:TYR:HA	10:eP1:662:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:fP1:581:LYS:HD2	10:fP1:674:TYR:HE2	1.85	0.41
13:kP1:53:TYR:HB3	13:kP1:61:ILE:HB	2.03	0.41
13:mP1:201:CYS:HB2	13:mP1:261:ILE:HD11	2.02	0.41
10:QP1:260:ILE:HD12	10:QP1:260:ILE:HA	1.96	0.41
14:UP1:313:ILE:HA	14:UP1:316:TYR:HD2	1.86	0.41
11:ZP1:321:GLN:HE22	10:cP1:254:LEU:HB3	1.85	0.41
10:dP1:562:ARG:HH21	10:dP1:733:LEU:HD23	1.84	0.41
10:eP1:312:LEU:HD13	10:eP1:315:ALA:HB3	2.03	0.41
13:iP1:53:TYR:HB3	13:iP1:61:ILE:HB	2.02	0.41
13:iP1:309:ARG:HA	13:iP1:309:ARG:HD3	1.84	0.41
10:QP1:435:ASP:OD1	10:QP1:436:GLY:N	2.54	0.41
14:UP1:329:GLU:HG2	15:VP1:134:PRO:HB2	2.03	0.41
14:UP1:705:LEU:HD12	14:UP1:711:LEU:HD22	2.01	0.41
11:YP1:247:VAL:HG21	11:YP1:258:LEU:HD13	2.02	0.41
10:dP1:659:TYR:HA	10:dP1:662:VAL:HG12	2.02	0.41
10:fP1:485:ILE:HB	10:fP1:537:TYR:HD1	1.86	0.41
17:jP1:201:THR:HG23	17:jP1:202:THR:HG23	2.02	0.41
13:qP1:201:CYS:HB2	13:qP1:261:ILE:HD11	2.03	0.41
13:rP1:217:ARG:HH22	13:rP1:276:LEU:H	1.69	0.41
10:QP1:581:LYS:HD2	10:QP1:674:TYR:HE2	1.85	0.41
11:RP1:550:LEU:HB3	11:RP1:574:ILE:HD13	2.02	0.41
15:WP1:96:ILE:HD12	15:WP1:96:ILE:HA	1.88	0.41
11:YP1:225:ILE:HG13	11:YP1:227:VAL:HB	2.01	0.41
11:YP1:713:LYS:HA	11:YP1:713:LYS:HD2	1.89	0.41
11:ZP1:433:ILE:HG23	11:ZP1:450:LEU:HD22	2.02	0.41
10:dP1:801:GLN:HB2	10:dP1:831:ARG:NH2	2.36	0.41
10:eP1:591:LEU:HD13	10:eP1:591:LEU:HA	1.94	0.41
10:eP1:742:ASP:HB2	10:eP1:745:HIS:HB2	2.02	0.41
10:fP1:419:GLY:HA2	10:fP1:524:ASP:HB2	2.03	0.41
13:iP1:217:ARG:HH22	13:iP1:276:LEU:H	1.69	0.41
13:pP1:201:CYS:HB2	13:pP1:261:ILE:HD11	2.02	0.41
13:pP1:217:ARG:HH22	13:pP1:276:LEU:H	1.69	0.41
13:rP1:201:CYS:HB2	13:rP1:261:ILE:HD11	2.03	0.41
13:sP1:317:TYR:N	13:sP1:347:ASN:O	2.52	0.41
13:tP1:53:TYR:HB3	13:tP1:61:ILE:HB	2.02	0.41
11:RP1:396:ARG:NH1	11:RP1:473:GLU:OE1	2.54	0.41
11:RP1:531:MET:HE1	11:RP1:652:ARG:HB2	2.03	0.41
12:SP1:1338:ALA:HA	12:SP1:1341:LEU:HD12	2.03	0.41
12:SP1:1415:ASP:OD1	12:SP1:1415:ASP:N	2.54	0.41
11:bP1:224:LEU:HD23	11:bP1:224:LEU:HA	1.94	0.41
10:dP1:491:PHE:HE2	10:dP1:743:LEU:HD22	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:fP1:300:HIS:HA	10:fP1:303:ILE:HG22	2.03	0.41
13:lP1:201:CYS:HB2	13:lP1:261:ILE:HD11	2.03	0.41
13:nP1:53:TYR:HB3	13:nP1:61:ILE:HB	2.03	0.41
10:QP1:332:LYS:HE2	11:YP1:332:ARG:HH22	1.86	0.40
10:QP1:364:ARG:NH2	11:RP1:222:TYR:CD1	2.89	0.40
14:UP1:398:LEU:O	14:UP1:402:LEU:N	2.54	0.40
11:ZP1:488:GLU:HA	11:ZP1:491:TYR:CE2	2.56	0.40
11:ZP1:525:ASP:HA	11:ZP1:528:VAL:HG22	2.03	0.40
10:fP1:805:PHE:CZ	10:fP1:824:GLU:HB2	2.56	0.40
13:nP1:217:ARG:HH22	13:nP1:276:LEU:H	1.69	0.40
13:sP1:121:ILE:HD12	13:sP1:121:ILE:HA	1.99	0.40
13:tP1:49:ASP:OD1	13:tP1:49:ASP:N	2.46	0.40
11:RP1:257:GLU:HA	11:RP1:260:ASN:HB2	2.04	0.40
11:RP1:269:TYR:HB2	11:RP1:334:MET:SD	2.60	0.40
11:RP1:430:ARG:HD2	11:RP1:457:ASN:HD21	1.86	0.40
12:SP1:1457:THR:N	12:SP1:1458:ALA:HA	2.30	0.40
11:YP1:730:ASP:HA	11:YP1:733:LEU:HD12	2.03	0.40
11:bP1:556:LEU:HB2	13:oP1:339:ARG:HE	1.85	0.40
10:eP1:336:ARG:O	10:eP1:339:SER:OG	2.37	0.40
10:fP1:854:GLN:HA	10:fP1:857:VAL:HG22	2.04	0.40
13:oP1:159:ASP:OD1	13:oP1:159:ASP:N	2.55	0.40
10:QP1:764:ASP:HB2	10:QP1:767:SER:HB3	2.04	0.40
12:SP1:1475:TYR:HA	12:SP1:1478:GLU:HG3	2.02	0.40
15:VP1:305:ASP:OD1	15:VP1:305:ASP:N	2.49	0.40
15:VP1:650:TYR:HE1	13:rP1:337:LEU:HG	1.86	0.40
15:WP1:310:GLU:HA	15:WP1:313:ARG:HG2	2.03	0.40
11:YP1:295:MET:SD	11:YP1:337:LEU:HD12	2.61	0.40
11:ZP1:220:LEU:HD11	11:ZP1:262:ILE:HB	2.03	0.40
11:ZP1:273:THR:HA	11:ZP1:276:VAL:HG22	2.03	0.40
11:aP1:857:ILE:HG12	11:aP1:860:ARG:HH21	1.86	0.40
10:dP1:366:LEU:HA	10:dP1:369:TRP:HB2	2.03	0.40
10:eP1:510:LYS:NZ	10:eP1:514:SER:HB3	2.34	0.40
13:hP1:201:CYS:HB2	13:hP1:261:ILE:HD11	2.02	0.40
13:hP1:217:ARG:HH22	13:hP1:276:LEU:H	1.69	0.40
17:jP1:338:SER:HA	17:jP1:341:ILE:HG22	2.04	0.40
13:nP1:309:ARG:HD3	13:nP1:309:ARG:HA	1.84	0.40
13:pP1:7:THR:HA	13:pP1:136:VAL:HG13	2.04	0.40
13:wP1:217:ARG:HH22	13:wP1:276:LEU:H	1.69	0.40
