



Full wwPDB EM Validation Report ⓘ

Mar 18, 2026 – 12:02 AM UTC

PDB ID : 8C5C / pdb_00008c5c
EMDB ID : EMD-16435
Title : microtubule decorated with tubulin oligomers in presence of APC C-terminal domain. (here only map corresponding to the 13-pf microtubule is represented)
Authors : Serre, L.; Arnal, I.
Deposited on : 2023-01-06
Resolution : 5.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

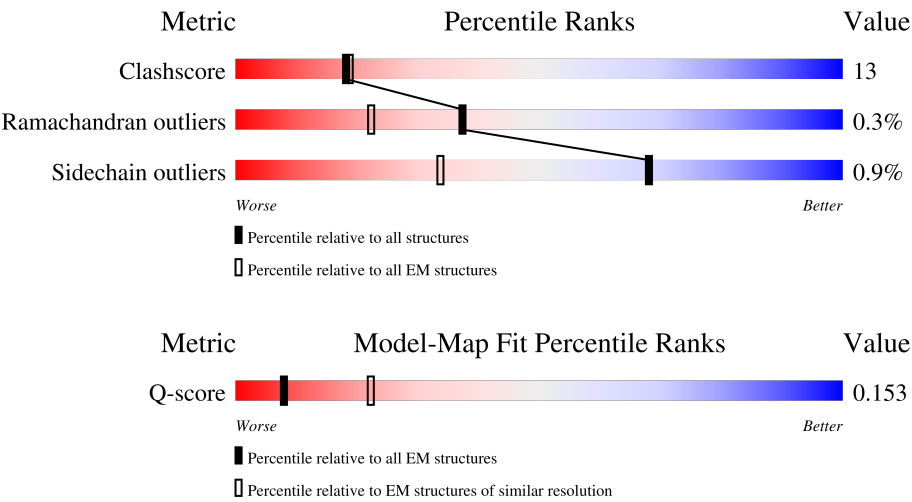
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.30 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.



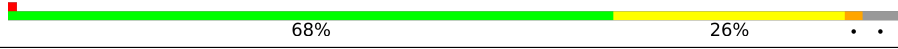
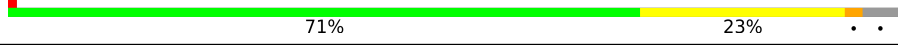
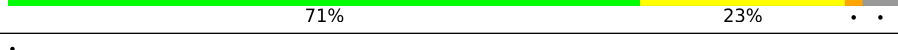
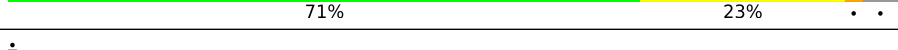
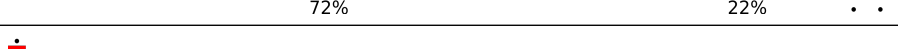
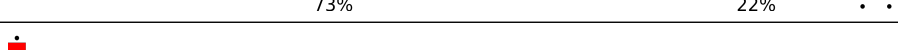
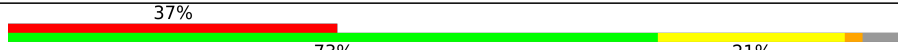
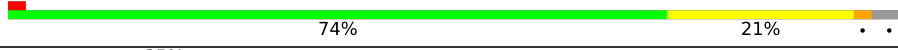
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	625 (4.80 - 5.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	446	70%24% . .
1	b	446	70%24% . .
1	c	446	71%22% . .
1	d	446	69%24% . .

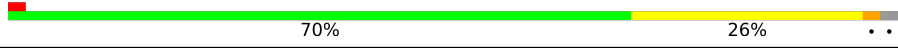
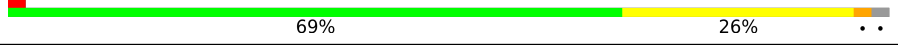
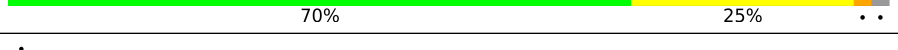
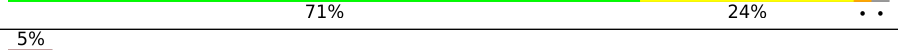
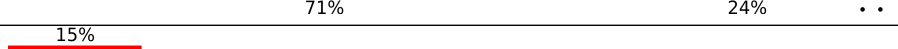
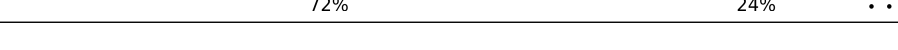
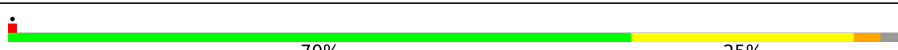
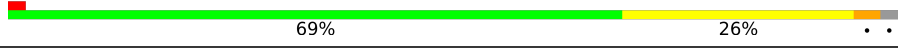
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Mol	Chain	Length	Quality of chain
1	e	446	
1	f	446	
1	g	446	
1	h	446	
1	i	446	
1	j	446	
1	k	446	
1	l	446	
1	m	446	
1	n	446	
1	o	446	
1	p	446	
1	q	446	
1	r	446	
1	s	446	
1	t	446	
1	u	446	
1	v	446	
1	w	446	
1	x	446	
1	y	446	
1	z	446	
2	A	451	
2	B	451	
2	C	451	

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Mol	Chain	Length	Quality of chain
2	D	451	
2	E	451	
2	F	451	
2	G	451	
2	H	451	
2	I	451	
2	J	451	
2	K	451	
2	L	451	
2	M	451	
2	N	451	
2	O	451	
2	P	451	
2	Q	451	
2	R	451	
2	S	451	
2	T	451	
2	U	451	
2	V	451	
2	W	451	
2	X	451	
2	Y	451	
2	Z	451	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TA1	c	601	-	-	X	-
3	TA1	i	601	-	-	X	-
4	GDP	a	602	-	-	X	-
4	GDP	b	602	-	-	X	-
4	GDP	c	602	-	-	X	-
4	GDP	d	602	-	-	X	-
4	GDP	e	602	-	-	X	-
4	GDP	f	602	-	-	X	-
4	GDP	g	602	-	-	X	-
4	GDP	h	602	-	-	X	-
4	GDP	i	602	-	-	X	-
4	GDP	j	602	-	-	X	-
4	GDP	k	602	-	-	X	-
4	GDP	l	602	-	-	X	-
4	GDP	m	602	-	-	X	-
6	GTP	N	502	-	-	X	-
6	GTP	O	502	-	-	X	-
6	GTP	P	502	-	-	X	-
6	GTP	Q	502	-	-	X	-
6	GTP	R	502	-	-	X	-
6	GTP	S	502	-	-	X	-
6	GTP	T	502	-	-	X	-
6	GTP	U	502	-	-	X	-
6	GTP	V	502	-	-	X	-
6	GTP	W	502	-	-	X	-
6	GTP	X	502	-	-	X	-
6	GTP	Y	502	-	-	X	-
6	GTP	Z	502	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 178971 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	b	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	c	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	d	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	e	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	f	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	g	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	h	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	i	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	j	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	k	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	l	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	m	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	n	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	o	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	p	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	q	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	s	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	t	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	u	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	v	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	w	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	x	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	y	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		
1	z	429	Total	C	N	O	S	0	0
			3376	2119	578	652	27		

- Molecule 2 is a protein called Tubulin alpha-1B chain.

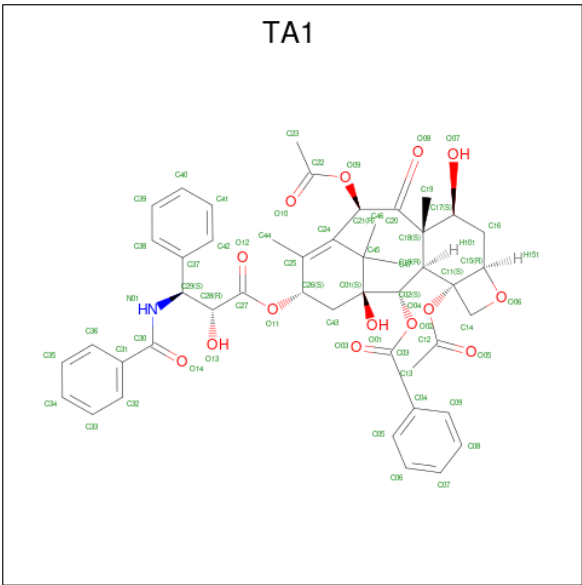
Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	O	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	P	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	Q	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	R	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	S	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	T	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	U	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	V	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		
2	W	441	Total	C	N	O	S	0	0
			3446	2180	585	659	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	Y	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	Z	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	A	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	B	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	C	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	D	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	E	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	F	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	G	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	H	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	I	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	J	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	K	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	L	441	Total 3446	C 2180	N 585	O 659	S 22	0	0
2	M	441	Total 3446	C 2180	N 585	O 659	S 22	0	0

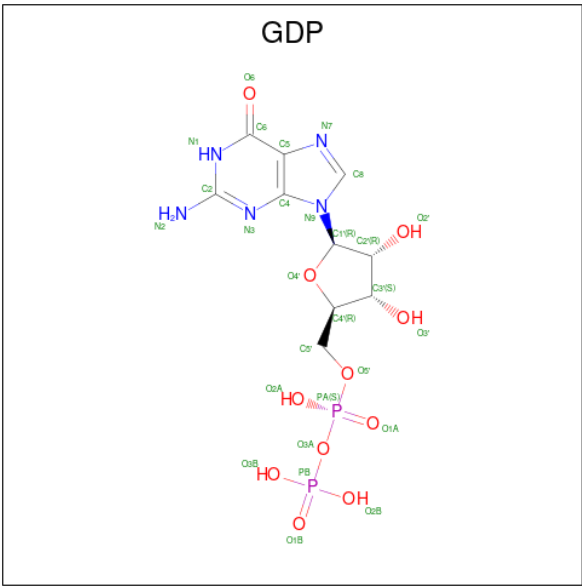
- Molecule 3 is TAXOL (CCD ID: TA1) (formula: $C_{47}H_{51}NO_{14}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	a	1	Total	C	N	O	0
			62	47	1	14	
3	b	1	Total	C	N	O	0
			62	47	1	14	
3	c	1	Total	C	N	O	0
			62	47	1	14	
3	d	1	Total	C	N	O	0
			62	47	1	14	
3	e	1	Total	C	N	O	0
			62	47	1	14	
3	f	1	Total	C	N	O	0
			62	47	1	14	
3	g	1	Total	C	N	O	0
			62	47	1	14	
3	h	1	Total	C	N	O	0
			62	47	1	14	
3	i	1	Total	C	N	O	0
			62	47	1	14	
3	j	1	Total	C	N	O	0
			62	47	1	14	
3	k	1	Total	C	N	O	0
			62	47	1	14	
3	l	1	Total	C	N	O	0
			62	47	1	14	
3	m	1	Total	C	N	O	0
			62	47	1	14	

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂)

(labeled as "Ligand of Interest" by depositor).

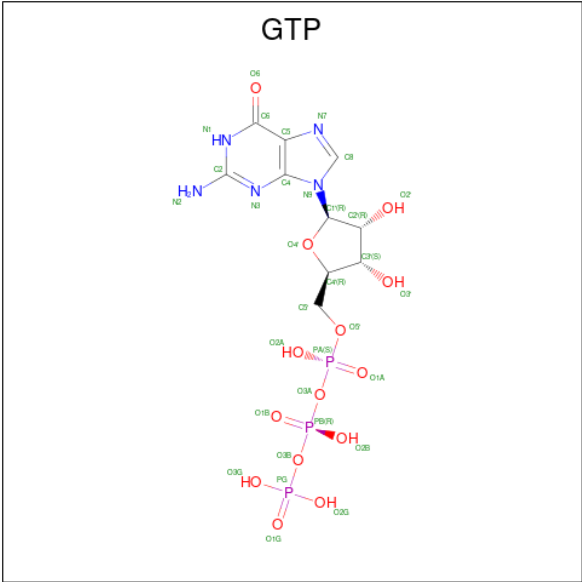


Mol	Chain	Residues	Atoms					AltConf
4	a	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	b	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	c	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	d	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	e	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	f	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	g	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	h	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	i	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	j	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	k	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	l	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	m	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	N	1	Total 1	Mg 1	0
5	O	1	Total 1	Mg 1	0
5	P	1	Total 1	Mg 1	0
5	Q	1	Total 1	Mg 1	0
5	R	1	Total 1	Mg 1	0
5	S	1	Total 1	Mg 1	0
5	T	1	Total 1	Mg 1	0
5	U	1	Total 1	Mg 1	0
5	V	1	Total 1	Mg 1	0
5	W	1	Total 1	Mg 1	0
5	X	1	Total 1	Mg 1	0
5	Y	1	Total 1	Mg 1	0
5	Z	1	Total 1	Mg 1	0

- Molecule 6 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).

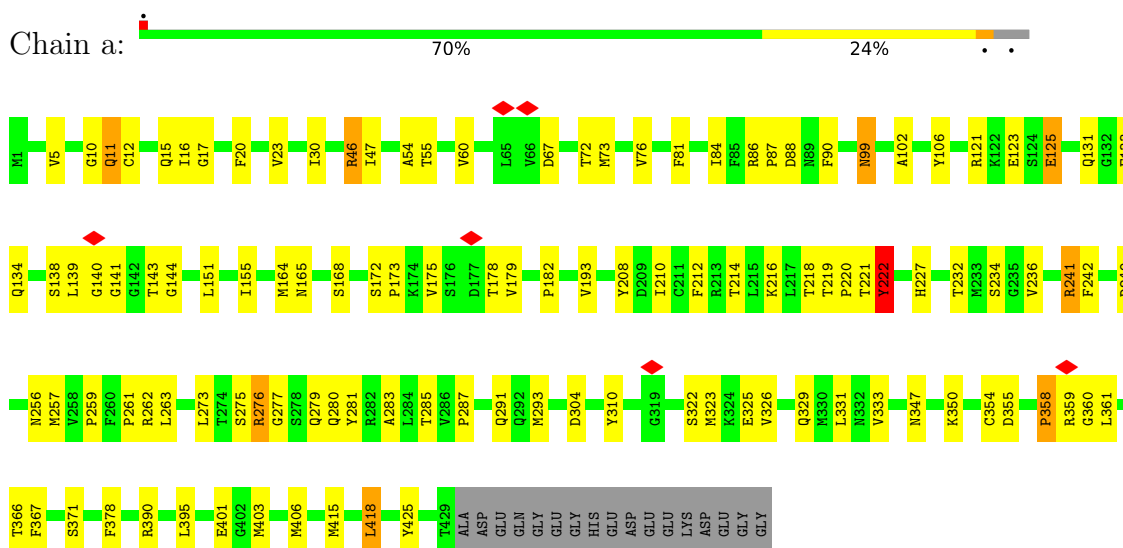


Mol	Chain	Residues	Atoms					AltConf
6	N	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	O	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	P	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	Q	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	R	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	S	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	T	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	U	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	V	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	W	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	X	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	Y	1	Total	C	N	O	P	0
			32	10	5	14	3	
6	Z	1	Total	C	N	O	P	0
			32	10	5	14	3	

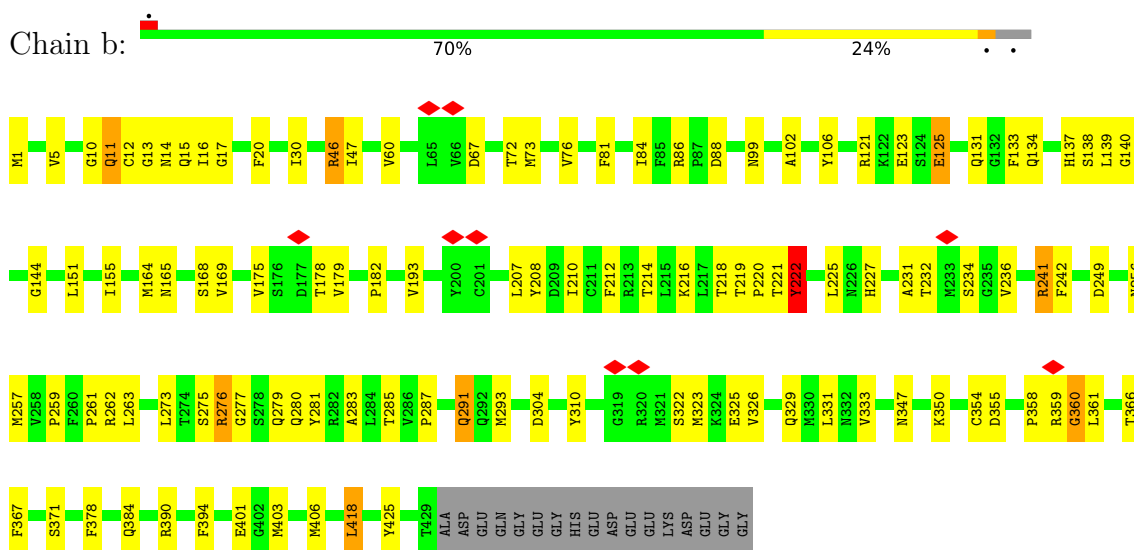
3 Residue-property plots [i](#)