10:QP1:364:ARG:HH22	11:RP1:221:LEU:HB3	1.85	0.40
10:QP1:644:ASP:OD1	10:QP1:644:ASP:N	2.53	0.40
11:RP1:275:PHE:HA	11:RP1:278:GLU:HG2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:RP1:657:VAL:HG21	11:RP1:758:THR:HG22	2.04	0.40
11:RP1:697:MET:HE2	11:RP1:697:MET:HB2	1.95	0.40
11:RP1:749:LYS:O	11:RP1:753:VAL:HG13	2.21	0.40
13:TP1:217:ARG:HH22	13:TP1:276:LEU:H	1.69	0.40
11:YP1:257:GLU:OE2	11:YP1:257:GLU:N	2.49	0.40
11:YP1:392:ARG:HH12	11:YP1:399:ILE:HA	1.86	0.40
10:dP1:545:LEU:HA	10:dP1:548:LEU:HG	2.02	0.40
10:fP1:510:LYS:HD2	10:fP1:510:LYS:C	2.46	0.40
10:fP1:791:LEU:O	10:fP1:795:ALA:N	2.54	0.40
13:kP1:192:LEU:HD23	13:kP1:192:LEU:HA	1.98	0.40
13:qP1:53:TYR:HB3	13:qP1:61:ILE:HB	2.03	0.40
11:RP1:707:ILE:HG22	11:RP1:724:HIS:NE2	2.37	0.40
12:SP1:472:PHE:HE2	12:SP1:481:ILE:HG12	1.86	0.40
12:SP1:1396:VAL:HB	12:SP1:1399:PRO:HD2	2.03	0.40
15:WP1:344:MET:O	15:WP1:348:SER:OG	2.38	0.40
11:YP1:707:ILE:HA	11:YP1:710:LYS:HG2	2.04	0.40
11:ZP1:653:LEU:HD12	11:ZP1:654:LEU:N	2.36	0.40
11:aP1:220:LEU:HD13	11:aP1:323:LEU:HD11	2.03	0.40
11:aP1:279:ASN:HA	11:aP1:282:PHE:HB2	2.04	0.40
11:bP1:525:ASP:OD1	11:bP1:525:ASP:N	2.55	0.40
11:bP1:533:LEU:HD13	11:bP1:553:LEU:HD22	2.04	0.40
10:dP1:435:ASP:OD1	10:dP1:436:GLY:N	2.55	0.40
13:mP1:7:THR:HA	13:mP1:136:VAL:HG13	2.04	0.40
13:oP1:217:ARG:HH22	13:oP1:276:LEU:H	1.69	0.40
13:rP1:53:TYR:HH	13:sP1:299:GLN:HE22	1.57	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	AP1	27/29 (93%)	27 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CP1	11/13 (85%)	11 (100%)	0	0	100	100
2	HP1	11/13 (85%)	11 (100%)	0	0	100	100
2	IP1	11/13 (85%)	11 (100%)	0	0	100	100
2	XP1	11/13 (85%)	11 (100%)	0	0	100	100
3	DP1	29/31 (94%)	29 (100%)	0	0	100	100
4	EP1	21/23 (91%)	21 (100%)	0	0	100	100
5	FP1	16/18 (89%)	16 (100%)	0	0	100	100
6	GP1	13/15 (87%)	13 (100%)	0	0	100	100
6	LP1	13/15 (87%)	13 (100%)	0	0	100	100
6	NP1	13/15 (87%)	13 (100%)	0	0	100	100
7	JP1	12/14 (86%)	12 (100%)	0	0	100	100
7	vP1	12/14 (86%)	12 (100%)	0	0	100	100
8	KP1	14/16 (88%)	14 (100%)	0	0	100	100
8	OP1	14/16 (88%)	14 (100%)	0	0	100	100
8	PP1	14/16 (88%)	14 (100%)	0	0	100	100
8	uP1	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
9	MP1	15/17 (88%)	15 (100%)	0	0	100	100
10	QP1	619/906 (68%)	580 (94%)	37 (6%)	2 (0%)	36	71
10	cP1	619/906 (68%)	579 (94%)	38 (6%)	2 (0%)	36	71
10	dP1	619/906 (68%)	580 (94%)	39 (6%)	0	100	100
10	eP1	619/906 (68%)	582 (94%)	36 (6%)	1 (0%)	43	78
10	fP1	619/906 (68%)	584 (94%)	34 (6%)	1 (0%)	43	78
11	RP1	543/896 (61%)	511 (94%)	32 (6%)	0	100	100
11	YP1	543/896 (61%)	504 (93%)	36 (7%)	3 (1%)	21	58
11	ZP1	541/896 (60%)	508 (94%)	31 (6%)	2 (0%)	30	67
11	aP1	541/896 (60%)	499 (92%)	39 (7%)	3 (1%)	21	58
11	bP1	543/896 (61%)	519 (96%)	24 (4%)	0	100	100
12	SP1	568/1625 (35%)	508 (89%)	48 (8%)	12 (2%)	5	29
13	TP1	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
13	hP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	iP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	kP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	lP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	mP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	nP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	oP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	pP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	qP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	rP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	sP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	tP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
13	wP1	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
14	UP1	559/1019 (55%)	516 (92%)	41 (7%)	2 (0%)	30	67
15	VP1	563/666 (84%)	520 (92%)	39 (7%)	4 (1%)	18	55
15	WP1	563/666 (84%)	521 (92%)	39 (7%)	3 (0%)	24	63
16	gP1	17/19 (90%)	17 (100%)	0	0	100	100
17	jP1	369/375 (98%)	354 (96%)	15 (4%)	0	100	100
All	All	14792/20001 (74%)	13891 (94%)	866 (6%)	35 (0%)	44	78