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

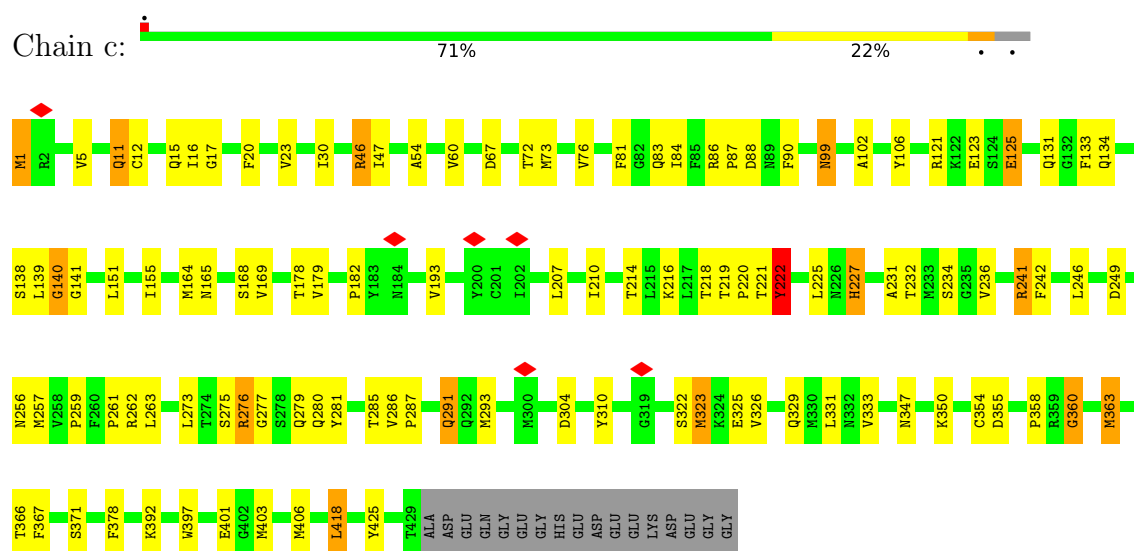
- Molecule 1: Tubulin beta chain



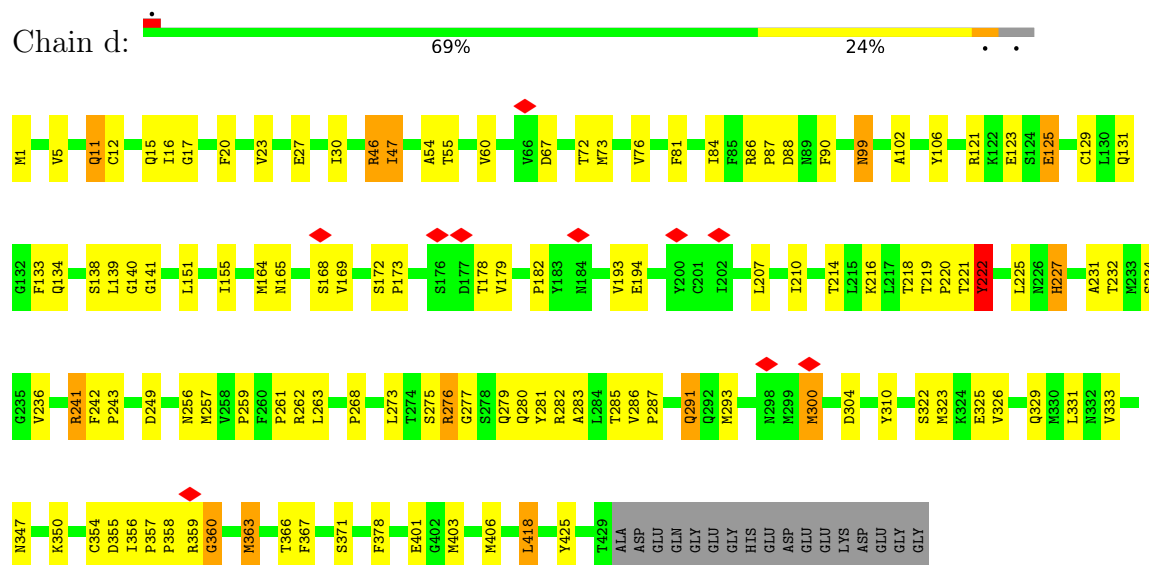
- Molecule 1: Tubulin beta chain



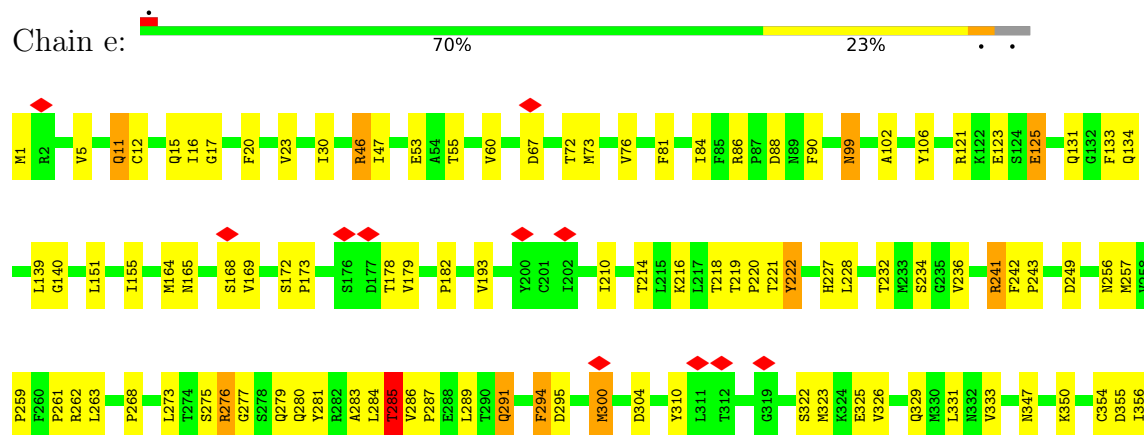
- Molecule 1: Tubulin beta chain



• Molecule 1: Tubulin beta chain



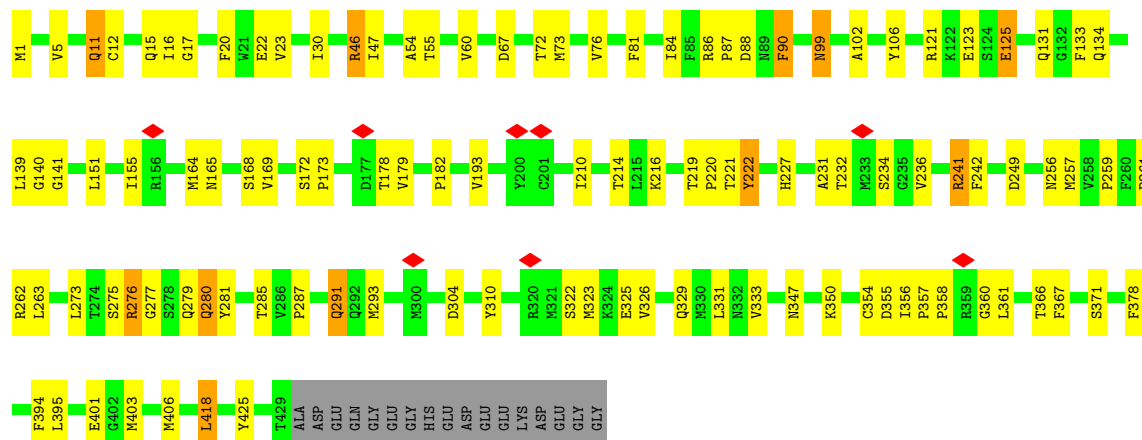
• Molecule 1: Tubulin beta chain





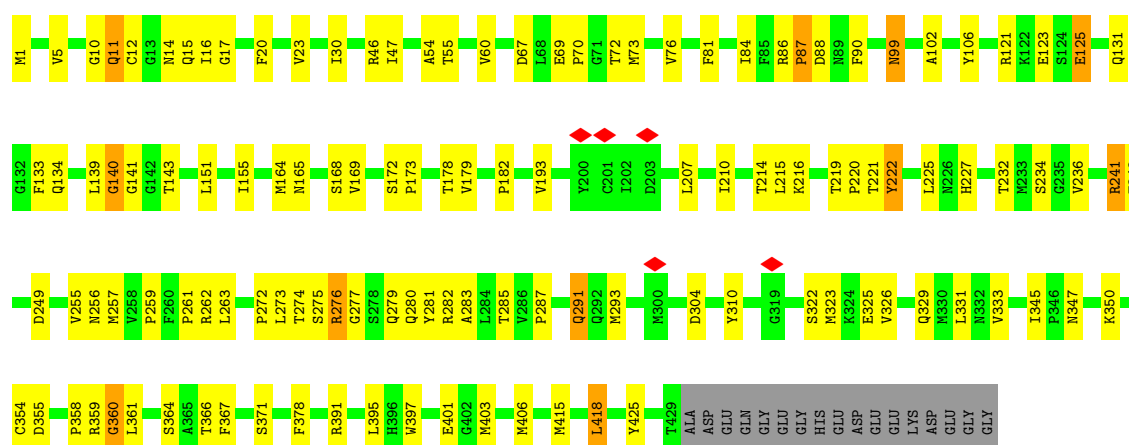
• Molecule 1: Tubulin beta chain

Chain f: 71% 22%



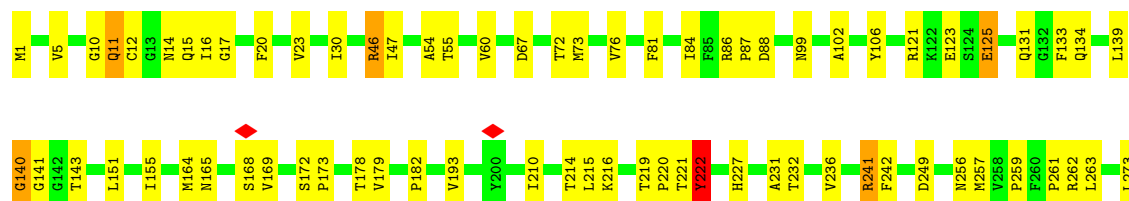
• Molecule 1: Tubulin beta chain

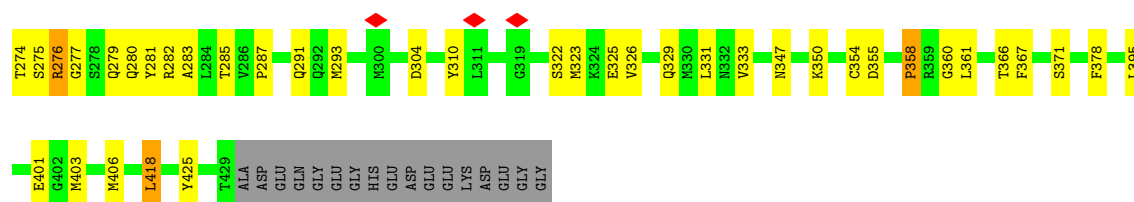
Chain g: 68% 26%



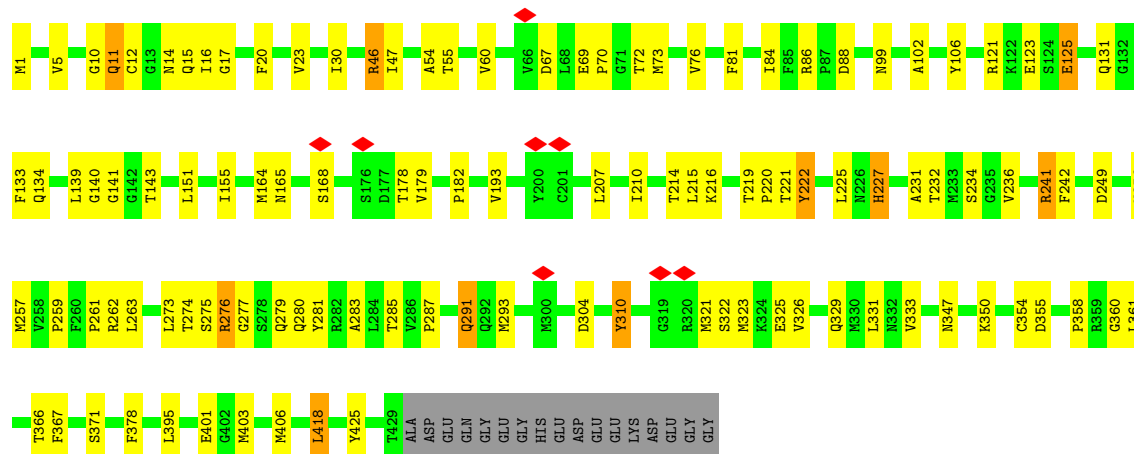
• Molecule 1: Tubulin beta chain

Chain h: 71% 23%

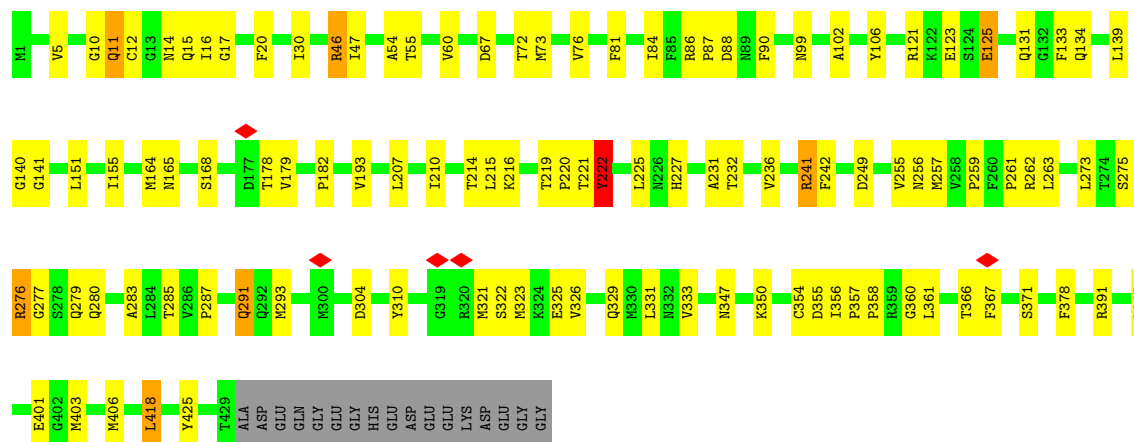




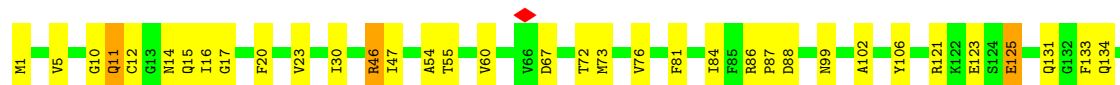
• Molecule 1: Tubulin beta chain

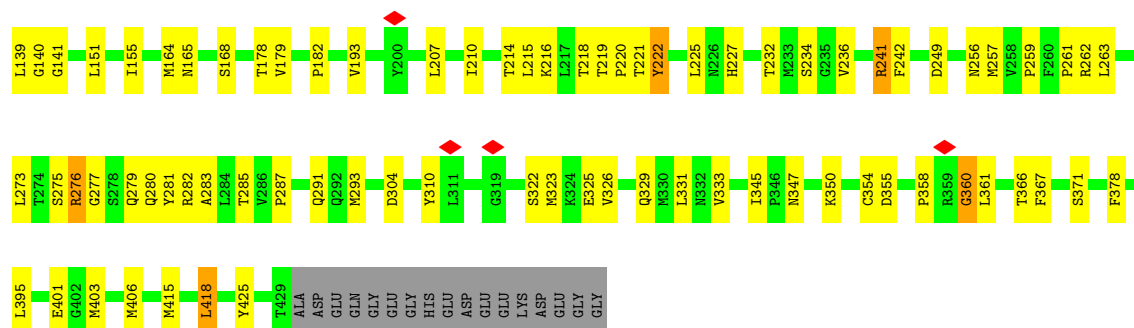


• Molecule 1: Tubulin beta chain



• Molecule 1: Tubulin beta chain

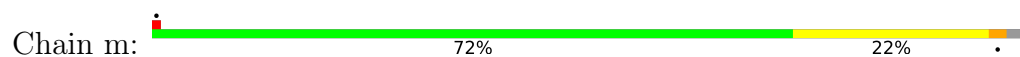


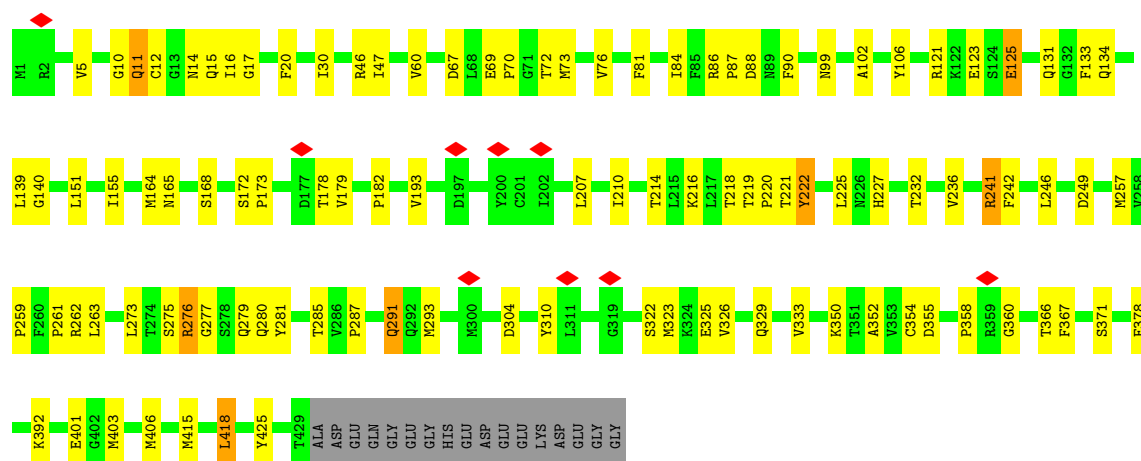


• Molecule 1: Tubulin beta chain

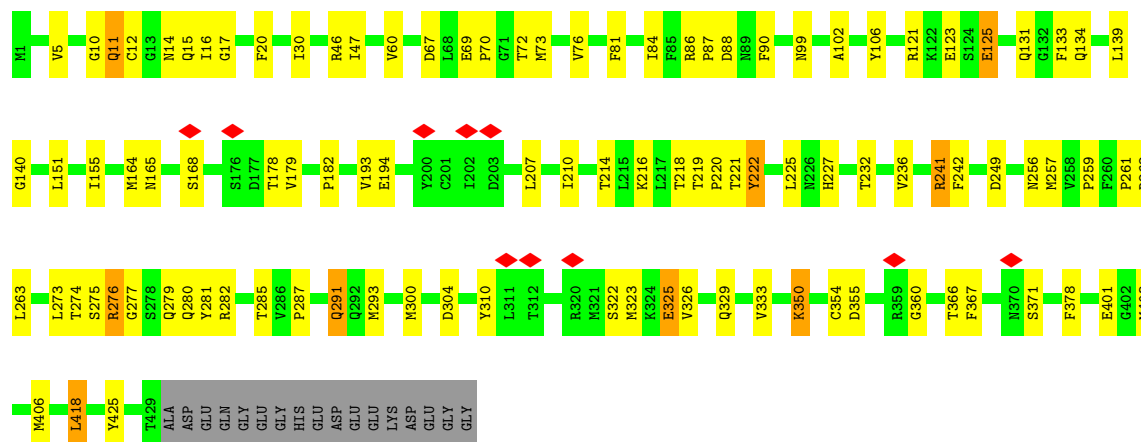


• Molecule 1: Tubulin beta chain

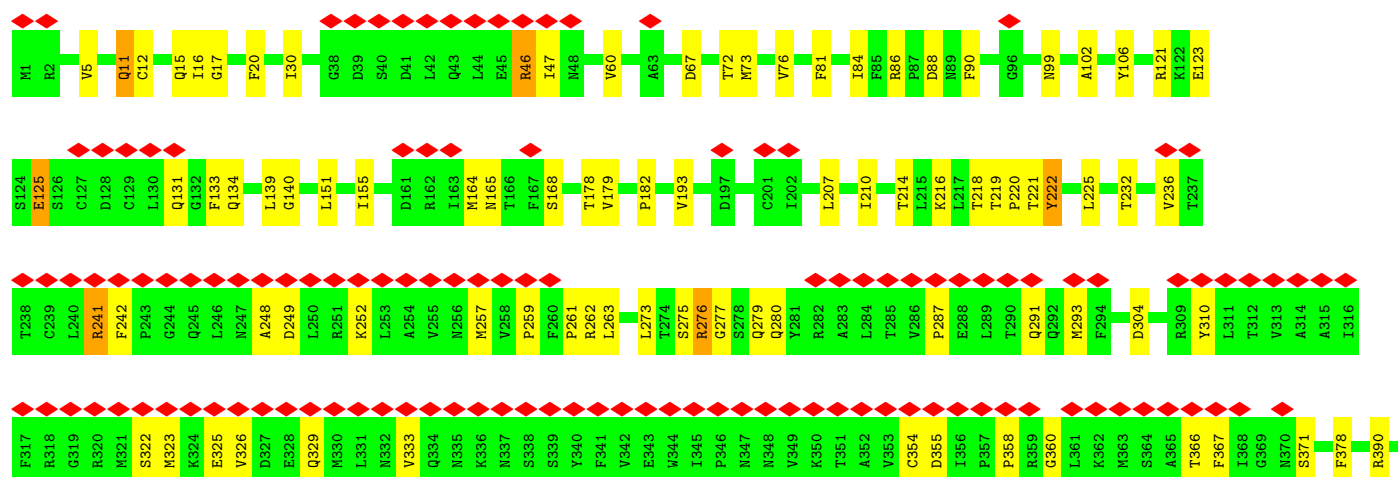
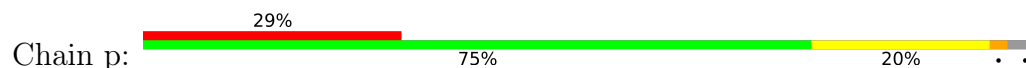


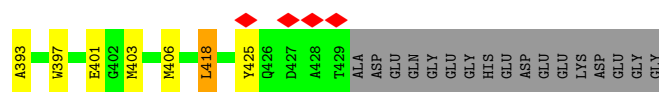


• Molecule 1: Tubulin beta chain

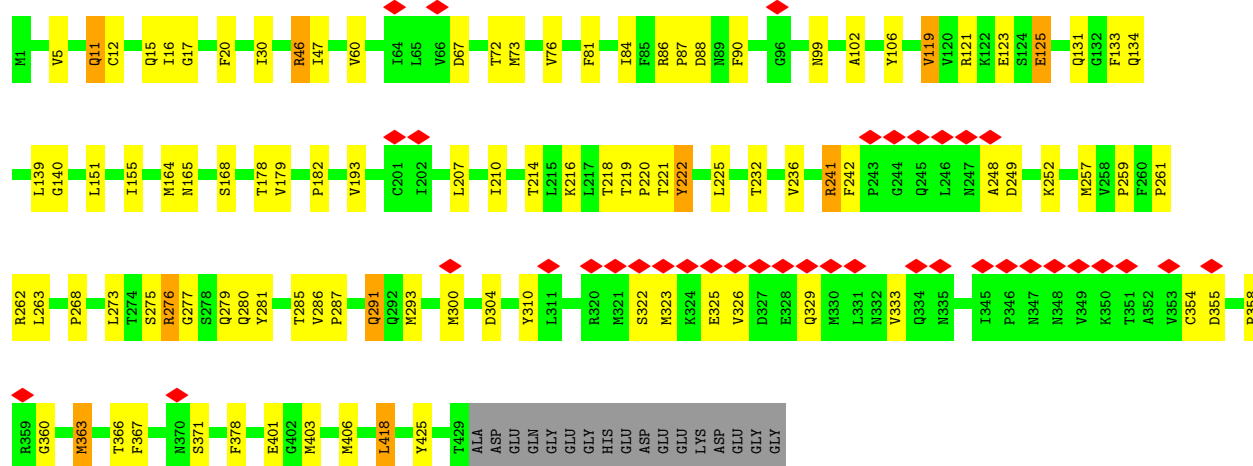
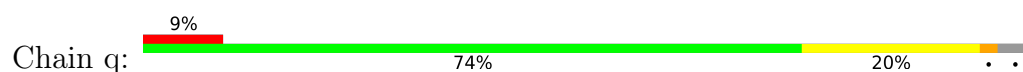


• Molecule 1: Tubulin beta chain

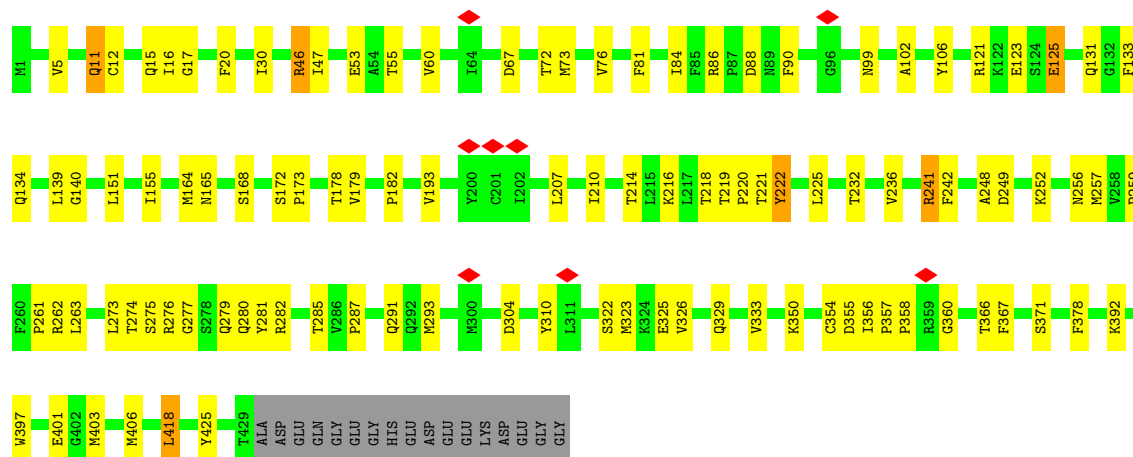




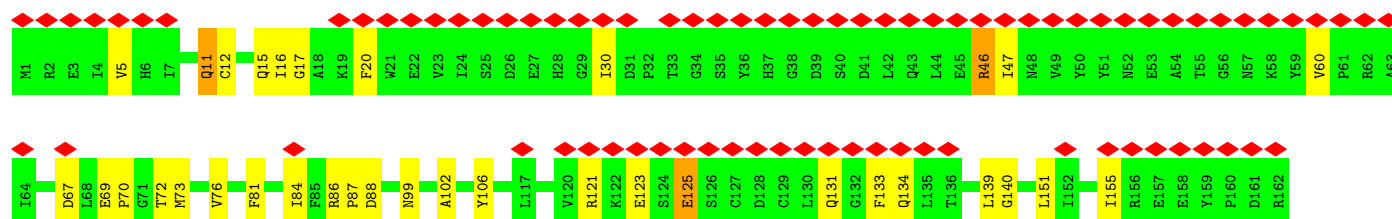
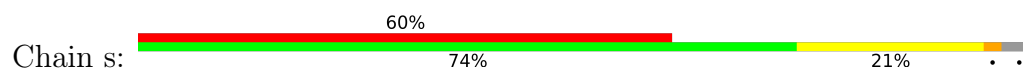
• Molecule 1: Tubulin beta chain

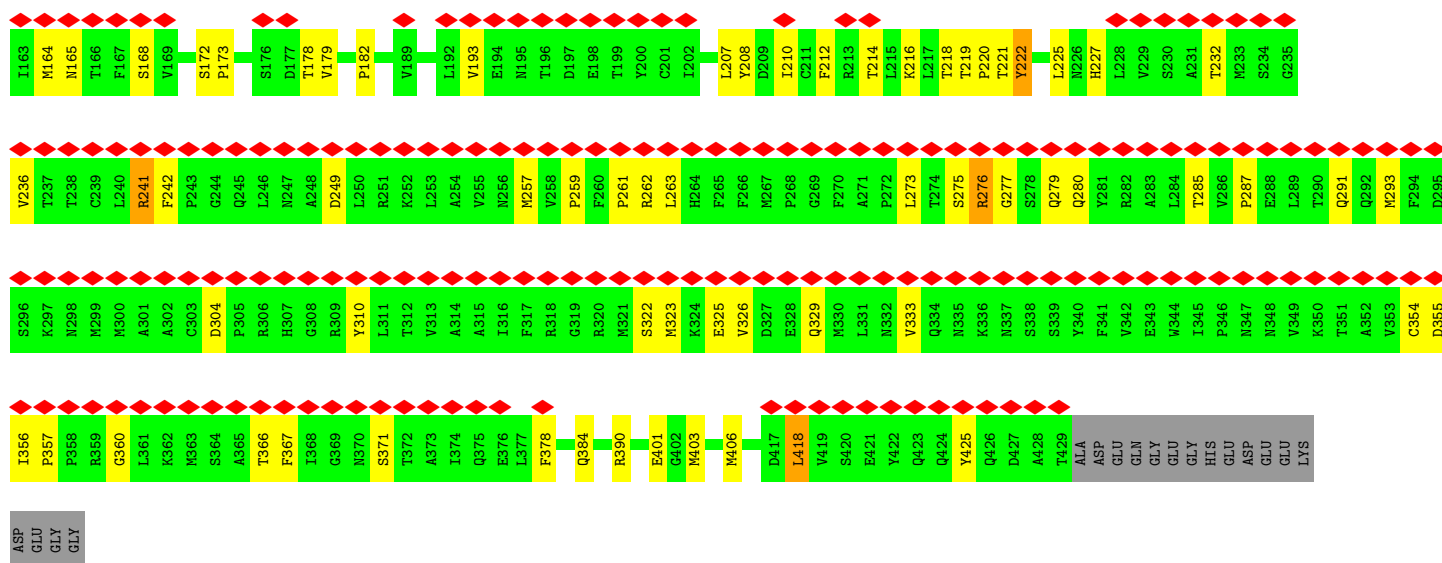


• Molecule 1: Tubulin beta chain

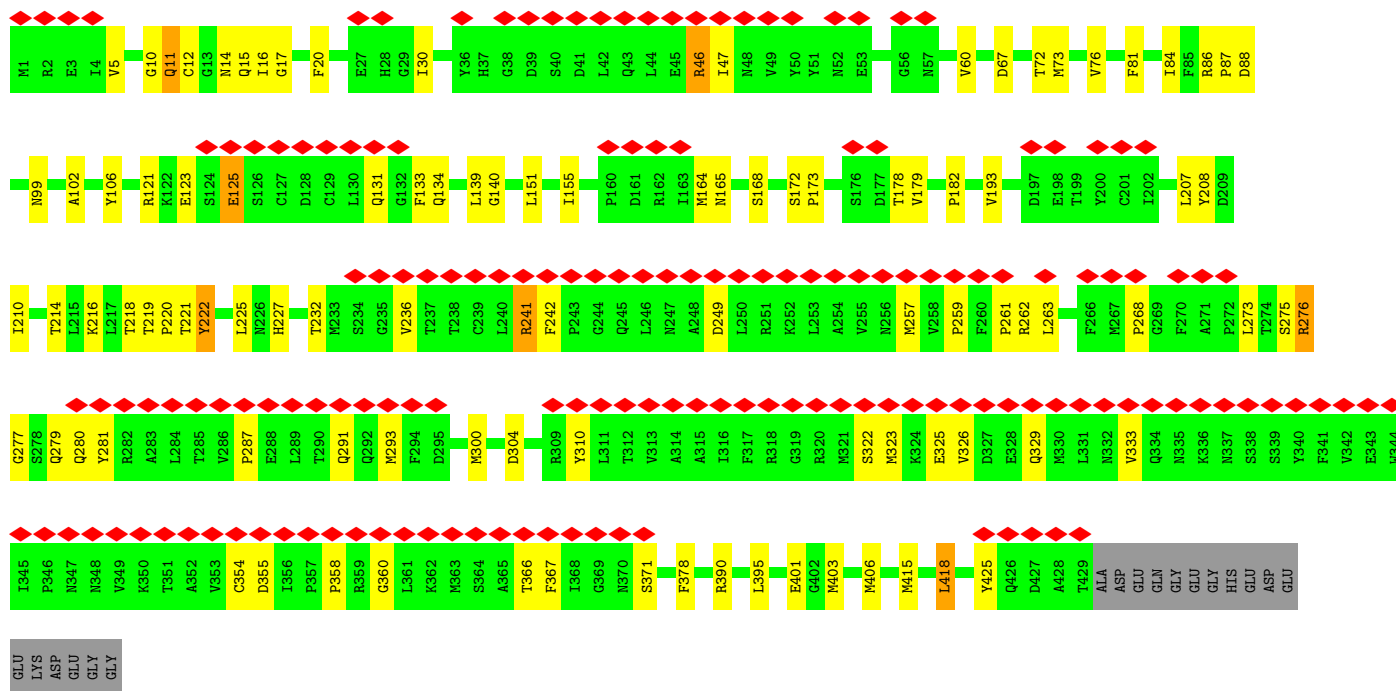


• Molecule 1: Tubulin beta chain

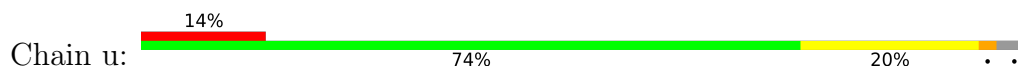


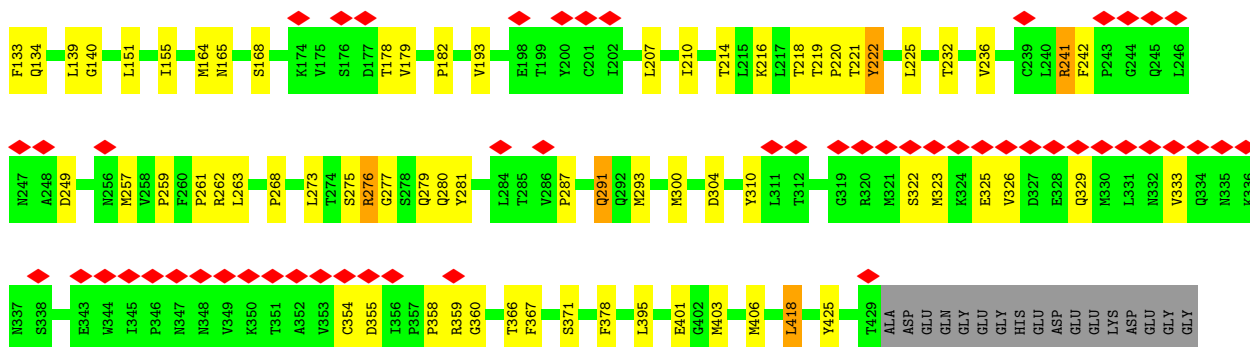


• Molecule 1: Tubulin beta chain

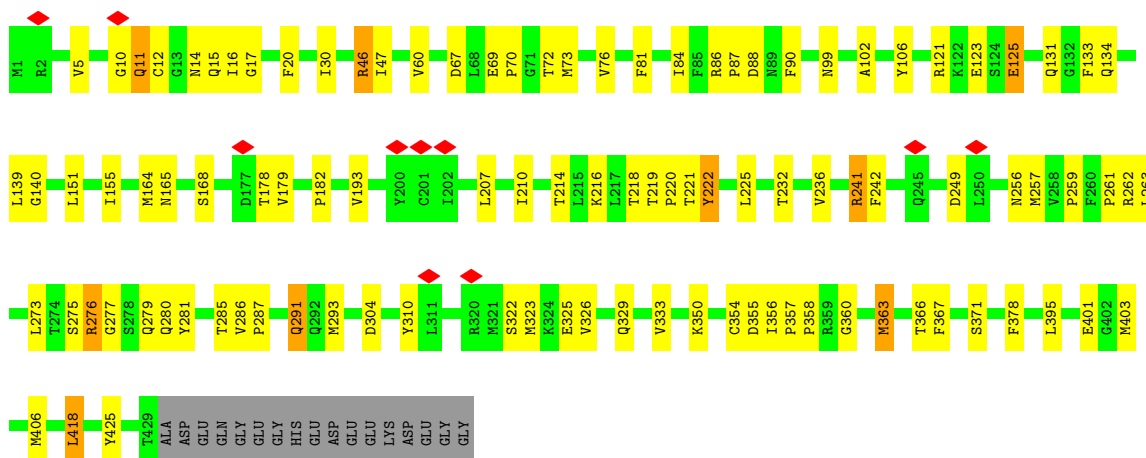


• Molecule 1: Tubulin beta chain

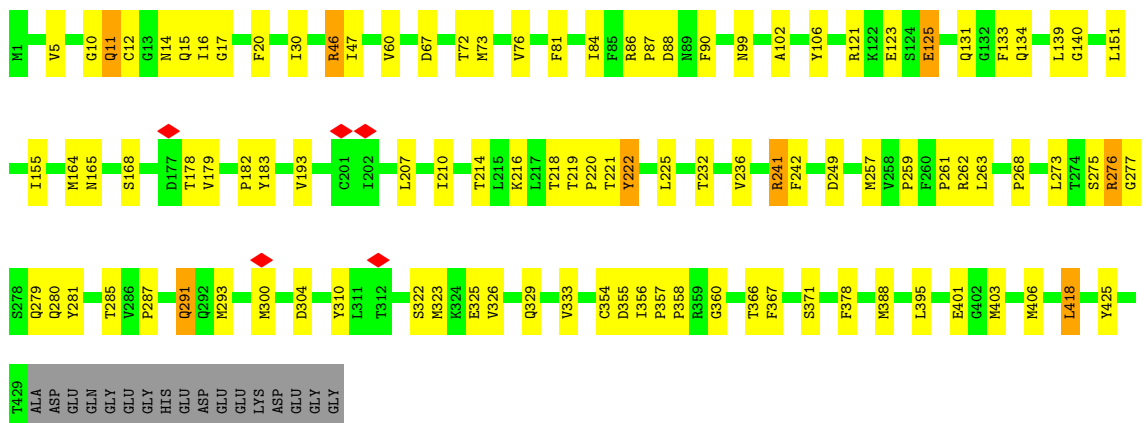
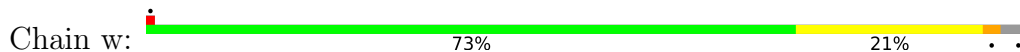