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	SP1	513	VAL
12	SP1	1460	VAL
12	SP1	1461	ASN
12	SP1	1510	SER
12	SP1	1533	THR
14	UP1	490	ILE
11	YP1	473	GLU
11	YP1	482	ALA
10	QP1	319	VAL
12	SP1	1459	LEU
11	YP1	481	GLN
11	ZP1	433	ILE
11	aP1	480	GLU
12	SP1	512	PRO
12	SP1	1502	PHE

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Mol	Chain	Res	Type
14	UP1	938	LEU
15	VP1	316	GLN
15	VP1	445	PRO
15	WP1	445	PRO
10	cP1	267	MET
10	cP1	268	CYS
10	fP1	840	PRO
12	SP1	313	ILE
12	SP1	1509	VAL
15	VP1	461	PRO
15	WP1	461	PRO
11	ZP1	432	THR
10	eP1	523	THR
10	QP1	861	LEU
12	SP1	1602	ASN
11	aP1	474	ILE
11	aP1	496	LYS
12	SP1	1534	GLU
15	VP1	573	ILE
15	WP1	573	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
10	QP1	561/798 (70%)	543 (97%)	18 (3%)	34	55
10	cP1	561/798 (70%)	558 (100%)	3 (0%)	81	82
10	dP1	561/798 (70%)	554 (99%)	7 (1%)	63	73
10	eP1	561/798 (70%)	556 (99%)	5 (1%)	70	77
10	fP1	561/798 (70%)	547 (98%)	14 (2%)	42	62
11	RP1	507/824 (62%)	502 (99%)	5 (1%)	68	76
11	YP1	507/824 (62%)	504 (99%)	3 (1%)	78	81
11	ZP1	506/824 (61%)	500 (99%)	6 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	aP1	505/824 (61%)	505 (100%)	0	100	100
11	bP1	507/824 (62%)	506 (100%)	1 (0%)	87	86
12	SP1	527/1471 (36%)	524 (99%)	3 (1%)	78	81
13	TP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	hP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	iP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	kP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	lP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	mP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	nP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	oP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	pP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	qP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	rP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	sP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	tP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
13	wP1	387/400 (97%)	368 (95%)	19 (5%)	22	44
14	UP1	523/933 (56%)	523 (100%)	0	100	100
15	VP1	518/595 (87%)	497 (96%)	21 (4%)	27	49
15	WP1	518/595 (87%)	500 (96%)	18 (4%)	32	53
17	jP1	314/318 (99%)	314 (100%)	0	100	100
All	All	13155/17622 (75%)	12785 (97%)	370 (3%)	38	59

All (370) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	QP1	254	LEU
10	QP1	314	ARG
10	QP1	337	LEU
10	QP1	363	LEU
10	QP1	365	ARG
10	QP1	366	LEU
10	QP1	367	LEU
10	QP1	369	TRP
10	QP1	508	VAL

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Mol	Chain	Res	Type
10	QP1	510	LYS
10	QP1	511	SER
10	QP1	515	PRO
10	QP1	516	LYS
10	QP1	517	ASP
10	QP1	862	VAL
10	QP1	863	LEU
10	QP1	864	LEU
10	QP1	866	THR
11	RP1	754	CYS
11	RP1	756	MET
11	RP1	761	LEU
11	RP1	762	GLN
11	RP1	763	ARG
12	SP1	1503	ARG
12	SP1	1505	LYS
12	SP1	1506	LEU
13	TP1	10	LEU
13	TP1	26	CYS
13	TP1	34	GLU
13	TP1	42	THR
13	TP1	56	ASP
13	TP1	79	ASN
13	TP1	80	SER
13	TP1	93	LEU
13	TP1	94	SER
13	TP1	138	CYS
13	TP1	181	VAL
13	TP1	221	GLN
13	TP1	229	ASN
13	TP1	231	LEU
13	TP1	279	ASP
13	TP1	306	SER
13	TP1	313	THR
13	TP1	328	VAL
13	TP1	419	ASP
15	VP1	1	MET
15	VP1	15	SER
15	VP1	39	THR
15	VP1	93	LEU
15	VP1	95	SER
15	VP1	117	LEU

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Mol	Chain	Res	Type
15	VP1	151	CYS
15	VP1	187	LEU
15	VP1	294	SER
15	VP1	298	SER
15	VP1	303	GLN
15	VP1	305	ASP
15	VP1	306	THR
15	VP1	310	GLU
15	VP1	312	HIS
15	VP1	315	LYS
15	VP1	316	GLN
15	VP1	402	LYS
15	VP1	477	VAL
15	VP1	538	SER
15	VP1	571	SER
15	WP1	1	MET
15	WP1	15	SER
15	WP1	39	THR
15	WP1	93	LEU
15	WP1	95	SER
15	WP1	117	LEU
15	WP1	151	CYS
15	WP1	187	LEU
15	WP1	294	SER
15	WP1	298	SER
15	WP1	306	THR
15	WP1	310	GLU
15	WP1	311	LEU
15	WP1	313	ARG
15	WP1	402	LYS
15	WP1	477	VAL
15	WP1	538	SER
15	WP1	571	SER
11	YP1	262	ILE
11	YP1	540	LYS
11	YP1	720	ASP
11	ZP1	491	TYR
11	ZP1	516	LYS
11	ZP1	652	ARG
11	ZP1	655	CYS
11	ZP1	658	TRP
11	ZP1	659	ILE

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Mol	Chain	Res	Type
11	bP1	503	MET
10	cP1	510	LYS
10	cP1	515	PRO
10	cP1	516	LYS
10	dP1	484	LEU
10	dP1	508	VAL
10	dP1	510	LYS
10	dP1	511	SER
10	dP1	515	PRO
10	dP1	517	ASP
10	dP1	540	THR
10	eP1	390	ARG
10	eP1	510	LYS
10	eP1	511	SER
10	eP1	515	PRO
10	eP1	516	LYS
10	fP1	293	LEU
10	fP1	508	VAL
10	fP1	510	LYS
10	fP1	511	SER
10	fP1	515	PRO
10	fP1	516	LYS
10	fP1	517	ASP
10	fP1	825	GLU
10	fP1	826	ASP
10	fP1	829	ASN
10	fP1	830	LYS
10	fP1	836	GLN
10	fP1	837	GLU
10	fP1	840	PRO
13	hP1	10	LEU
13	hP1	26	CYS
13	hP1	34	GLU
13	hP1	42	THR
13	hP1	56	ASP
13	hP1	79	ASN
13	hP1	80	SER
13	hP1	93	LEU
13	hP1	94	SER
13	hP1	138	CYS
13	hP1	181	VAL
13	hP1	221	GLN

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Mol	Chain	Res	Type
13	hP1	229	ASN
13	hP1	231	LEU
13	hP1	279	ASP
13	hP1	306	SER
13	hP1	313	THR
13	hP1	328	VAL
13	hP1	419	ASP
13	iP1	10	LEU
13	iP1	26	CYS
13	iP1	34	GLU
13	iP1	42	THR
13	iP1	56	ASP
13	iP1	79	ASN
13	iP1	80	SER
13	iP1	93	LEU
13	iP1	94	SER
13	iP1	138	CYS
13	iP1	181	VAL
13	iP1	221	GLN
13	iP1	229	ASN
13	iP1	231	LEU
13	iP1	279	ASP
13	iP1	306	SER
13	iP1	313	THR
13	iP1	328	VAL
13	iP1	419	ASP
13	kP1	10	LEU
13	kP1	26	CYS
13	kP1	34	GLU
13	kP1	42	THR
13	kP1	56	ASP
13	kP1	79	ASN
13	kP1	80	SER
13	kP1	93	LEU
13	kP1	94	SER
13	kP1	138	CYS
13	kP1	181	VAL
13	kP1	221	GLN
13	kP1	229	ASN
13	kP1	231	LEU
13	kP1	279	ASP
13	kP1	306	SER