• Molecule 1: Tubulin beta chain

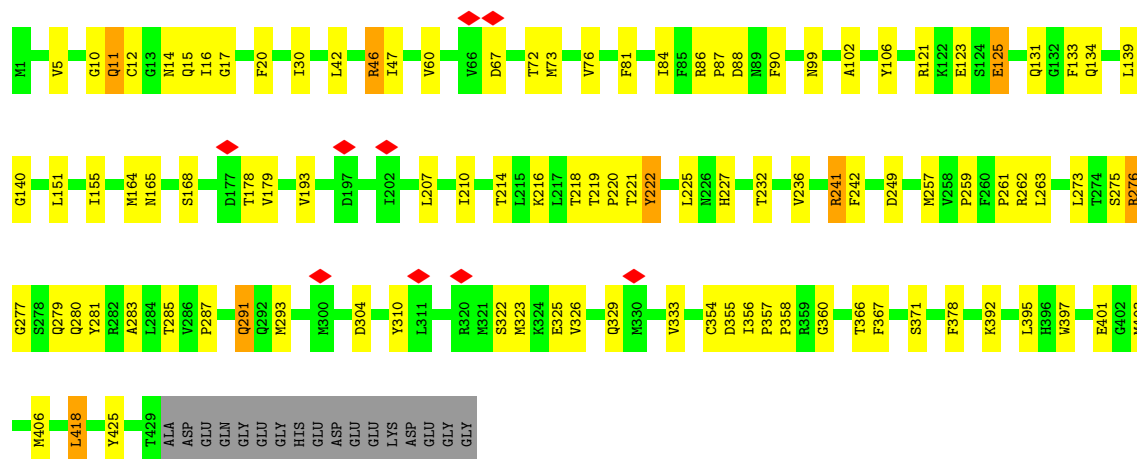


• Molecule 1: Tubulin beta chain

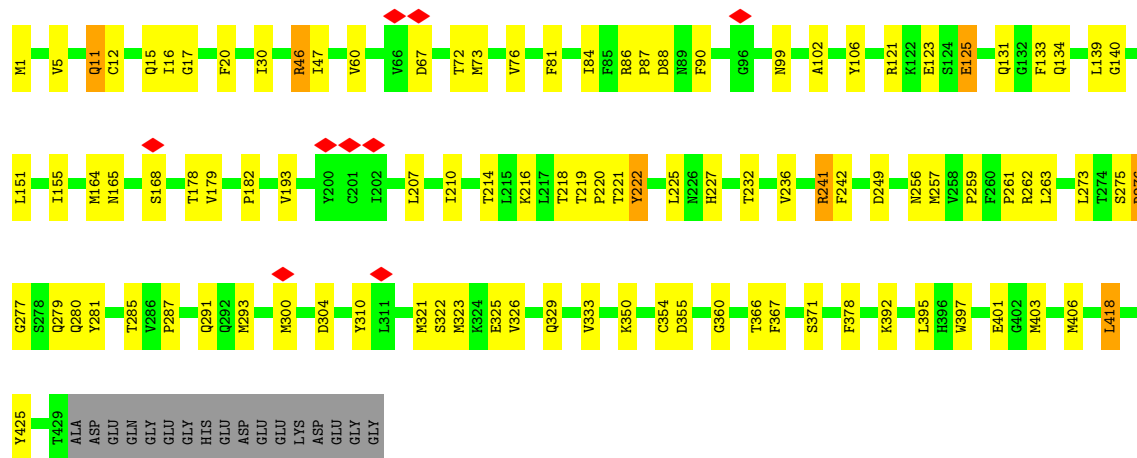


• Molecule 1: Tubulin beta chain

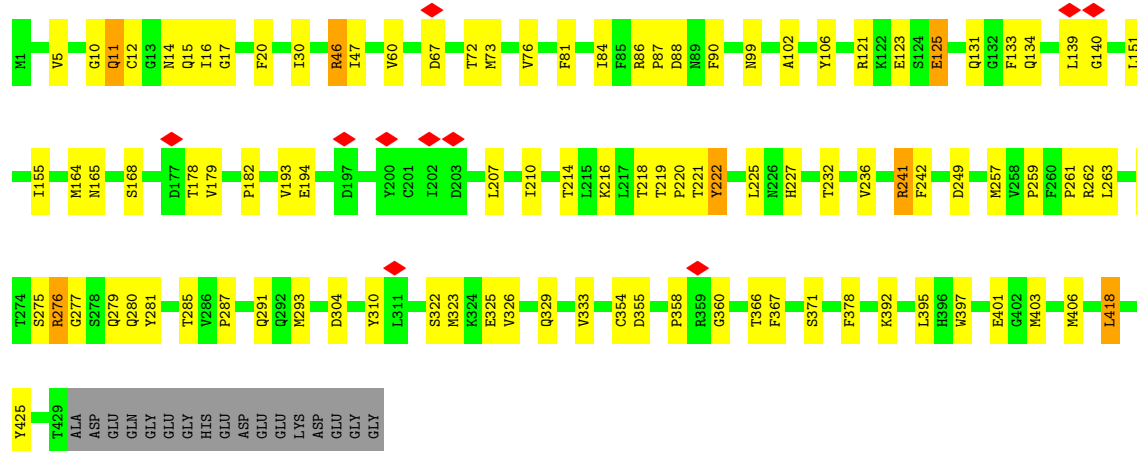




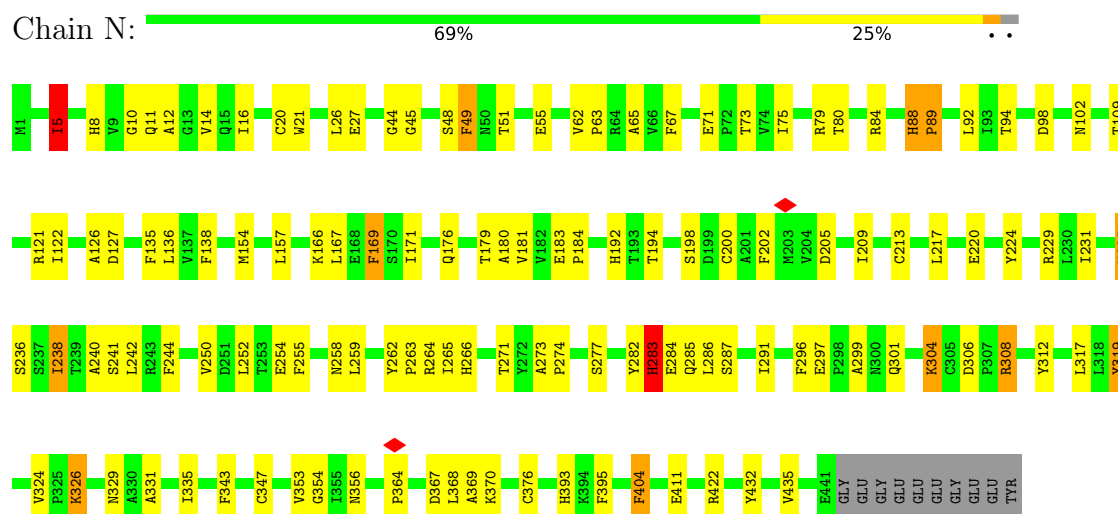
• Molecule 1: Tubulin beta chain



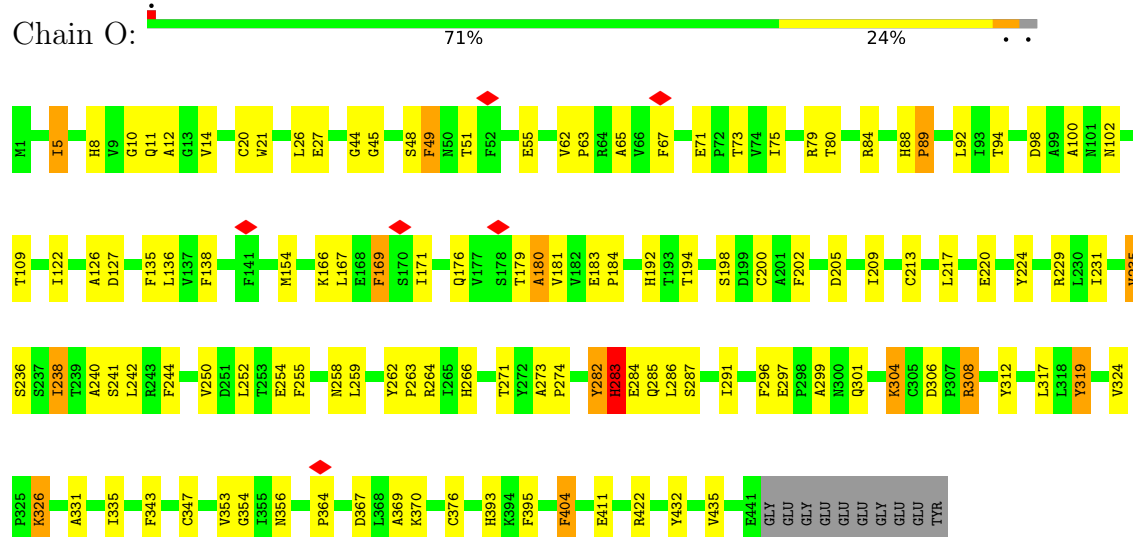
• Molecule 1: Tubulin beta chain



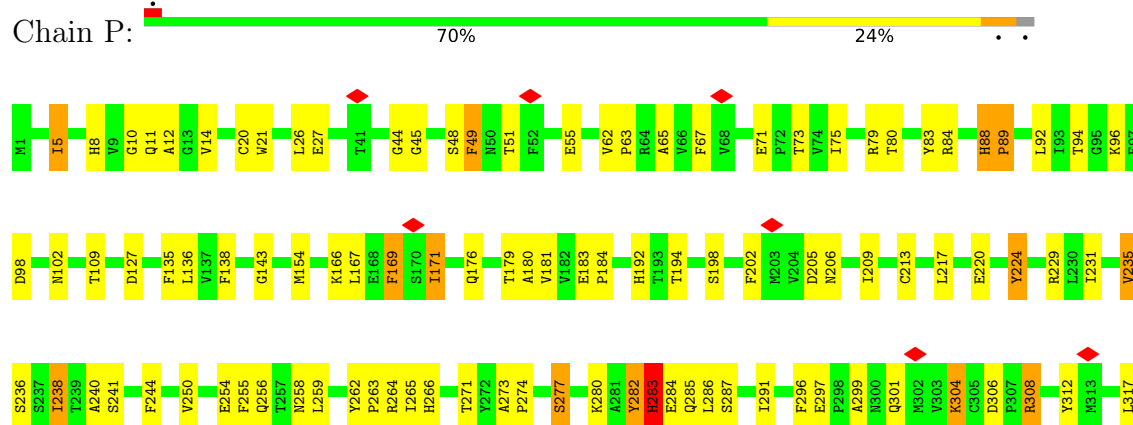
- Molecule 2: Tubulin alpha-1B chain

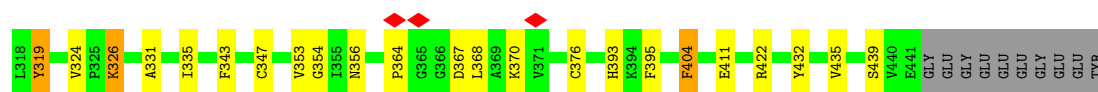


- Molecule 2: Tubulin alpha-1B chain



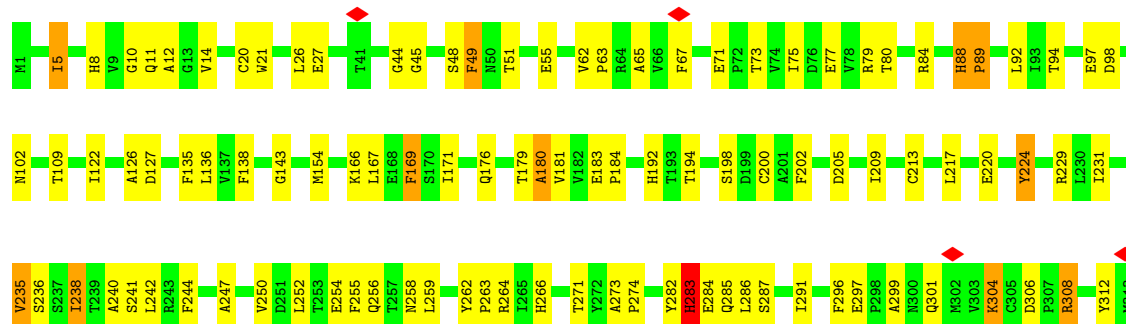
- Molecule 2: Tubulin alpha-1B chain





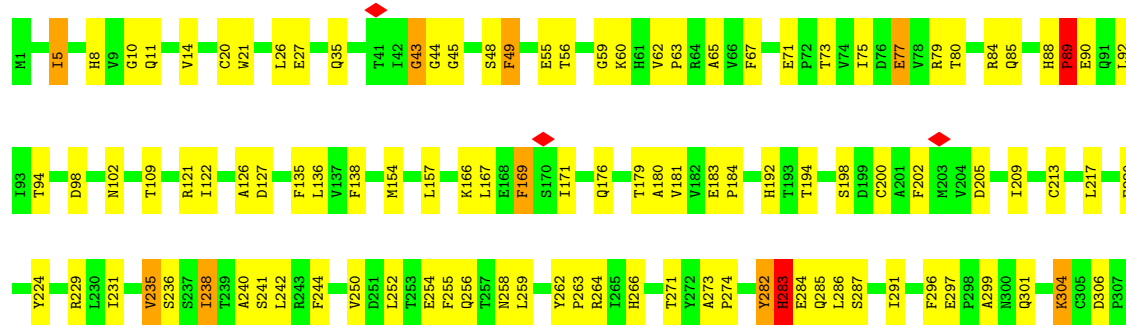
• Molecule 2: Tubulin alpha-1B chain

Chain Q: 69% 25%



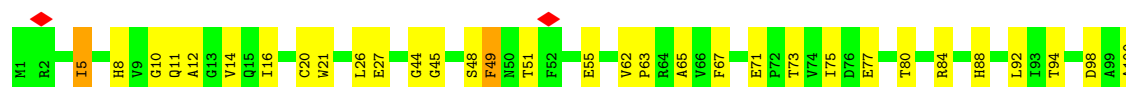
• Molecule 2: Tubulin alpha-1B chain

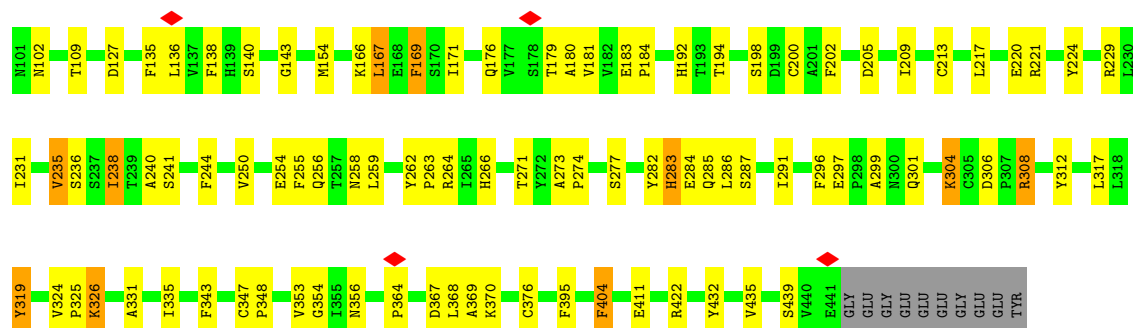
Chain R: 69% 25%



• Molecule 2: Tubulin alpha-1B chain

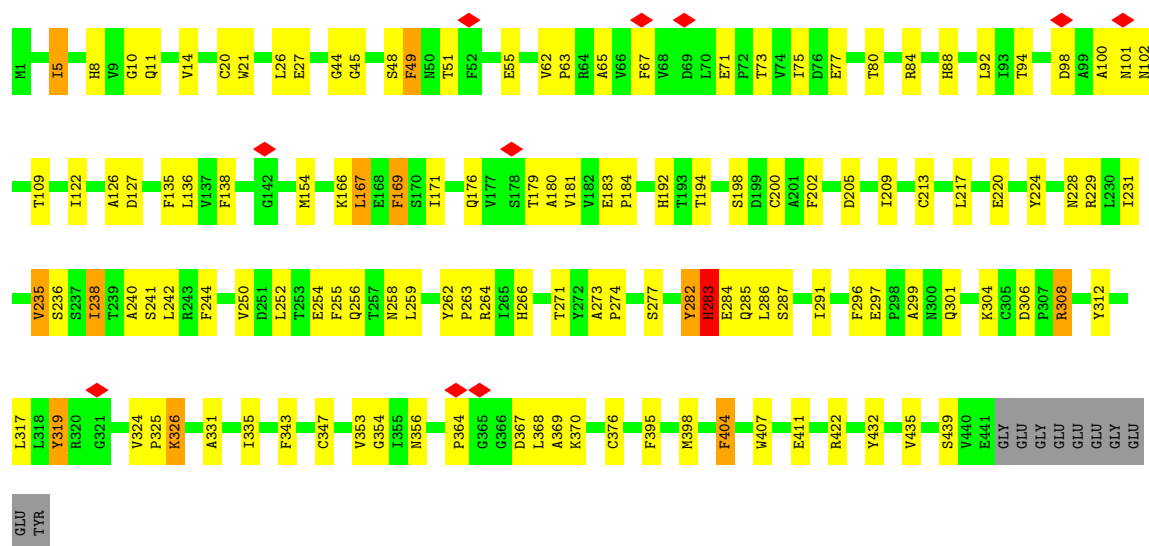
Chain S: 70% 25%





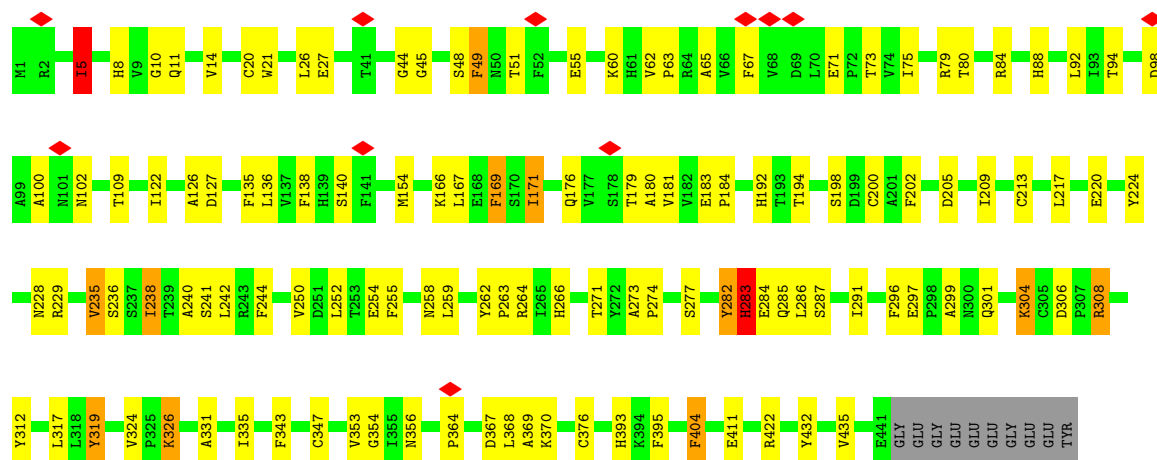
• Molecule 2: Tubulin alpha-1B chain