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Mol	Chain	Res	Type
13	kP1	313	THR
13	kP1	328	VAL
13	kP1	419	ASP
13	lP1	10	LEU
13	lP1	26	CYS
13	lP1	34	GLU
13	lP1	42	THR
13	lP1	56	ASP
13	lP1	79	ASN
13	lP1	80	SER
13	lP1	93	LEU
13	lP1	94	SER
13	lP1	138	CYS
13	lP1	181	VAL
13	lP1	221	GLN
13	lP1	229	ASN
13	lP1	231	LEU
13	lP1	279	ASP
13	lP1	306	SER
13	lP1	313	THR
13	lP1	328	VAL
13	lP1	419	ASP
13	mP1	10	LEU
13	mP1	26	CYS
13	mP1	34	GLU
13	mP1	42	THR
13	mP1	56	ASP
13	mP1	79	ASN
13	mP1	80	SER
13	mP1	93	LEU
13	mP1	94	SER
13	mP1	138	CYS
13	mP1	181	VAL
13	mP1	221	GLN
13	mP1	229	ASN
13	mP1	231	LEU
13	mP1	279	ASP
13	mP1	306	SER
13	mP1	313	THR
13	mP1	328	VAL
13	mP1	419	ASP
13	nP1	10	LEU

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Mol	Chain	Res	Type
13	nP1	26	CYS
13	nP1	34	GLU
13	nP1	42	THR
13	nP1	56	ASP
13	nP1	79	ASN
13	nP1	80	SER
13	nP1	93	LEU
13	nP1	94	SER
13	nP1	138	CYS
13	nP1	181	VAL
13	nP1	221	GLN
13	nP1	229	ASN
13	nP1	231	LEU
13	nP1	279	ASP
13	nP1	306	SER
13	nP1	313	THR
13	nP1	328	VAL
13	nP1	419	ASP
13	oP1	10	LEU
13	oP1	26	CYS
13	oP1	34	GLU
13	oP1	42	THR
13	oP1	56	ASP
13	oP1	79	ASN
13	oP1	80	SER
13	oP1	93	LEU
13	oP1	94	SER
13	oP1	138	CYS
13	oP1	181	VAL
13	oP1	221	GLN
13	oP1	229	ASN
13	oP1	231	LEU
13	oP1	279	ASP
13	oP1	306	SER
13	oP1	313	THR
13	oP1	328	VAL
13	oP1	419	ASP
13	pP1	10	LEU
13	pP1	26	CYS
13	pP1	34	GLU
13	pP1	42	THR
13	pP1	56	ASP

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Mol	Chain	Res	Type
13	pP1	79	ASN
13	pP1	80	SER
13	pP1	93	LEU
13	pP1	94	SER
13	pP1	138	CYS
13	pP1	181	VAL
13	pP1	221	GLN
13	pP1	229	ASN
13	pP1	231	LEU
13	pP1	279	ASP
13	pP1	306	SER
13	pP1	313	THR
13	pP1	328	VAL
13	pP1	419	ASP
13	qP1	10	LEU
13	qP1	26	CYS
13	qP1	34	GLU
13	qP1	42	THR
13	qP1	56	ASP
13	qP1	79	ASN
13	qP1	80	SER
13	qP1	93	LEU
13	qP1	94	SER
13	qP1	138	CYS
13	qP1	181	VAL
13	qP1	221	GLN
13	qP1	229	ASN
13	qP1	231	LEU
13	qP1	279	ASP
13	qP1	306	SER
13	qP1	313	THR
13	qP1	328	VAL
13	qP1	419	ASP
13	rP1	10	LEU
13	rP1	26	CYS
13	rP1	34	GLU
13	rP1	42	THR
13	rP1	56	ASP
13	rP1	79	ASN
13	rP1	80	SER
13	rP1	93	LEU
13	rP1	94	SER

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Mol	Chain	Res	Type
13	rP1	138	CYS
13	rP1	181	VAL
13	rP1	221	GLN
13	rP1	229	ASN
13	rP1	231	LEU
13	rP1	279	ASP
13	rP1	306	SER
13	rP1	313	THR
13	rP1	328	VAL
13	rP1	419	ASP
13	sP1	10	LEU
13	sP1	26	CYS
13	sP1	34	GLU
13	sP1	42	THR
13	sP1	56	ASP
13	sP1	79	ASN
13	sP1	80	SER
13	sP1	93	LEU
13	sP1	94	SER
13	sP1	138	CYS
13	sP1	181	VAL
13	sP1	221	GLN
13	sP1	229	ASN
13	sP1	231	LEU
13	sP1	279	ASP
13	sP1	306	SER
13	sP1	313	THR
13	sP1	328	VAL
13	sP1	419	ASP
13	tP1	10	LEU
13	tP1	26	CYS
13	tP1	34	GLU
13	tP1	42	THR
13	tP1	56	ASP
13	tP1	79	ASN
13	tP1	80	SER
13	tP1	93	LEU
13	tP1	94	SER
13	tP1	138	CYS
13	tP1	181	VAL
13	tP1	221	GLN
13	tP1	229	ASN

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Mol	Chain	Res	Type
13	tP1	231	LEU
13	tP1	279	ASP
13	tP1	306	SER
13	tP1	313	THR
13	tP1	328	VAL
13	tP1	419	ASP
13	wP1	10	LEU
13	wP1	26	CYS
13	wP1	34	GLU
13	wP1	42	THR
13	wP1	56	ASP
13	wP1	79	ASN
13	wP1	80	SER
13	wP1	93	LEU
13	wP1	94	SER
13	wP1	138	CYS
13	wP1	181	VAL
13	wP1	221	GLN
13	wP1	229	ASN
13	wP1	231	LEU
13	wP1	279	ASP
13	wP1	306	SER
13	wP1	313	THR
13	wP1	328	VAL
13	wP1	419	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

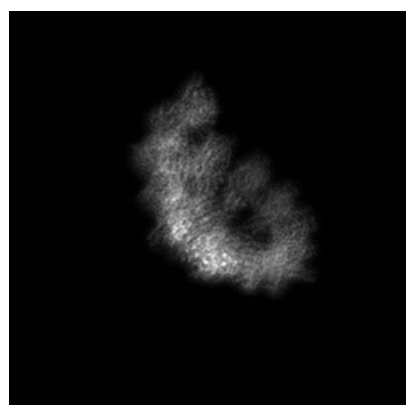
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10491. These allow visual inspection of the internal detail of the map and identification of artifacts.