Chain T: 69% 26%

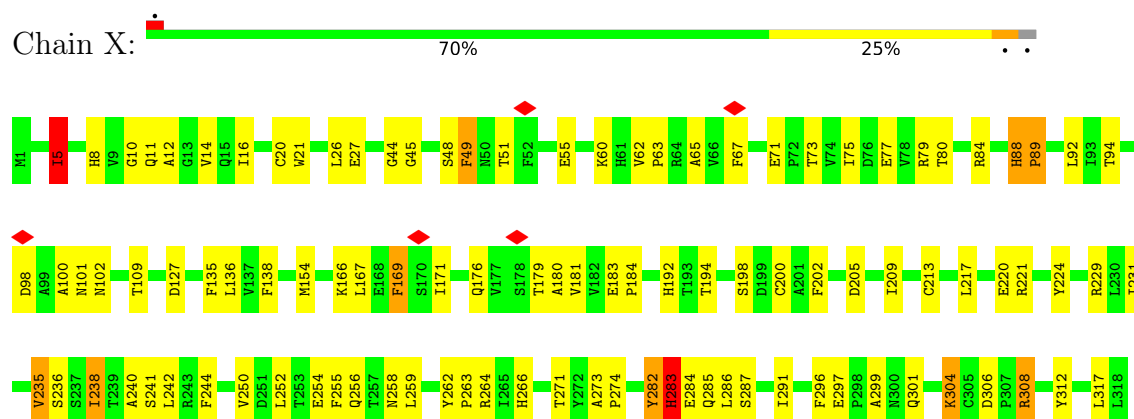


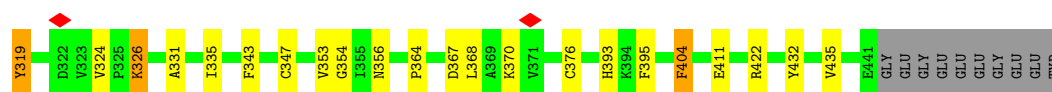
• Molecule 2: Tubulin alpha-1B chain

Chain U: 70% 25%



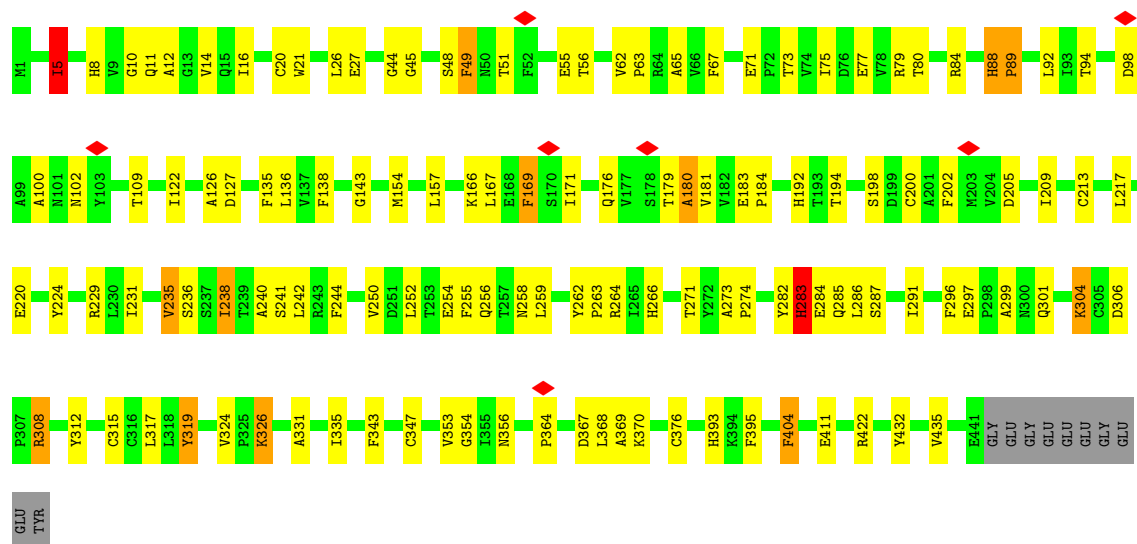
• Molecule 2: Tubulin alpha-1B chain





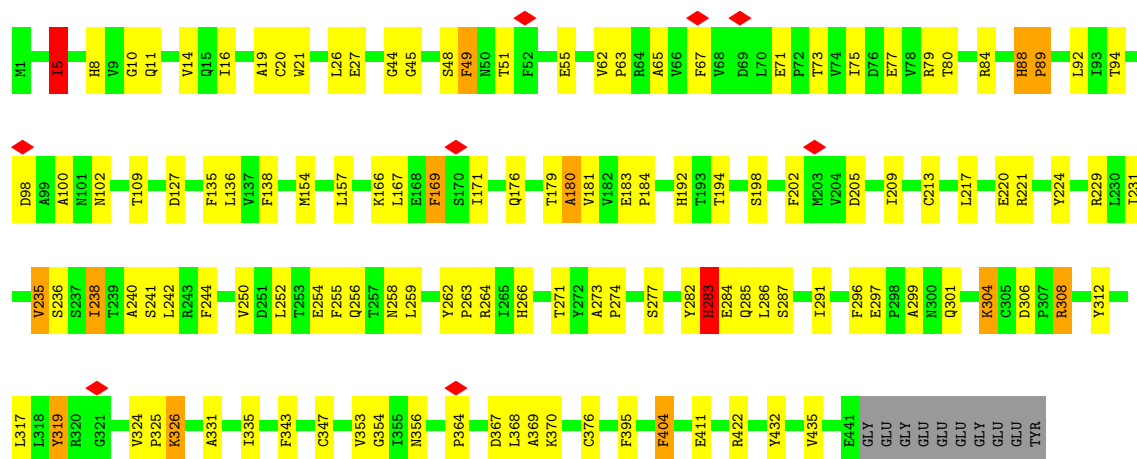
• Molecule 2: Tubulin alpha-1B chain

Chain Y: 69% 26%



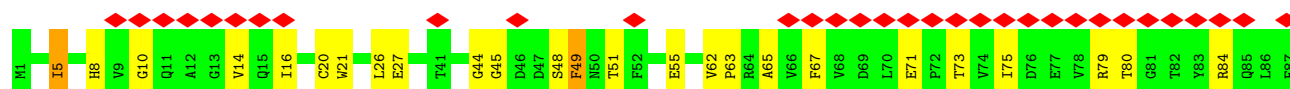
• Molecule 2: Tubulin alpha-1B chain

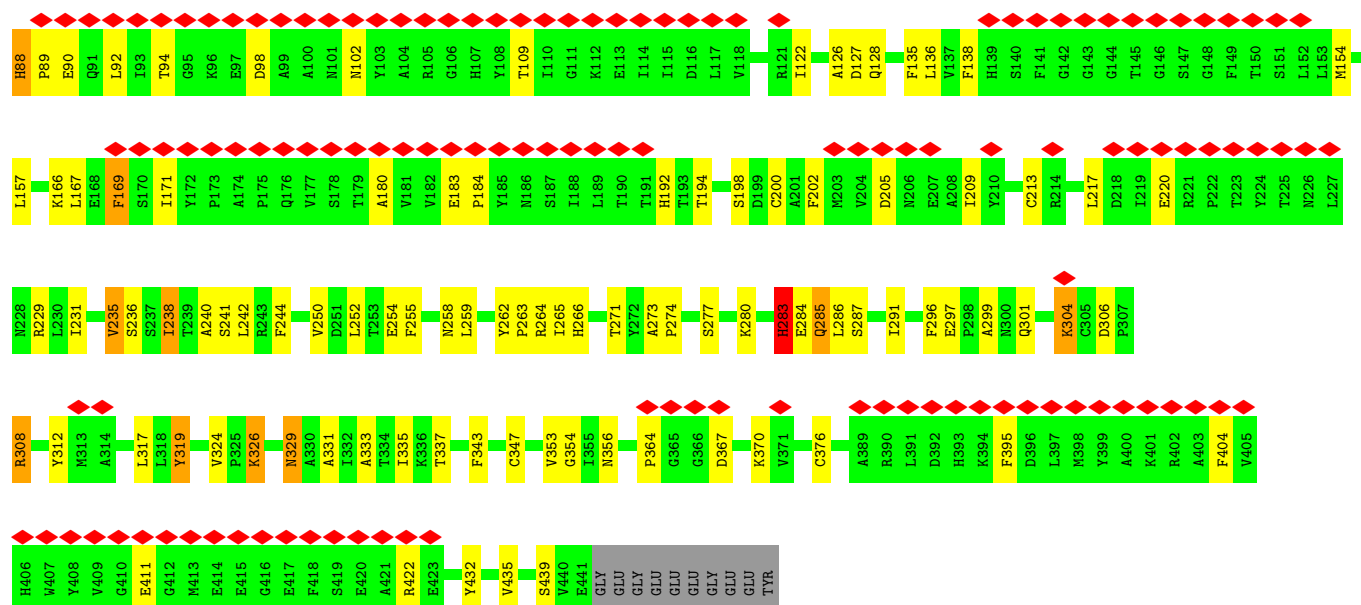
Chain Z: 70% 25%



• Molecule 2: Tubulin alpha-1B chain

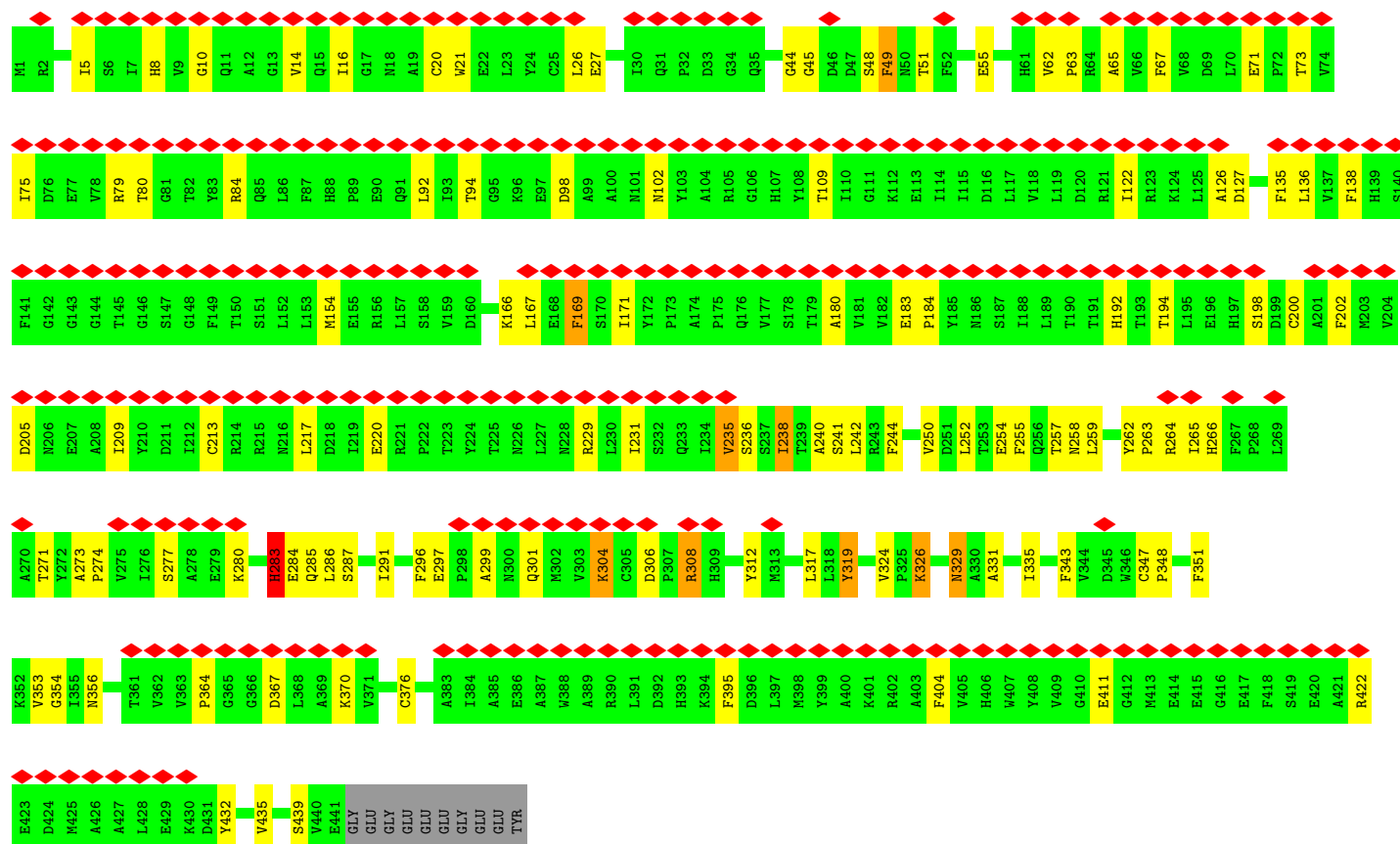
Chain A: 35% 71% 24%



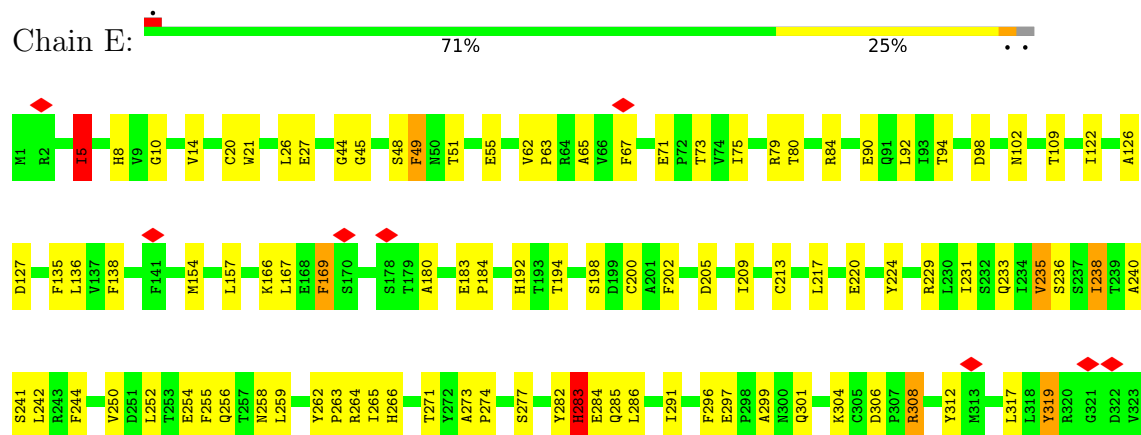


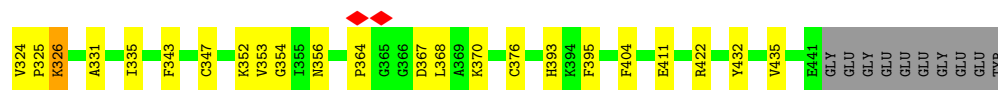
• Molecule 2: Tubulin alpha-1B chain

Chain B: 60% 71% 24%



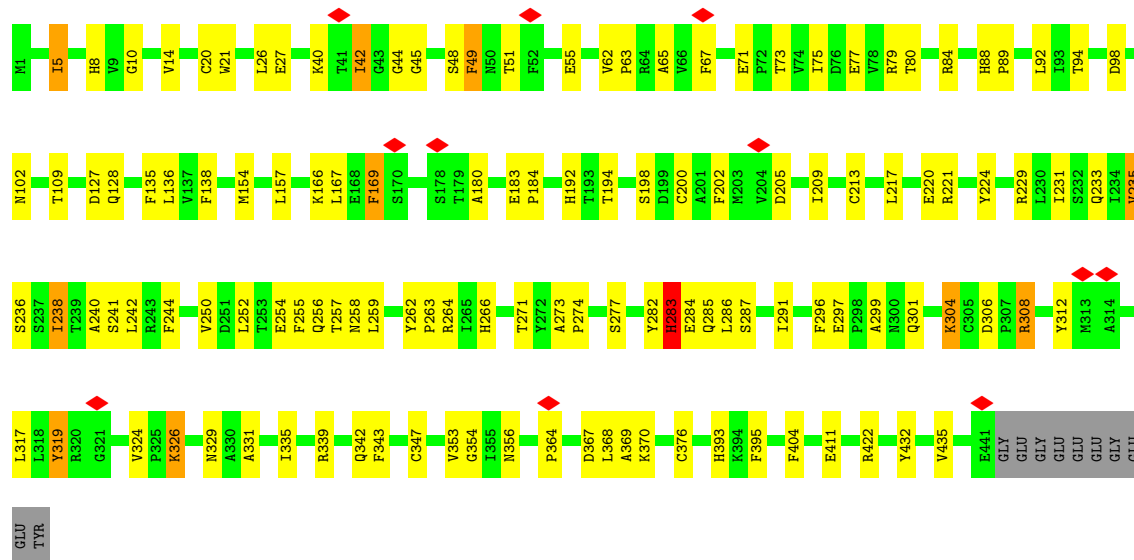
• Molecule 2: Tubulin alpha-1B chain





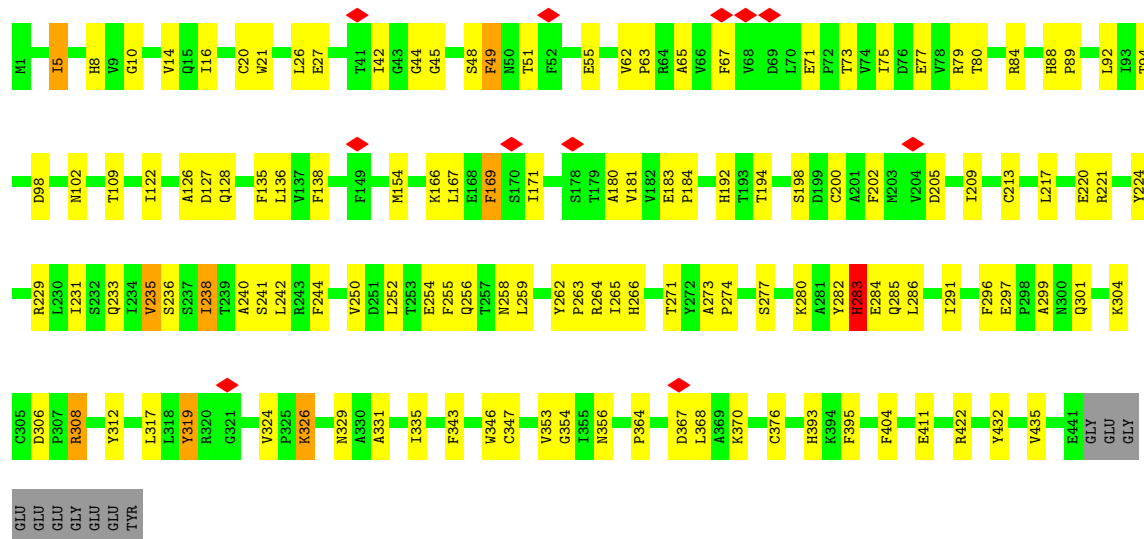
• Molecule 2: Tubulin alpha-1B chain

Chain F: 70% 26% ..



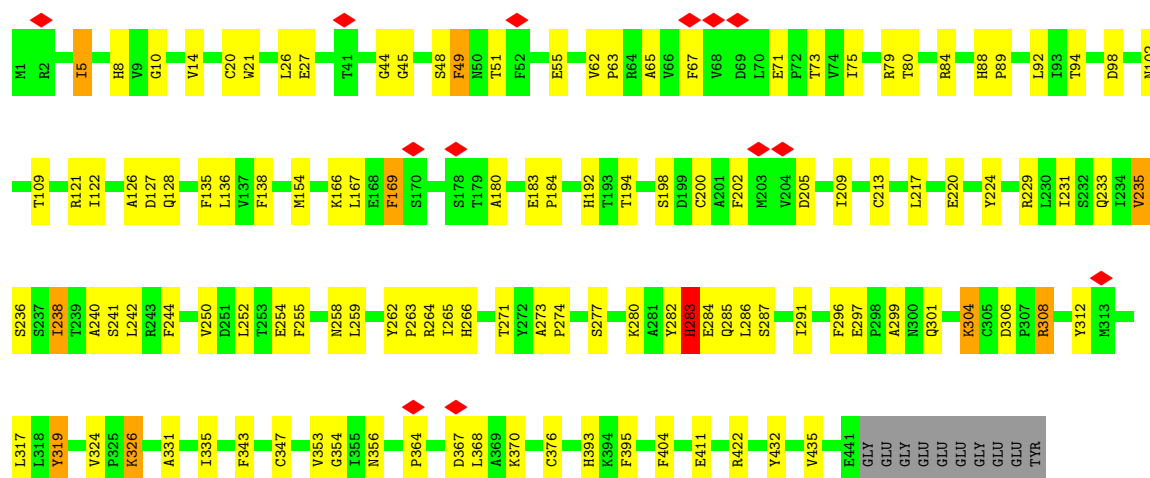
• Molecule 2: Tubulin alpha-1B chain

Chain G: 69% 26% ..