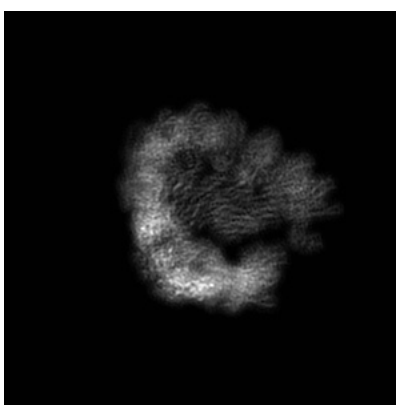
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

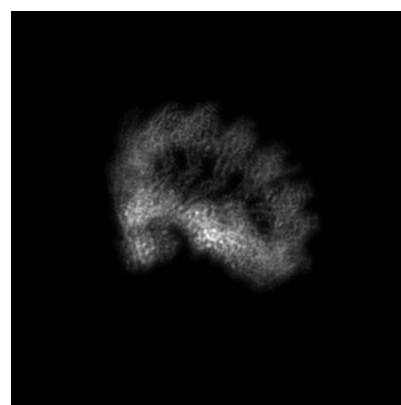
6.1.1 Primary map



X



Y



Z

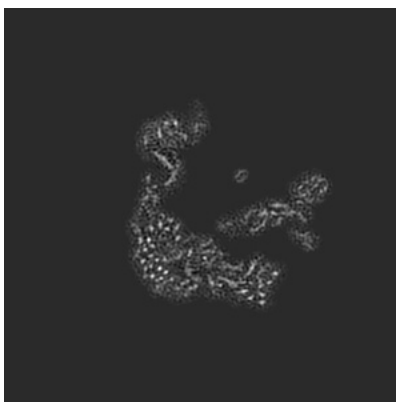
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

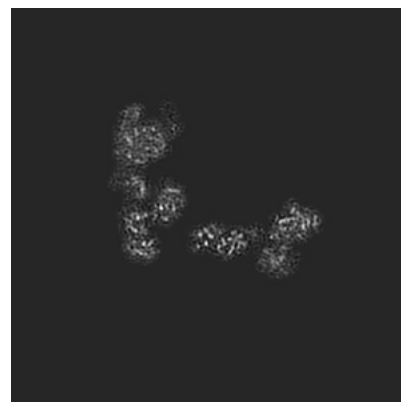
6.2.1 Primary map



X Index: 128



Y Index: 128

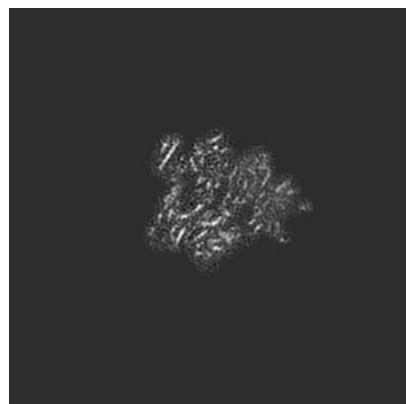


Z Index: 128

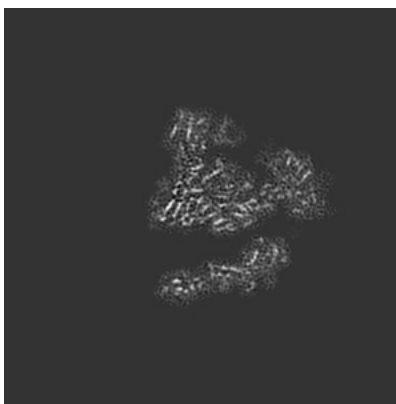
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

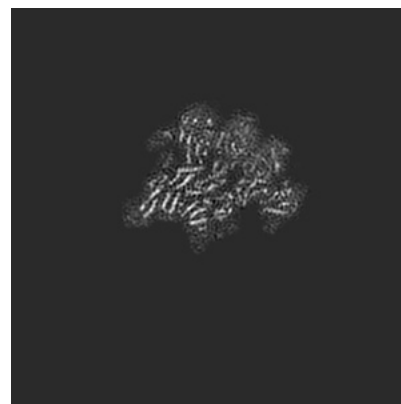
6.3.1 Primary map



X Index: 81



Y Index: 109

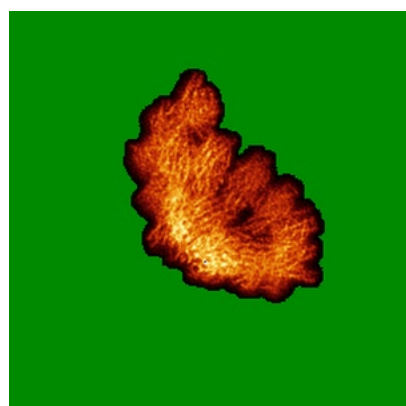


Z Index: 94

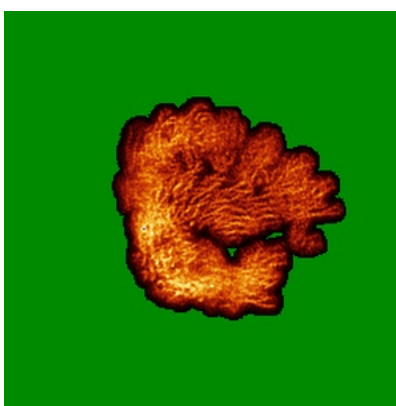
The images above show the largest variance slices of the map in three orthogonal directions.

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

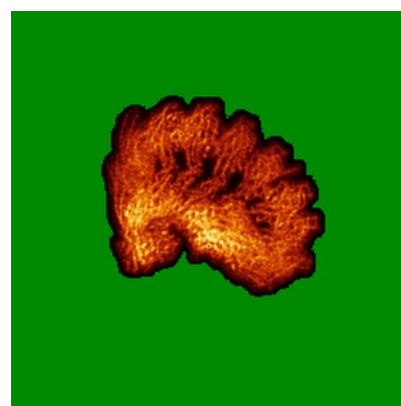
6.4.1 Primary map



X



Y

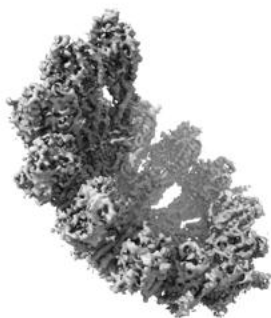


Z

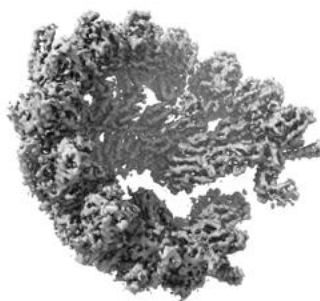
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

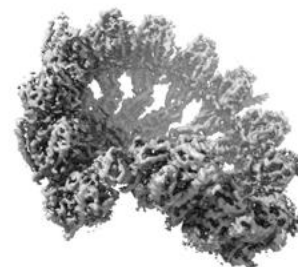
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