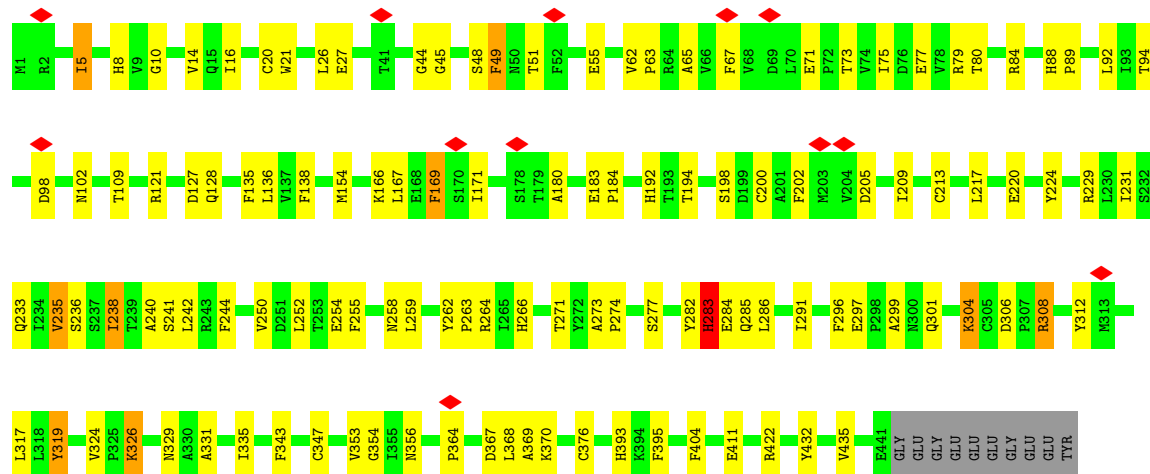
• Molecule 2: Tubulin alpha-1B chain

Chain H: 71% 25% ..



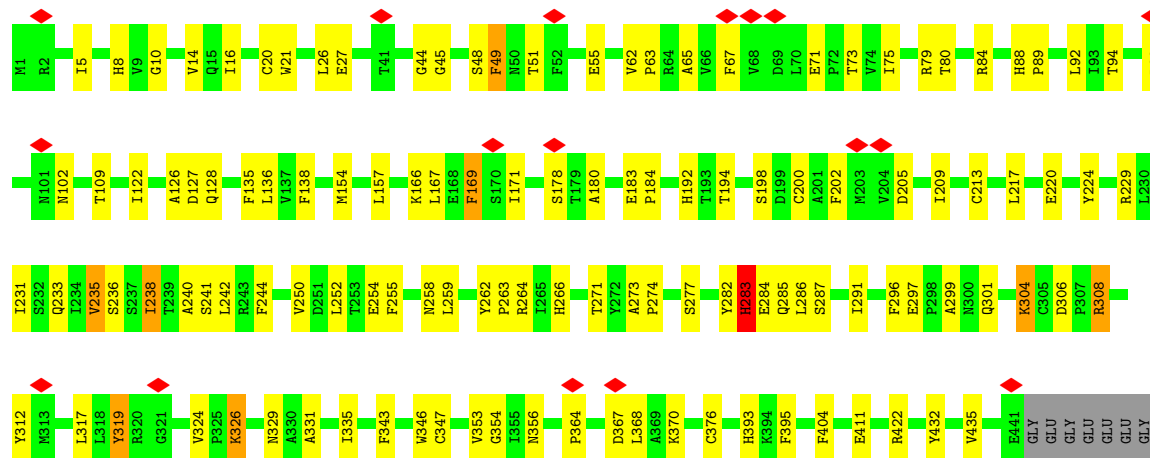
• Molecule 2: Tubulin alpha-1B chain

Chain I: 71% 25%



• Molecule 2: Tubulin alpha-1B chain

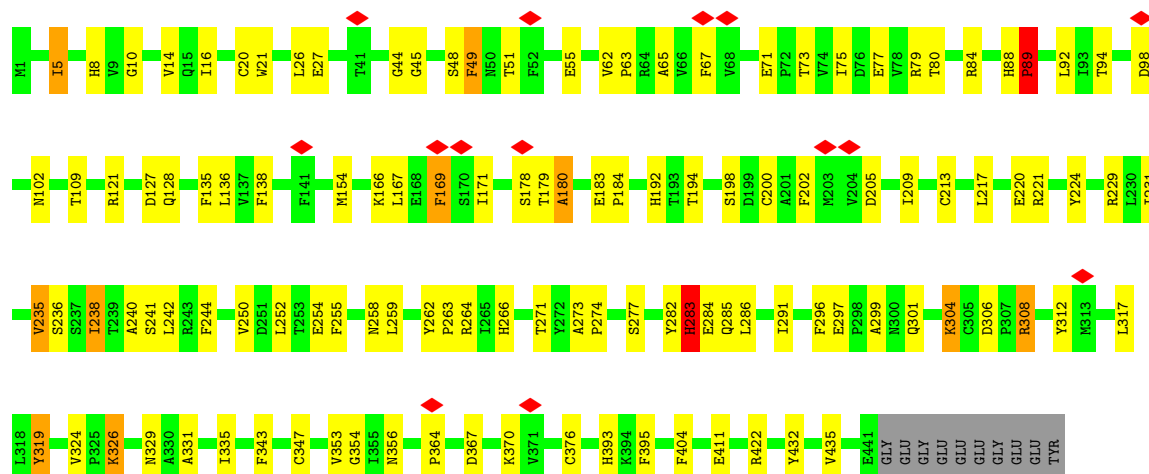
Chain J: 70% 25%



GLU
GLU
TYR

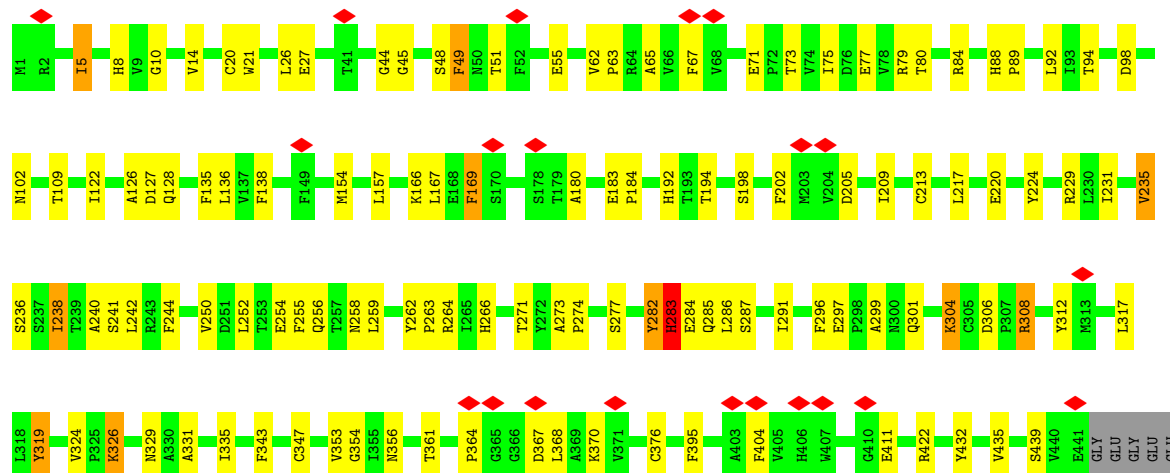
• Molecule 2: Tubulin alpha-1B chain

Chain K:  71% 24%



• Molecule 2: Tubulin alpha-1B chain

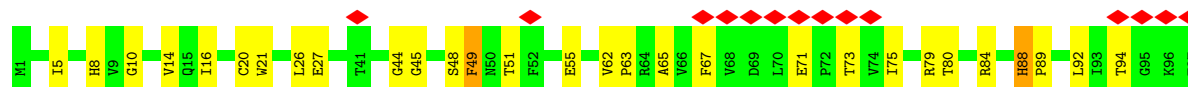
Chain L:  5% 71% 24%

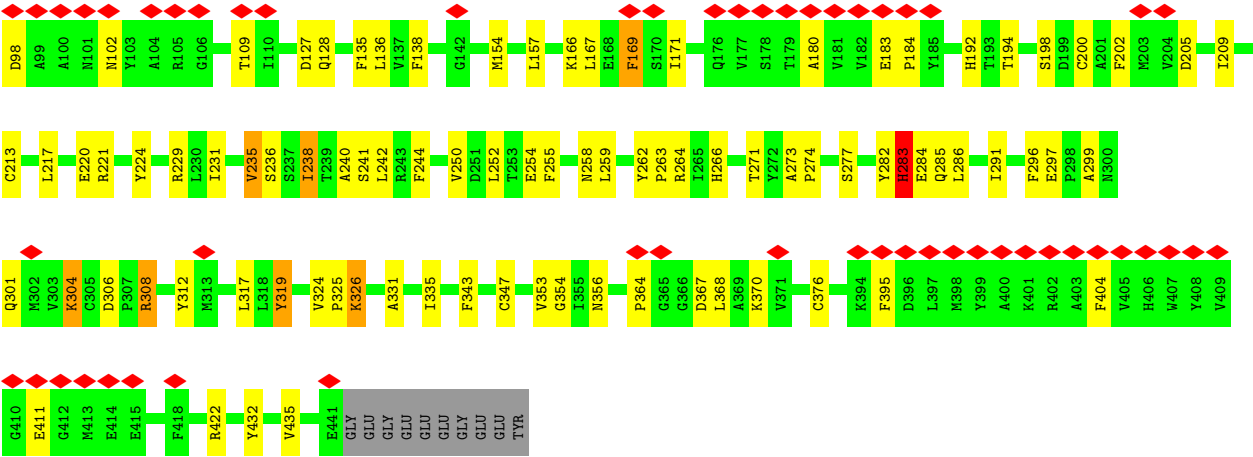


GLU
GLY
GLU
GLU
TYR

• Molecule 2: Tubulin alpha-1B chain

Chain M:  15% 72% 24%





4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-27.68°, rise=9.54 Å, axial sym=C1	Depositor
Number of segments used	11670	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.167	Depositor
Minimum map value	-0.157	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	627.2, 627.2, 627.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.96, 1.96, 1.96	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, TA1, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.74	0/3451	1.51	31/4674 (0.7%)
1	b	0.73	0/3451	1.51	29/4674 (0.6%)
1	c	0.75	1/3451 (0.0%)	1.52	33/4674 (0.7%)
1	d	0.76	2/3451 (0.1%)	1.52	35/4674 (0.7%)
1	e	1.01	4/3451 (0.1%)	1.59	36/4674 (0.8%)
1	f	0.75	1/3451 (0.0%)	1.50	31/4674 (0.7%)
1	g	0.76	0/3451	1.51	32/4674 (0.7%)
1	h	0.75	0/3451	1.51	29/4674 (0.6%)
1	i	0.74	0/3451	1.50	29/4674 (0.6%)
1	j	0.75	0/3451	1.50	30/4674 (0.6%)
1	k	0.76	0/3451	1.50	28/4674 (0.6%)
1	l	0.74	0/3451	1.51	31/4674 (0.7%)
1	m	0.74	0/3451	1.51	28/4674 (0.6%)
1	n	0.75	1/3451 (0.0%)	1.52	34/4674 (0.7%)
1	o	0.75	1/3451 (0.0%)	1.52	36/4674 (0.8%)
1	p	0.73	0/3451	1.52	31/4674 (0.7%)
1	q	0.74	0/3451	1.51	35/4674 (0.7%)
1	r	0.73	0/3451	1.52	32/4674 (0.7%)
1	s	0.72	0/3451	1.50	30/4674 (0.6%)
1	t	0.74	0/3451	1.50	27/4674 (0.6%)
1	u	0.73	0/3451	1.51	31/4674 (0.7%)
1	v	0.73	0/3451	1.51	34/4674 (0.7%)
1	w	0.73	0/3451	1.51	32/4674 (0.7%)
1	x	0.74	1/3451 (0.0%)	1.52	34/4674 (0.7%)
1	y	0.74	1/3451 (0.0%)	1.52	32/4674 (0.7%)
1	z	0.75	1/3451 (0.0%)	1.52	34/4674 (0.7%)
2	A	0.80	1/3524 (0.0%)	1.51	34/4784 (0.7%)
2	B	0.78	0/3524	1.50	32/4784 (0.7%)
2	C	0.77	0/3524	1.53	43/4784 (0.9%)
2	D	0.79	1/3524 (0.0%)	1.55	46/4784 (1.0%)
2	E	0.79	1/3524 (0.0%)	1.53	39/4784 (0.8%)
2	F	0.78	0/3524	1.55	43/4784 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	G	0.78	0/3524	1.54	41/4784 (0.9%)
2	H	0.79	0/3524	1.54	40/4784 (0.8%)
2	I	0.78	0/3524	1.53	43/4784 (0.9%)
2	J	0.78	0/3524	1.52	40/4784 (0.8%)
2	K	0.79	1/3524 (0.0%)	1.54	45/4784 (0.9%)
2	L	0.76	0/3524	1.52	38/4784 (0.8%)
2	M	0.77	1/3524 (0.0%)	1.52	34/4784 (0.7%)
2	N	0.78	1/3524 (0.0%)	1.53	40/4784 (0.8%)
2	O	0.77	0/3524	1.53	38/4784 (0.8%)
2	P	0.81	4/3524 (0.1%)	1.56	38/4784 (0.8%)
2	Q	0.79	1/3524 (0.0%)	1.55	42/4784 (0.9%)
2	R	1.09	1/3524 (0.0%)	1.55	41/4784 (0.9%)
2	S	0.77	0/3524	1.52	38/4784 (0.8%)
2	T	0.79	1/3524 (0.0%)	1.54	40/4784 (0.8%)
2	U	0.77	0/3524	1.53	37/4784 (0.8%)
2	V	0.77	1/3524 (0.0%)	1.53	39/4784 (0.8%)
2	W	0.78	1/3524 (0.0%)	1.53	41/4784 (0.9%)
2	X	0.79	2/3524 (0.1%)	1.53	38/4784 (0.8%)
2	Y	0.79	1/3524 (0.0%)	1.53	41/4784 (0.9%)
2	Z	0.80	2/3524 (0.1%)	1.53	40/4784 (0.8%)
All	All	0.78	33/181350 (0.0%)	1.52	1855/245908 (0.8%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	e	0	1
1	h	0	1
1	i	0	1
2	A	0	1
2	B	0	1
2	C	0	1
2	D	0	1
2	E	0	1
2	F	0	1
2	G	0	1
2	H	0	1
2	I	0	1
2	J	0	1
2	K	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
2	L	0	1
2	M	0	1
2	N	0	1
2	O	0	1
2	P	0	1
2	Q	0	1
2	R	0	1
2	S	0	1
2	T	0	1
2	U	0	1
2	V	0	1
2	W	0	1
2	X	0	1
2	Y	0	1
2	Z	0	1
All	All	0	29

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	43	GLY	C-N	44.65	1.98	1.33
1	e	294	PHE	C-N	34.87	1.83	1.33
2	A	88	HIS	CE1-NE2	12.88	1.45	1.32
2	W	88	HIS	CE1-NE2	-9.48	1.23	1.32
2	N	88	HIS	CE1-NE2	-9.35	1.23	1.32
2	Q	88	HIS	CE1-NE2	-9.35	1.23	1.32
1	e	227	HIS	CE1-NE2	8.12	1.40	1.32
2	Z	88	HIS	CE1-NE2	-8.00	1.24	1.32
1	e	285	THR	C-O	-7.71	1.16	1.24
2	P	283	HIS	ND1-CE1	7.52	1.40	1.32
2	P	88	HIS	CE1-NE2	-7.45	1.25	1.32
2	X	283	HIS	CE1-NE2	7.38	1.40	1.32
2	X	88	HIS	CE1-NE2	-7.28	1.25	1.32
2	P	283	HIS	CE1-NE2	7.24	1.39	1.32
1	n	227	HIS	CE1-NE2	7.21	1.39	1.32
2	T	398	MET	CG-SD	6.83	1.97	1.80
1	o	227	HIS	CE1-NE2	6.78	1.39	1.32
1	c	227	HIS	CE1-NE2	6.73	1.39	1.32
1	z	227	HIS	CE1-NE2	6.73	1.39	1.32
1	y	227	HIS	CE1-NE2	6.52	1.39	1.32
2	D	352	LYS	CG-CD	-6.28	1.33	1.52
2	M	88	HIS	CE1-NE2	6.10	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	283	HIS	CB-CG	6.00	1.58	1.50
1	x	227	HIS	CE1-NE2	5.98	1.38	1.32
2	Y	88	HIS	CE1-NE2	-5.92	1.26	1.32
1	e	285	THR	C-N	5.89	1.40	1.33
1	d	227	HIS	CE1-NE2	5.88	1.38	1.32
2	E	352	LYS	CG-CD	-5.79	1.35	1.52
2	V	88	HIS	CE1-NE2	-5.43	1.27	1.32
1	d	27	GLU	CD-OE2	5.27	1.35	1.25
1	f	22	GLU	CD-OE2	5.27	1.35	1.25
2	Z	283	HIS	CE1-NE2	5.14	1.37	1.32
2	K	179	THR	CA-C	5.09	1.59	1.52