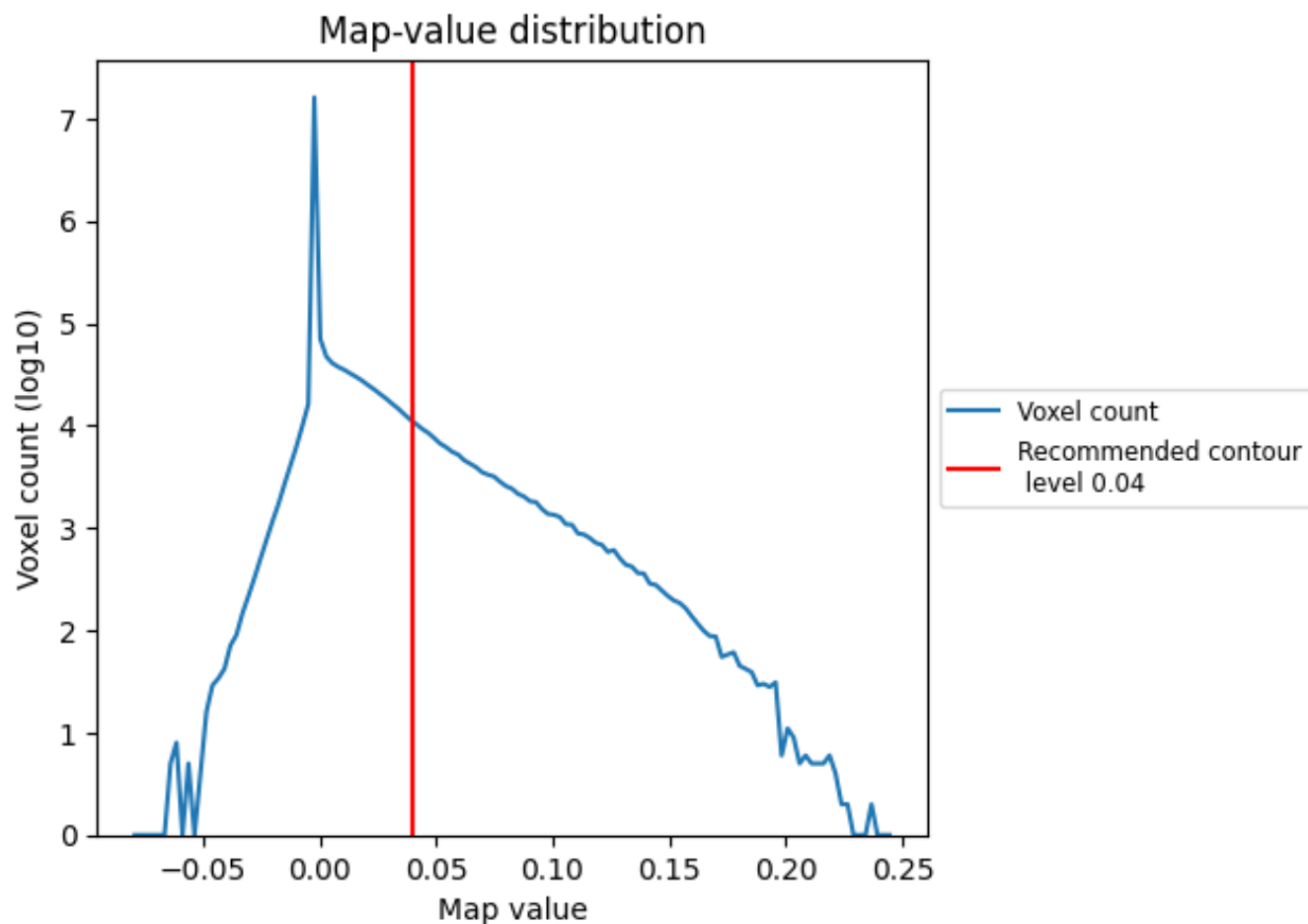
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

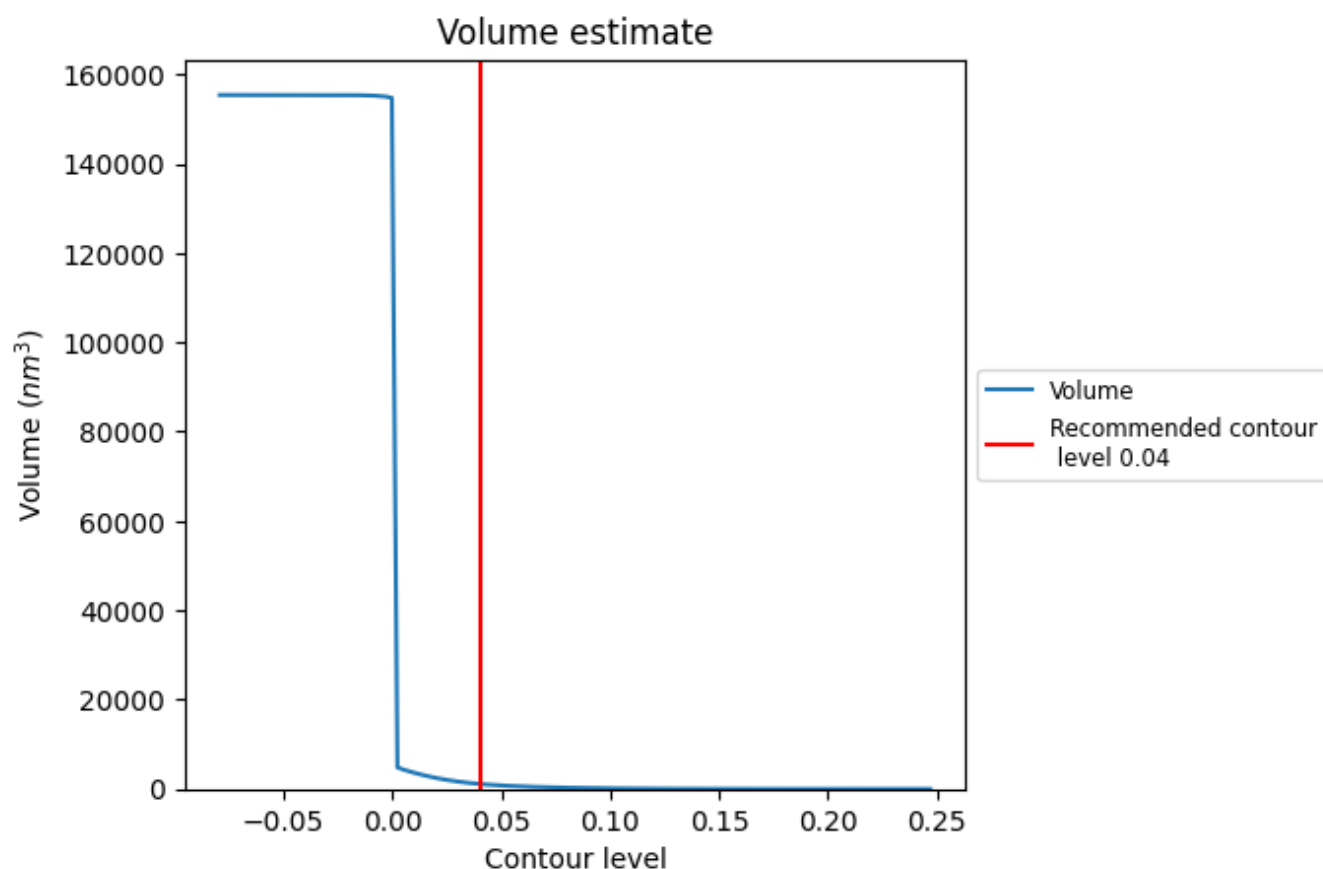
This section contains the results of statistical analysis of the map.

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.