All (1855) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	283	HIS	CA-CB-CG	18.53	132.33	113.80
1	p	99	ASN	CB-CA-C	17.35	136.37	111.73
1	e	294	PHE	CA-C-N	-16.20	95.10	122.64
1	e	294	PHE	C-N-CA	-16.20	95.10	122.64
1	r	99	ASN	CB-CA-C	15.89	134.45	111.89
1	n	99	ASN	CB-CA-C	15.28	133.59	111.89
1	y	99	ASN	CB-CA-C	15.22	133.50	111.89
1	u	99	ASN	CB-CA-C	15.16	133.42	111.89
1	q	99	ASN	CB-CA-C	15.16	133.41	111.89
1	s	99	ASN	CB-CA-C	15.15	133.41	111.89
1	x	99	ASN	CB-CA-C	15.12	133.37	111.89
1	t	99	ASN	CB-CA-C	15.10	133.33	111.89
1	o	99	ASN	CB-CA-C	15.09	133.31	111.89
1	z	99	ASN	CB-CA-C	15.07	133.29	111.89
1	v	99	ASN	CB-CA-C	15.05	133.26	111.89
1	d	99	ASN	CB-CA-C	15.02	133.21	111.89
1	b	99	ASN	CB-CA-C	14.95	133.11	111.89
1	c	99	ASN	CB-CA-C	14.89	133.04	111.89
1	w	99	ASN	CB-CA-C	14.86	133.00	111.89
1	l	99	ASN	CB-CA-C	14.85	132.97	111.89
1	e	99	ASN	CB-CA-C	14.80	132.91	111.89
1	e	294	PHE	O-C-N	14.78	139.84	122.25
1	m	99	ASN	CB-CA-C	14.77	132.86	111.89
1	a	99	ASN	CB-CA-C	14.70	132.76	111.89
1	h	99	ASN	CB-CA-C	14.61	132.64	111.89
1	i	99	ASN	CB-CA-C	14.59	132.61	111.89
1	f	99	ASN	CB-CA-C	14.22	132.09	111.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	k	99	ASN	CB-CA-C	13.99	131.75	111.89
1	g	99	ASN	CB-CA-C	13.80	131.49	111.89
1	j	99	ASN	CB-CA-C	13.63	131.24	111.89
2	Q	247	ALA	N-CA-CB	-12.97	90.25	109.83
2	P	370	LYS	CB-CG-CD	11.96	138.81	111.30
1	z	222	TYR	CA-CB-CG	11.89	135.31	113.90
1	p	99	ASN	CB-CG-ND2	11.81	134.11	116.40
1	p	99	ASN	OD1-CG-ND2	-11.31	111.28	122.60
2	K	178	SER	CA-C-O	-11.23	108.94	121.40
1	p	242	PHE	CA-CB-CG	-11.03	102.77	113.80
1	t	242	PHE	CA-CB-CG	-10.88	102.92	113.80
1	s	242	PHE	CA-CB-CG	-10.88	102.92	113.80
2	U	376	CYS	CB-CA-C	-10.78	91.75	109.53
2	T	376	CYS	CB-CA-C	-10.73	91.82	109.53
2	V	376	CYS	CB-CA-C	-10.72	91.83	109.53
2	S	376	CYS	CB-CA-C	-10.71	91.86	109.53
2	W	376	CYS	CB-CA-C	-10.71	91.86	109.53
2	R	376	CYS	CB-CA-C	-10.69	91.89	109.53
2	P	376	CYS	CB-CA-C	-10.66	91.94	109.53
2	X	376	CYS	CB-CA-C	-10.64	91.98	109.53
2	N	376	CYS	CB-CA-C	-10.63	91.99	109.53
2	O	376	CYS	CB-CA-C	-10.63	91.99	109.53
2	Q	376	CYS	CB-CA-C	-10.63	91.99	109.53
2	C	376	CYS	CB-CA-C	-10.61	92.03	109.53
2	G	376	CYS	CB-CA-C	-10.60	92.03	109.53
2	F	376	CYS	CB-CA-C	-10.60	92.04	109.53
2	I	376	CYS	CB-CA-C	-10.58	92.07	109.53
2	M	376	CYS	CB-CA-C	-10.58	92.08	109.53
2	E	376	CYS	CB-CA-C	-10.57	92.08	109.53
2	H	376	CYS	CB-CA-C	-10.56	92.10	109.53
2	J	376	CYS	CB-CA-C	-10.50	92.21	109.53
2	Z	376	CYS	CB-CA-C	-10.46	92.27	109.53
2	L	376	CYS	CB-CA-C	-10.45	92.28	109.53
1	r	242	PHE	CA-CB-CG	-10.45	103.35	113.80
2	Q	247	ALA	CB-CA-C	-10.45	92.38	109.72
2	A	376	CYS	CB-CA-C	-10.44	92.30	109.53
2	Y	376	CYS	CB-CA-C	-10.40	92.38	109.53
2	K	376	CYS	CB-CA-C	-10.38	92.41	109.53
1	y	222	TYR	CA-CB-CG	10.35	132.52	113.90
1	u	242	PHE	CA-CB-CG	-10.34	103.46	113.80
2	D	376	CYS	CB-CA-C	-10.33	92.49	109.53
1	y	242	PHE	CA-CB-CG	-10.26	103.54	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	376	CYS	CB-CA-C	-10.26	92.24	109.48
1	z	242	PHE	CA-CB-CG	-10.18	103.62	113.80
1	o	222	TYR	CA-CB-CG	10.15	132.16	113.90
1	v	242	PHE	CA-CB-CG	-10.15	103.65	113.80
1	w	242	PHE	CA-CB-CG	-10.08	103.72	113.80
1	n	222	TYR	CA-CB-CG	10.07	132.03	113.90
1	o	242	PHE	CA-CB-CG	-10.04	103.76	113.80
2	P	224	TYR	CA-CB-CG	10.01	131.92	113.90
1	b	242	PHE	CA-CB-CG	-10.01	103.79	113.80
1	g	242	PHE	CA-CB-CG	-10.00	103.80	113.80
1	a	242	PHE	CA-CB-CG	-9.99	103.81	113.80
1	x	242	PHE	CA-CB-CG	-9.98	103.81	113.80
1	i	242	PHE	CA-CB-CG	-9.97	103.83	113.80
1	n	242	PHE	CA-CB-CG	-9.96	103.84	113.80
1	h	242	PHE	CA-CB-CG	-9.96	103.84	113.80
1	m	242	PHE	CA-CB-CG	-9.96	103.84	113.80
1	w	222	TYR	CA-CB-CG	9.95	131.81	113.90
1	q	242	PHE	CA-CB-CG	-9.91	103.89	113.80
1	c	242	PHE	CA-CB-CG	-9.91	103.89	113.80
1	j	242	PHE	CA-CB-CG	-9.88	103.92	113.80
1	k	242	PHE	CA-CB-CG	-9.86	103.94	113.80
1	l	242	PHE	CA-CB-CG	-9.83	103.97	113.80
1	x	222	TYR	CA-CB-CG	9.82	131.58	113.90
1	e	242	PHE	CA-CB-CG	-9.82	103.98	113.80
1	d	242	PHE	CA-CB-CG	-9.79	104.00	113.80
1	f	242	PHE	CA-CB-CG	-9.75	104.05	113.80
1	v	222	TYR	CA-CB-CG	9.61	131.19	113.90
1	s	222	TYR	CA-CB-CG	9.56	131.11	113.90
1	t	222	TYR	CA-CB-CG	9.56	131.12	113.90
1	u	222	TYR	CA-CB-CG	9.56	131.12	113.90
2	H	283	HIS	CA-CB-CG	9.18	122.98	113.80
2	K	283	HIS	CA-CB-CG	9.00	122.80	113.80
1	a	222	TYR	CA-CB-CG	8.96	130.02	113.90
1	q	222	TYR	CA-CB-CG	8.82	129.78	113.90
1	b	222	TYR	CA-CB-CG	8.72	129.60	113.90
2	Y	235	VAL	N-CA-CB	-8.68	97.56	110.58
1	r	222	TYR	CA-CB-CG	8.66	129.48	113.90
2	X	235	VAL	N-CA-CB	-8.65	97.61	110.58
2	Z	235	VAL	N-CA-CB	-8.64	97.61	110.58
2	D	235	VAL	N-CA-CB	-8.63	97.64	110.58
2	V	235	VAL	N-CA-CB	-8.62	97.65	110.58
2	N	235	VAL	N-CA-CB	-8.62	97.65	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	235	VAL	N-CA-CB	-8.61	97.66	110.58
2	W	235	VAL	N-CA-CB	-8.60	97.69	110.58
2	U	235	VAL	N-CA-CB	-8.58	97.71	110.58
2	B	283	HIS	CA-CB-CG	8.58	122.38	113.80
2	B	235	VAL	N-CA-CB	-8.57	97.72	110.58
2	A	235	VAL	N-CA-CB	-8.56	97.74	110.58
2	E	235	VAL	N-CA-CB	-8.56	97.74	110.58
2	R	235	VAL	N-CA-CB	-8.55	97.75	110.58
2	J	235	VAL	N-CA-CB	-8.56	97.75	110.58
2	O	235	VAL	N-CA-CB	-8.55	97.76	110.58
2	G	235	VAL	N-CA-CB	-8.52	97.80	110.58
2	S	235	VAL	N-CA-CB	-8.52	97.80	110.58
1	p	222	TYR	CA-CB-CG	8.51	129.22	113.90
2	G	283	HIS	CA-CB-CG	8.51	122.31	113.80
2	Q	235	VAL	N-CA-CB	-8.49	97.84	110.58
2	C	235	VAL	N-CA-CB	-8.49	97.84	110.58
2	T	235	VAL	N-CA-CB	-8.48	97.86	110.58
2	P	235	VAL	N-CA-CB	-8.47	97.88	110.58
2	I	235	VAL	N-CA-CB	-8.46	97.89	110.58
2	T	283	HIS	CA-CB-CG	8.46	122.25	113.80
2	L	235	VAL	N-CA-CB	-8.45	97.91	110.58
2	H	235	VAL	N-CA-CB	-8.44	97.92	110.58
2	F	235	VAL	N-CA-CB	-8.41	97.96	110.58
2	M	235	VAL	N-CA-CB	-8.40	97.98	110.58
2	Y	283	HIS	CA-CB-CG	8.25	122.05	113.80
1	m	222	TYR	CA-CB-CG	8.16	128.59	113.90
2	A	283	HIS	CA-CB-CG	8.13	121.93	113.80
2	V	283	HIS	CA-CB-CG	8.10	121.90	113.80
2	I	283	HIS	CA-CB-CG	8.06	121.86	113.80
2	M	283	HIS	CA-CB-CG	8.02	121.82	113.80
2	X	283	HIS	CA-CB-CG	8.00	121.80	113.80
2	R	283	HIS	CA-CB-CG	8.00	121.80	113.80
2	J	283	HIS	CA-CB-CG	7.99	121.79	113.80
2	D	283	HIS	CA-CB-CG	7.97	121.77	113.80
2	K	178	SER	O-C-N	7.97	133.38	122.78
2	N	283	HIS	CA-CB-CG	7.85	121.65	113.80
2	Z	283	HIS	CA-CB-CG	7.85	121.65	113.80
2	W	283	HIS	CA-CB-CG	7.78	121.58	113.80
2	U	283	HIS	CA-CB-CG	7.78	121.58	113.80
2	D	229	ARG	CG-CD-NE	-7.77	94.91	112.00
1	m	222	TYR	CA-C-N	7.76	128.72	120.03
1	m	222	TYR	C-N-CA	7.76	128.72	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Q	283	HIS	CA-CB-CG	7.73	121.53	113.80
1	p	140	GLY	CA-C-N	7.62	130.14	122.30
1	p	140	GLY	C-N-CA	7.62	130.14	122.30
2	O	282	TYR	CA-C-N	-7.61	111.19	122.07
2	O	282	TYR	C-N-CA	-7.61	111.19	122.07
1	w	222	TYR	CA-C-N	7.61	128.55	120.03
1	w	222	TYR	C-N-CA	7.61	128.55	120.03
2	P	282	TYR	O-C-N	-7.59	112.11	121.83
2	K	180	ALA	CA-C-O	-7.57	112.19	120.36
2	M	370	LYS	CB-CG-CD	7.56	128.69	111.30
1	l	222	TYR	CA-C-N	7.55	128.49	120.03
1	l	222	TYR	C-N-CA	7.55	128.49	120.03
2	R	85	GLN	OE1-CD-NE2	7.55	130.15	122.60
1	e	368	ILE	CB-CG1-CD1	7.55	129.65	113.80
2	Q	247	ALA	CA-C-O	-7.52	112.91	121.19
1	v	222	TYR	CA-C-N	7.51	128.44	120.03
1	v	222	TYR	C-N-CA	7.51	128.44	120.03
1	e	140	GLY	CA-C-N	7.49	130.02	122.30
1	e	140	GLY	C-N-CA	7.49	130.02	122.30
1	t	222	TYR	CA-C-N	7.45	128.38	120.03
1	t	222	TYR	C-N-CA	7.45	128.38	120.03
2	O	229	ARG	CG-CD-NE	-7.45	95.62	112.00
1	e	222	TYR	CA-CB-CG	7.44	127.30	113.90
1	u	222	TYR	CA-C-N	7.43	128.36	120.03
1	u	222	TYR	C-N-CA	7.43	128.36	120.03
2	N	282	TYR	CA-C-N	-7.43	111.44	122.07
2	N	282	TYR	C-N-CA	-7.43	111.44	122.07
1	t	140	GLY	CA-C-N	7.42	129.94	122.30
1	t	140	GLY	C-N-CA	7.42	129.94	122.30
1	q	358	PRO	N-CA-CB	7.39	110.34	103.39
1	d	222	TYR	CA-CB-CG	7.39	127.20	113.90
1	s	222	TYR	CA-C-N	7.39	128.30	120.03
1	s	222	TYR	C-N-CA	7.39	128.30	120.03
1	o	350	LYS	CB-CG-CD	7.38	128.28	111.30
1	f	222	TYR	CA-C-N	7.38	128.29	120.03
1	f	222	TYR	C-N-CA	7.38	128.29	120.03
1	h	140	GLY	CA-C-N	7.37	129.90	122.30
1	h	140	GLY	C-N-CA	7.37	129.90	122.30
2	R	282	TYR	CA-C-N	-7.36	111.54	122.07
2	R	282	TYR	C-N-CA	-7.36	111.54	122.07
1	s	140	GLY	CA-C-N	7.36	129.88	122.30
1	s	140	GLY	C-N-CA	7.36	129.88	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	283	HIS	CA-CB-CG	7.33	121.13	113.80
2	D	370	LYS	CB-CG-CD	7.33	128.16	111.30
1	c	222	TYR	CA-CB-CG	7.32	127.08	113.90
2	Y	282	TYR	CA-C-N	-7.31	111.62	122.07
2	Y	282	TYR	C-N-CA	-7.31	111.62	122.07
1	x	222	TYR	CA-C-N	7.30	128.21	120.03
1	x	222	TYR	C-N-CA	7.30	128.21	120.03
1	g	276	ARG	CB-CG-CD	7.30	128.09	111.30
1	a	140	GLY	CA-C-N	7.30	129.81	122.30
1	a	140	GLY	C-N-CA	7.30	129.81	122.30
1	i	140	GLY	CA-C-N	7.29	129.81	122.30
1	i	140	GLY	C-N-CA	7.29	129.81	122.30
1	y	222	TYR	CA-C-N	7.28	128.19	120.03
1	y	222	TYR	C-N-CA	7.28	128.19	120.03
1	a	222	TYR	CA-C-N	7.27	128.17	120.03
1	a	222	TYR	C-N-CA	7.27	128.17	120.03
1	c	140	GLY	CA-C-N	7.25	129.77	122.30
1	c	140	GLY	C-N-CA	7.25	129.77	122.30
2	Z	282	TYR	CA-C-N	-7.24	111.72	122.07
2	Z	282	TYR	C-N-CA	-7.24	111.72	122.07
1	z	222	TYR	CA-C-N	7.23	128.12	120.03
1	z	222	TYR	C-N-CA	7.23	128.12	120.03
1	q	140	GLY	CA-C-N	7.22	129.74	122.30
1	q	140	GLY	C-N-CA	7.22	129.74	122.30
1	j	140	GLY	CA-C-N	7.22	129.74	122.30
1	j	140	GLY	C-N-CA	7.22	129.74	122.30
1	f	222	TYR	CA-CB-CG	7.21	126.87	113.90
1	u	140	GLY	CA-C-N	7.21	129.72	122.30
1	u	140	GLY	C-N-CA	7.21	129.72	122.30
2	R	404	PHE	CA-CB-CG	7.21	121.01	113.80
1	e	222	TYR	CA-C-N	7.20	128.09	120.03
1	e	222	TYR	C-N-CA	7.20	128.09	120.03
2	W	282	TYR	CA-C-N	-7.20	111.78	122.07
2	W	282	TYR	C-N-CA	-7.20	111.78	122.07
2	X	282	TYR	CA-C-N	-7.18	111.80	122.07
2	X	282	TYR	C-N-CA	-7.18	111.80	122.07
2	Q	282	TYR	CA-C-N	-7.16	111.84	122.07
2	Q	282	TYR	C-N-CA	-7.16	111.84	122.07
1	o	222	TYR	CA-C-N	7.16	128.04	120.03
1	o	222	TYR	C-N-CA	7.16	128.04	120.03
2	H	224	TYR	CA-CB-CG	7.15	126.77	113.90
1	i	222	TYR	CA-C-N	7.13	128.02	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	i	222	TYR	C-N-CA	7.13	128.02	120.03
2	X	89	PRO	N-CD-CG	-7.13	92.51	103.20
1	j	222	TYR	CA-C-N	7.12	128.01	120.03
1	j	222	TYR	C-N-CA	7.12	128.01	120.03
2	C	282	TYR	CA-C-N	-7.12	111.89	122.07
2	C	282	TYR	C-N-CA	-7.12	111.89	122.07
1	k	276	ARG	CB-CG-CD	7.12	127.67	111.30
1	b	222	TYR	CA-C-N	7.10	127.99	120.03
1	b	222	TYR	C-N-CA	7.10	127.99	120.03
2	Q	229	ARG	CG-CD-NE	-7.08	96.41	112.00
1	m	140	GLY	CA-C-N	7.08	129.59	122.30
1	m	140	GLY	C-N-CA	7.08	129.59	122.30
1	k	222	TYR	CA-C-N	7.07	127.95	120.03
1	k	222	TYR	C-N-CA	7.07	127.95	120.03
2	E	283	HIS	CA-CB-CG	7.07	120.87	113.80
1	p	222	TYR	CA-C-N	7.07	127.95	120.03
1	p	222	TYR	C-N-CA	7.07	127.95	120.03
2	D	338	LYS	CG-CD-CE	7.06	127.54	111.30
1	g	222	TYR	CA-C-N	7.06	127.94	120.03
1	g	222	TYR	C-N-CA	7.06	127.94	120.03
1	g	87	PRO	N-CA-CB	7.05	110.65	103.25
1	h	276	ARG	CB-CG-CD	7.04	127.49	111.30
1	a	276	ARG	CB-CG-CD	7.04	127.48	111.30
1	n	222	TYR	CA-C-N	7.03	127.91	120.03
1	n	222	TYR	C-N-CA	7.03	127.91	120.03
1	q	222	TYR	CA-C-N	7.03	127.90	120.03
1	q	222	TYR	C-N-CA	7.03	127.90	120.03
2	R	229	ARG	CG-CD-NE	-7.01	96.58	112.00
1	l	140	GLY	CA-C-N	7.00	129.51	122.30
1	l	140	GLY	C-N-CA	7.00	129.51	122.30
2	P	404	PHE	CA-CB-CG	6.99	120.79	113.80
2	Q	404	PHE	CA-CB-CG	6.99	120.79	113.80
2	A	404	PHE	CA-CB-CG	6.99	120.78	113.80
1	r	222	TYR	CA-C-N	6.98	127.85	120.03
1	r	222	TYR	C-N-CA	6.98	127.85	120.03
2	G	404	PHE	CA-CB-CG	6.98	120.78	113.80
2	L	404	PHE	CA-CB-CG	6.98	120.78	113.80
1	z	178	THR	CB-CA-C	-6.96	98.51	109.72