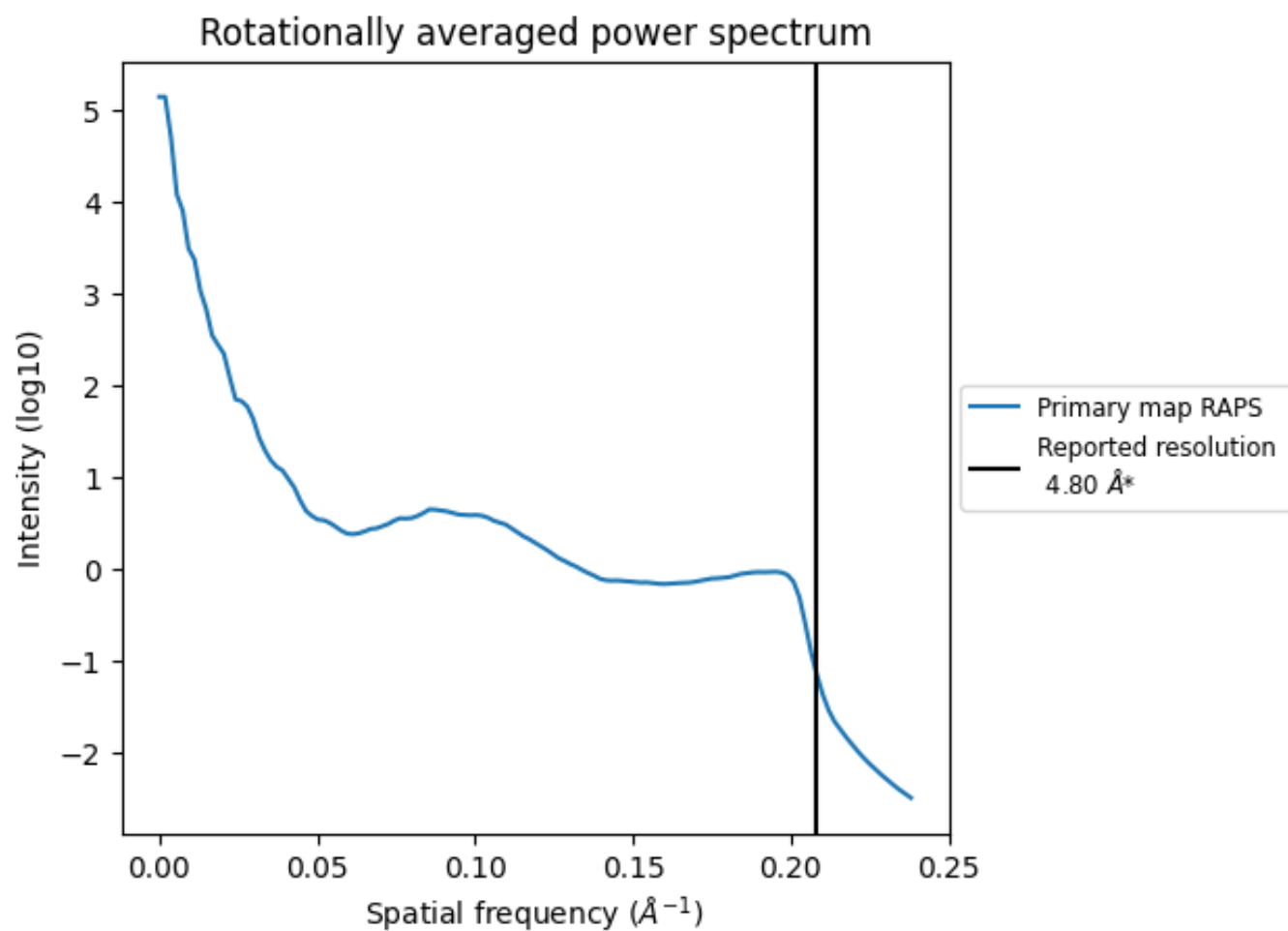
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1128 nm³; this corresponds to an approximate mass of 1019 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 0.208 Å⁻¹

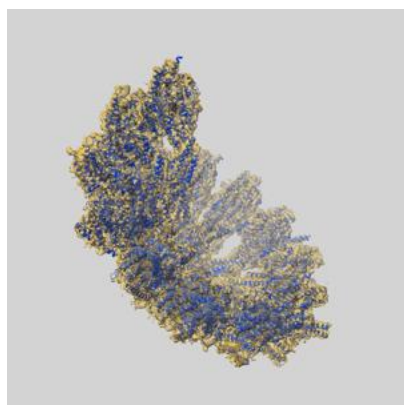
8 Fourier-Shell correlation

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

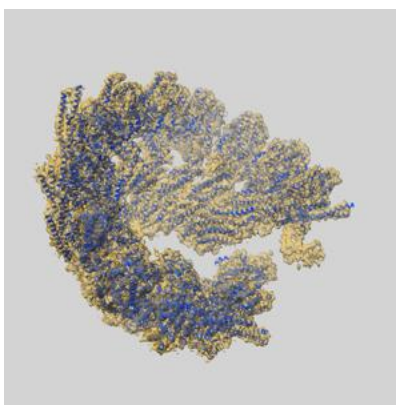
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10491 and PDB model 6TF9. Per-residue inclusion information can be found in section [3](#) on page [9](#).

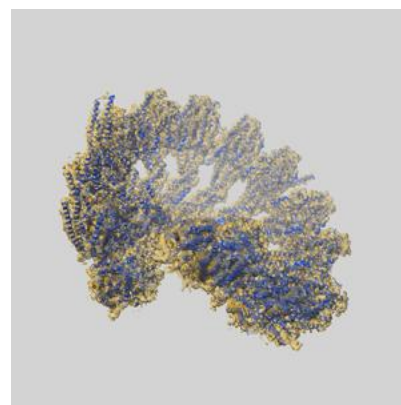
9.1 Map-model overlay [i](#)



X



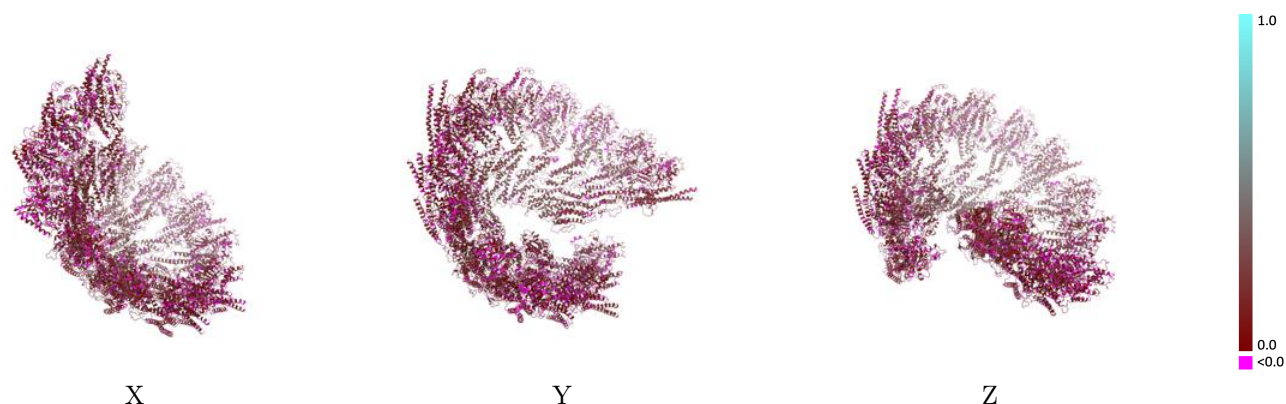
Y



Z

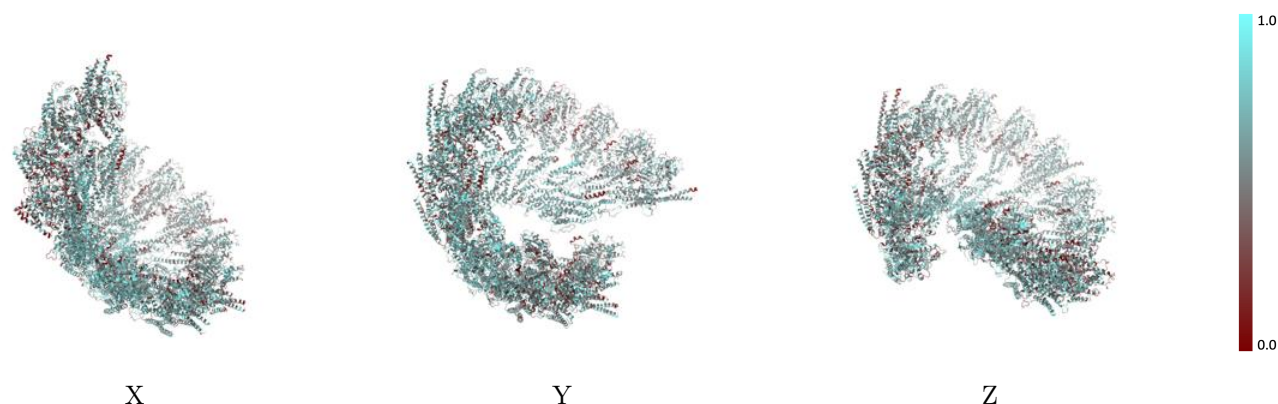
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



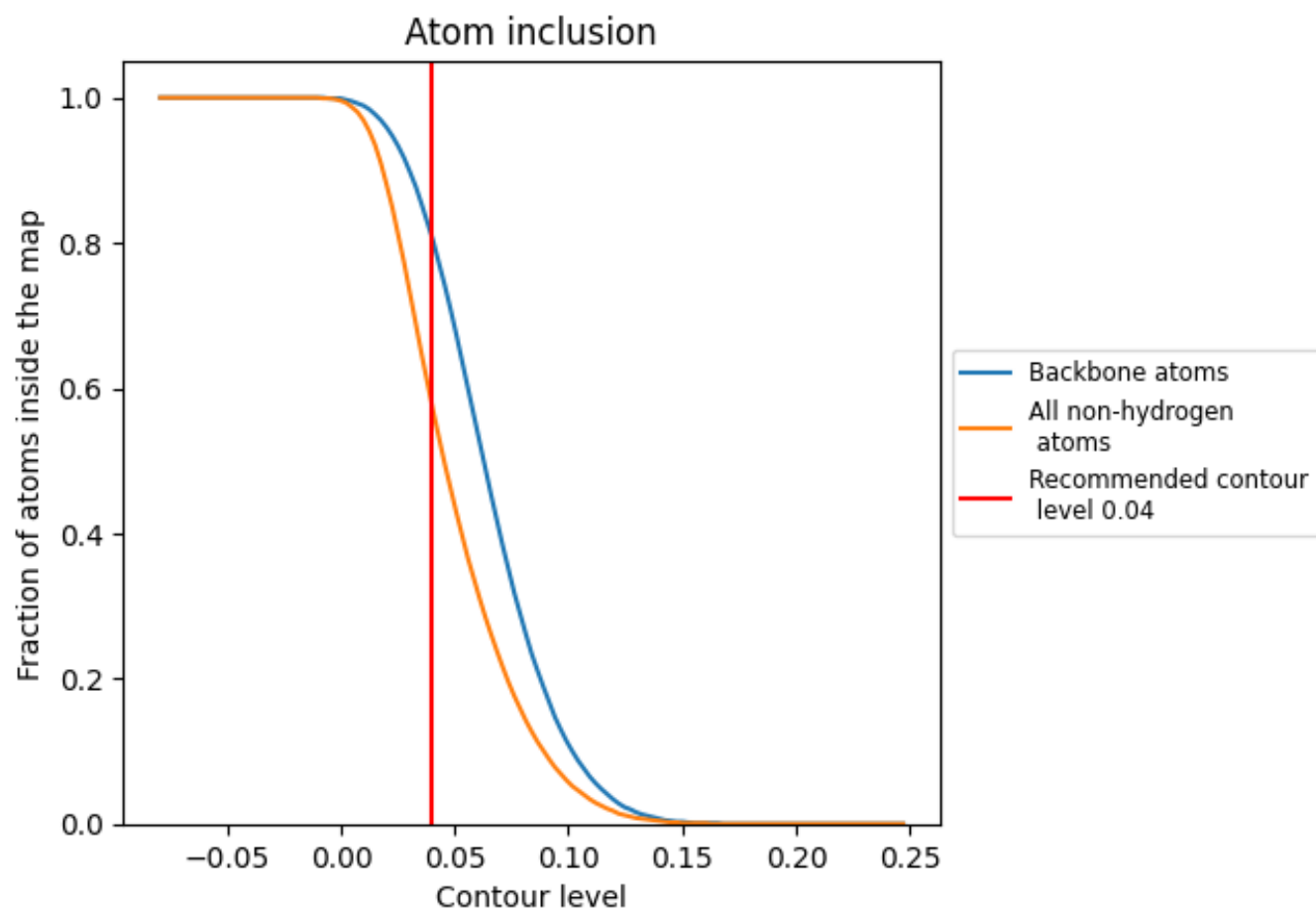
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion ⓘ



At the recommended contour level, 81% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5770	0.1380
AP1	0.8430	0.2100
CP1	0.8790	0.2540
DP1	0.9420	0.2650
EP1	0.9050	0.2110
FP1	0.9450	0.2230
GP1	0.8160	0.2090
HP1	0.8330	0.2060
IP1	0.8940	0.2410
JP1	0.8450	0.2340
KP1	0.9260	0.2570
LP1	0.8950	0.2290
MP1	0.8950	0.2170
NP1	0.9210	0.2450
OP1	0.9010	0.2680
PP1	0.8640	0.2350
QP1	0.5930	0.1340
RP1	0.6190	0.1540
SP1	0.6060	0.1500
TP1	0.5360	0.1180
UP1	0.6380	0.1760
VP1	0.5500	0.1180
WP1	0.6290	0.1740
XP1	0.9550	0.2430
YP1	0.6190	0.1450
ZP1	0.6460	0.1630
aP1	0.6280	0.1690
bP1	0.6350	0.1690
cP1	0.5670	0.1260
dP1	0.5800	0.1420
eP1	0.6170	0.1710
fP1	0.5670	0.1340
gP1	0.8960	0.2780
hP1	0.5550	0.1240
iP1	0.4690	0.0950



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Chain	Atom inclusion	Q-score
jP1	 0.5520	 0.1690
kP1	 0.5030	 0.1020
lP1	 0.5580	 0.1080
mP1	 0.5600	 0.1260
nP1	 0.5050	 0.1010
oP1	 0.5480	 0.1340
pP1	 0.5920	 0.1340
qP1	 0.5680	 0.1230
rP1	 0.4530	 0.0970
sP1	 0.4730	 0.0890
tP1	 0.5330	 0.1160
uP1	 0.7530	 0.1820
vP1	 0.9440	 0.2670
wP1	 0.5330	 0.1430