1	d	222	TYR	CA-C-N	6.96	127.82	120.03
1	d	222	TYR	C-N-CA	6.96	127.82	120.03
1	x	257	MET	N-CA-C	-6.95	105.34	114.31
2	B	404	PHE	CA-CB-CG	6.95	120.75	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	e	178	THR	CB-CA-C	-6.95	98.53	109.72
2	N	229	ARG	CG-CD-NE	-6.95	96.71	112.00
1	y	178	THR	CB-CA-C	-6.95	98.53	109.72
1	e	286	VAL	CA-CB-CG2	6.94	122.20	110.40
1	e	276	ARG	CB-CG-CD	6.92	127.21	111.30
2	H	404	PHE	CA-CB-CG	6.92	120.72	113.80
1	n	178	THR	CB-CA-C	-6.92	98.58	109.72
2	R	43	GLY	CA-C-O	-6.91	108.54	120.57
2	U	229	ARG	CG-CD-NE	-6.91	96.79	112.00
2	M	404	PHE	CA-CB-CG	6.91	120.71	113.80
1	o	178	THR	CB-CA-C	-6.91	98.60	109.72
1	c	178	THR	CB-CA-C	-6.90	98.61	109.72
2	Y	404	PHE	CA-CB-CG	6.90	120.70	113.80
2	S	404	PHE	CA-CB-CG	6.89	120.69	113.80
1	r	140	GLY	CA-C-N	6.89	129.40	122.30
1	r	140	GLY	C-N-CA	6.89	129.40	122.30
2	P	229	ARG	CG-CD-NE	-6.89	96.84	112.00
2	X	229	ARG	CG-CD-NE	-6.89	96.84	112.00
2	Y	229	ARG	CG-CD-NE	-6.89	96.85	112.00
2	C	224	TYR	CA-CB-CG	6.88	126.29	113.90
1	c	222	TYR	CA-C-N	6.87	127.73	120.03
1	c	222	TYR	C-N-CA	6.87	127.73	120.03
2	Z	404	PHE	CA-CB-CG	6.87	120.67	113.80
2	T	229	ARG	CG-CD-NE	-6.87	96.89	112.00
1	d	178	THR	CB-CA-C	-6.86	98.67	109.72
1	u	257	MET	N-CA-C	-6.86	105.84	114.56
2	F	283	HIS	CA-CB-CG	6.86	120.66	113.80
1	h	222	TYR	CA-C-N	6.86	127.71	120.03
1	h	222	TYR	C-N-CA	6.86	127.71	120.03
2	T	282	TYR	CA-C-N	-6.86	112.27	122.07
2	T	282	TYR	C-N-CA	-6.86	112.27	122.07
2	O	283	HIS	CA-CB-CG	6.86	120.66	113.80
2	Z	229	ARG	CG-CD-NE	-6.85	96.92	112.00
2	M	229	ARG	CG-CD-NE	-6.85	96.93	112.00
1	p	257	MET	N-CA-C	-6.84	105.87	114.56
2	V	404	PHE	CA-CB-CG	6.84	120.64	113.80
2	L	229	ARG	CG-CD-NE	-6.83	96.97	112.00
2	V	229	ARG	CG-CD-NE	-6.83	96.97	112.00
2	F	404	PHE	CA-CB-CG	6.83	120.63	113.80
2	J	404	PHE	CA-CB-CG	6.83	120.63	113.80
2	O	404	PHE	CA-CB-CG	6.82	120.62	113.80
1	r	99	ASN	CB-CG-ND2	6.82	126.64	116.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	180	ALA	CA-C-N	-6.82	110.72	121.02
2	F	180	ALA	C-N-CA	-6.82	110.72	121.02
2	C	229	ARG	CG-CD-NE	-6.82	97.00	112.00
1	m	276	ARG	CB-CG-CD	6.81	126.97	111.30
2	P	49	PHE	N-CA-C	-6.81	104.94	113.18
2	S	282	TYR	CA-C-N	-6.81	112.33	122.07
2	S	282	TYR	C-N-CA	-6.81	112.33	122.07
2	V	282	TYR	CA-C-N	-6.81	112.34	122.07
2	V	282	TYR	C-N-CA	-6.81	112.34	122.07
1	s	257	MET	N-CA-C	-6.81	105.92	114.56
2	N	404	PHE	CA-CB-CG	6.80	120.61	113.80
1	x	140	GLY	CA-C-N	6.80	129.31	122.30
1	x	140	GLY	C-N-CA	6.80	129.31	122.30
2	W	404	PHE	CA-CB-CG	6.80	120.60	113.80
2	A	229	ARG	CG-CD-NE	-6.80	97.04	112.00
2	T	404	PHE	CA-CB-CG	6.80	120.60	113.80
2	W	229	ARG	CG-CD-NE	-6.79	97.06	112.00
2	U	404	PHE	CA-CB-CG	6.79	120.59	113.80
2	A	49	PHE	N-CA-C	-6.79	104.97	113.18
2	F	282	TYR	CA-C-N	-6.79	112.37	122.07
2	F	282	TYR	C-N-CA	-6.79	112.37	122.07
2	R	49	PHE	N-CA-C	-6.78	104.97	113.18
1	r	358	PRO	N-CA-CB	6.78	109.77	103.39
2	Q	49	PHE	N-CA-C	-6.77	104.99	113.18
2	X	49	PHE	N-CA-C	-6.76	105.00	113.18
2	S	192	HIS	CA-CB-CG	-6.76	107.04	113.80
2	O	49	PHE	N-CA-C	-6.76	105.00	113.18
2	C	404	PHE	CA-CB-CG	6.76	120.56	113.80
2	P	192	HIS	CA-CB-CG	-6.75	107.05	113.80
2	U	282	TYR	CA-C-N	-6.74	112.42	122.07
2	U	282	TYR	C-N-CA	-6.74	112.42	122.07
2	E	49	PHE	N-CA-C	-6.74	105.02	113.18
2	E	229	ARG	CG-CD-NE	-6.74	97.17	112.00
2	U	192	HIS	CA-CB-CG	-6.74	107.06	113.80
2	T	192	HIS	CA-CB-CG	-6.73	107.07	113.80
2	I	404	PHE	CA-CB-CG	6.73	120.53	113.80
1	t	257	MET	N-CA-C	-6.73	106.02	114.56
2	M	49	PHE	N-CA-C	-6.73	105.04	113.18
2	K	229	ARG	CG-CD-NE	-6.72	97.21	112.00
2	L	49	PHE	N-CA-C	-6.72	105.04	113.18
2	N	192	HIS	CA-CB-CG	-6.72	107.08	113.80
1	g	140	GLY	CA-C-N	6.72	129.22	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	g	140	GLY	C-N-CA	6.72	129.22	122.30
2	O	192	HIS	CA-CB-CG	-6.72	107.08	113.80
2	Y	49	PHE	N-CA-C	-6.71	105.06	113.18
2	S	49	PHE	N-CA-C	-6.71	105.06	113.18
2	V	192	HIS	CA-CB-CG	-6.71	107.09	113.80
2	Y	192	HIS	CA-CB-CG	-6.71	107.09	113.80
2	H	180	ALA	CA-C-N	-6.71	110.89	121.02
2	H	180	ALA	C-N-CA	-6.71	110.89	121.02
2	S	229	ARG	CG-CD-NE	-6.71	97.24	112.00
2	W	192	HIS	CA-CB-CG	-6.71	107.09	113.80
2	J	49	PHE	N-CA-C	-6.71	105.06	113.18
1	y	140	GLY	CA-C-N	6.71	129.21	122.30
1	y	140	GLY	C-N-CA	6.71	129.21	122.30
2	D	192	HIS	CA-CB-CG	-6.70	107.10	113.80
2	D	404	PHE	CA-CB-CG	6.70	120.50	113.80
2	F	192	HIS	CA-CB-CG	-6.70	107.10	113.80
2	C	49	PHE	N-CA-C	-6.70	105.08	113.18
2	T	49	PHE	N-CA-C	-6.69	105.08	113.18
2	D	352	LYS	CB-CG-CD	6.69	126.69	111.30
2	E	192	HIS	CA-CB-CG	-6.69	107.11	113.80
2	G	192	HIS	CA-CB-CG	-6.69	107.11	113.80
2	C	192	HIS	CA-CB-CG	-6.69	107.11	113.80
2	J	192	HIS	CA-CB-CG	-6.69	107.11	113.80
2	Z	49	PHE	N-CA-C	-6.69	105.09	113.18
2	Z	192	HIS	CA-CB-CG	-6.69	107.11	113.80
2	F	224	TYR	CA-CB-CG	6.68	125.93	113.90
2	B	229	ARG	CG-CD-NE	-6.68	97.30	112.00
2	S	283	HIS	CA-CB-CG	6.68	120.48	113.80
2	N	49	PHE	N-CA-C	-6.68	105.10	113.18
2	Q	192	HIS	CA-CB-CG	-6.68	107.12	113.80
2	E	352	LYS	CB-CG-CD	6.68	126.66	111.30
2	H	229	ARG	CG-CD-NE	-6.68	97.30	112.00
2	D	49	PHE	N-CA-C	-6.68	105.10	113.18
2	R	192	HIS	CA-CB-CG	-6.67	107.12	113.80
2	K	404	PHE	CA-CB-CG	6.67	120.47	113.80
2	B	192	HIS	CA-CB-CG	-6.67	107.13	113.80
2	K	49	PHE	N-CA-C	-6.67	105.11	113.18
2	A	192	HIS	CA-CB-CG	-6.67	107.13	113.80
2	K	192	HIS	CA-CB-CG	-6.66	107.14	113.80
2	H	49	PHE	N-CA-C	-6.66	105.12	113.18
2	L	192	HIS	CA-CB-CG	-6.66	107.14	113.80
2	I	229	ARG	CG-CD-NE	-6.66	97.35	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	49	PHE	N-CA-C	-6.66	105.13	113.18
2	F	229	ARG	CG-CD-NE	-6.66	97.36	112.00
2	M	192	HIS	CA-CB-CG	-6.66	107.14	113.80
2	W	49	PHE	N-CA-C	-6.65	105.14	113.18
2	X	192	HIS	CA-CB-CG	-6.65	107.15	113.80
2	I	49	PHE	N-CA-C	-6.64	105.14	113.18
2	I	192	HIS	CA-CB-CG	-6.64	107.16	113.80
1	n	257	MET	N-CA-C	-6.64	105.74	114.31
1	j	276	ARG	CB-CG-CD	6.64	126.57	111.30
2	H	192	HIS	CA-CB-CG	-6.64	107.16	113.80
2	G	180	ALA	CA-C-N	-6.64	111.00	121.02
2	G	180	ALA	C-N-CA	-6.64	111.00	121.02
2	B	49	PHE	N-CA-C	-6.62	105.16	113.18
2	G	224	TYR	CA-CB-CG	6.62	125.82	113.90
2	V	49	PHE	N-CA-C	-6.62	105.17	113.18
2	U	49	PHE	N-CA-C	-6.62	105.17	113.18
1	c	276	ARG	CB-CG-CD	6.61	126.50	111.30
1	l	222	TYR	CA-CB-CG	6.61	125.79	113.90
1	l	276	ARG	CB-CG-CD	6.61	126.50	111.30
1	b	257	MET	N-CA-C	-6.60	105.80	114.31
1	v	140	GLY	CA-C-N	6.60	129.09	122.30
1	v	140	GLY	C-N-CA	6.60	129.09	122.30
2	X	404	PHE	CA-CB-CG	6.59	120.39	113.80
1	w	257	MET	N-CA-C	-6.59	105.81	114.31
2	G	49	PHE	N-CA-C	-6.59	105.21	113.18
1	a	257	MET	N-CA-C	-6.58	105.82	114.31
2	E	404	PHE	CA-CB-CG	6.58	120.38	113.80
2	J	229	ARG	CG-CD-NE	-6.57	97.54	112.00
1	j	257	MET	N-CA-C	-6.57	105.84	114.31
2	G	229	ARG	CG-CD-NE	-6.57	97.55	112.00
2	Y	89	PRO	N-CD-CG	-6.56	93.36	103.20
2	K	180	ALA	CA-C-N	-6.56	111.11	121.02
2	K	180	ALA	C-N-CA	-6.56	111.11	121.02
2	R	368	LEU	N-CA-CB	6.55	119.81	110.44
1	q	257	MET	N-CA-C	-6.55	105.86	114.31
2	I	224	TYR	CA-CB-CG	6.54	125.68	113.90
1	d	140	GLY	CA-C-N	6.54	129.04	122.30
1	d	140	GLY	C-N-CA	6.54	129.04	122.30
1	b	140	GLY	CA-C-N	6.54	129.03	122.30
1	b	140	GLY	C-N-CA	6.54	129.03	122.30
1	u	182	PRO	CB-CA-C	-6.53	102.75	112.55
1	i	257	MET	N-CA-C	-6.53	105.88	114.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	h	257	MET	N-CA-C	-6.53	105.89	114.31
1	g	257	MET	N-CA-C	-6.53	105.89	114.31
1	t	182	PRO	CB-CA-C	-6.52	102.77	112.55
1	w	140	GLY	CA-C-N	6.52	129.01	122.30
1	w	140	GLY	C-N-CA	6.52	129.01	122.30
1	e	294	PHE	CA-C-O	-6.51	111.90	119.59
1	y	182	PRO	CB-CA-C	-6.51	102.79	112.55
1	d	257	MET	N-CA-C	-6.50	105.92	114.31
2	A	367	ASP	CB-CA-C	6.49	120.60	109.24
2	B	367	ASP	CB-CA-C	6.49	120.61	109.24
1	z	140	GLY	CA-C-N	6.49	128.99	122.30
1	z	140	GLY	C-N-CA	6.49	128.99	122.30
1	m	257	MET	N-CA-C	-6.48	105.95	114.31
1	n	140	GLY	CA-C-N	6.47	128.97	122.30
1	n	140	GLY	C-N-CA	6.47	128.97	122.30
2	E	367	ASP	CB-CA-C	6.46	120.54	109.24
1	r	257	MET	N-CA-C	-6.45	105.98	114.31
1	s	182	PRO	CB-CA-C	-6.45	102.88	112.55
1	w	182	PRO	CB-CA-C	-6.45	102.88	112.55
1	p	182	PRO	CB-CA-C	-6.45	102.88	112.55
2	K	367	ASP	CB-CA-C	6.44	120.52	109.24
1	z	182	PRO	CB-CA-C	-6.44	102.89	112.55
1	h	182	PRO	CB-CA-C	-6.44	102.89	112.55
1	l	257	MET	N-CA-C	-6.44	106.00	114.31
1	n	182	PRO	CB-CA-C	-6.44	102.90	112.55
1	z	257	MET	N-CA-C	-6.43	106.01	114.31
2	L	224	TYR	CA-CB-CG	6.43	125.48	113.90
2	C	283	HIS	CA-CB-CG	6.43	120.23	113.80
1	k	257	MET	N-CA-C	-6.43	106.02	114.31
1	k	182	PRO	CB-CA-C	-6.41	102.93	112.55
1	c	257	MET	N-CA-C	-6.41	106.04	114.31
1	e	257	MET	N-CA-C	-6.40	106.05	114.31
1	f	276	ARG	CB-CG-CD	6.40	126.01	111.30
2	L	367	ASP	CB-CA-C	6.39	120.43	109.24
2	M	367	ASP	CB-CA-C	6.39	120.42	109.24
2	N	367	ASP	CB-CA-C	6.38	120.41	109.24
2	H	367	ASP	CB-CA-C	6.38	120.41	109.24
1	o	182	PRO	CB-CA-C	-6.38	102.98	112.55
1	m	182	PRO	CB-CA-C	-6.38	102.98	112.55
1	o	140	GLY	CA-C-N	6.38	128.87	122.30
1	o	140	GLY	C-N-CA	6.38	128.87	122.30
2	R	89	PRO	N-CD-CG	-6.37	93.64	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	d	182	PRO	CB-CA-C	-6.37	103.00	112.55
1	f	140	GLY	CA-C-N	6.37	128.86	122.30
1	f	140	GLY	C-N-CA	6.37	128.86	122.30
1	i	182	PRO	CB-CA-C	-6.37	103.00	112.55
2	J	367	ASP	CB-CA-C	6.37	120.39	109.24
1	e	182	PRO	CB-CA-C	-6.37	103.00	112.55
1	l	182	PRO	CB-CA-C	-6.37	103.00	112.55
1	b	182	PRO	CB-CA-C	-6.36	103.00	112.55
2	O	89	PRO	N-CD-CG	-6.36	93.67	103.20
2	P	367	ASP	CB-CA-C	6.35	120.36	109.24
2	I	180	ALA	CA-C-N	-6.35	111.43	121.02
2	I	180	ALA	C-N-CA	-6.35	111.43	121.02
2	Z	367	ASP	CB-CA-C	6.35	120.35	109.24
1	q	182	PRO	CB-CA-C	-6.34	103.03	112.55
1	a	182	PRO	CB-CA-C	-6.34	103.04	112.55
2	I	367	ASP	CB-CA-C	6.34	120.34	109.24
2	Y	319	TYR	CB-CA-C	-6.34	97.77	109.37
1	f	182	PRO	CB-CA-C	-6.34	103.04	112.55
2	O	367	ASP	CB-CA-C	6.34	120.33	109.24
1	f	257	MET	N-CA-C	-6.33	106.14	114.31
2	W	367	ASP	CB-CA-C	6.33	120.32	109.24
1	j	182	PRO	CB-CA-C	-6.33	103.05	112.55
2	Z	319	TYR	CB-CA-C	-6.33	97.78	109.37
1	v	257	MET	N-CA-C	-6.33	106.14	114.31
2	V	367	ASP	CB-CA-C	6.33	120.32	109.24
1	r	182	PRO	CB-CA-C	-6.33	103.06	112.55
1	g	182	PRO	CB-CA-C	-6.33	103.06	112.55
1	c	182	PRO	CB-CA-C	-6.32	103.07	112.55
2	X	367	ASP	CB-CA-C	6.32	120.30	109.24
2	V	370	LYS	CB-CG-CD	6.32	125.83	111.30
2	Y	367	ASP	CB-CA-C	6.32	120.29	109.24
2	E	224	TYR	CA-CB-CG	6.32	125.27	113.90
2	F	367	ASP	CB-CA-C	6.32	120.29	109.24
2	G	367	ASP	CB-CA-C	6.32	120.29	109.24
2	D	367	ASP	CB-CA-C	6.31	120.29	109.24
2	E	319	TYR	CB-CA-C	-6.31	97.82	109.37
1	i	276	ARG	CB-CG-CD	6.30	125.79	111.30
2	C	319	TYR	CB-CA-C	-6.30	97.85	109.37
2	P	319	TYR	CB-CA-C	-6.29	97.85	109.37
1	v	182	PRO	CB-CA-C	-6.29	103.11	112.55
2	R	319	TYR	CB-CA-C	-6.29	97.85	109.37
2	F	370	LYS	CB-CG-CD	6.29	125.78	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	319	TYR	CB-CA-C	-6.29	97.86	109.37
2	D	180	ALA	CA-C-N	-6.29	111.52	121.02
2	D	180	ALA	C-N-CA	-6.29	111.52	121.02
2	A	319	TYR	CB-CA-C	-6.29	97.86	109.37
2	D	229	ARG	CB-CA-C	-6.29	98.60	110.67
1	o	257	MET	N-CA-C	-6.29	106.20	114.31
1	r	241	ARG	CB-CA-C	-6.29	97.96	109.15
2	C	367	ASP	CB-CA-C	6.29	120.24	109.24
1	y	257	MET	N-CA-C	-6.28	106.21	114.31
2	Q	367	ASP	CB-CA-C	6.28	120.22	109.24
2	R	367	ASP	CB-CA-C	6.28	120.22	109.24
2	S	367	ASP	CB-CA-C	6.28	120.22	109.24
1	l	257	MET	CA-C-N	-6.27	116.35	123.25
1	l	257	MET	C-N-CA	-6.27	116.35	123.25
2	G	319	TYR	CB-CA-C	-6.27	97.89	109.37
2	K	224	TYR	CA-CB-CG	6.26	125.18	113.90
2	I	370	LYS	CB-CG-CD	6.26	125.70	111.30
1	d	60	VAL	CA-C-O	6.26	123.26	119.19
2	K	319	TYR	CB-CA-C	-6.25	97.92	109.37
2	J	319	TYR	CB-CA-C	-6.25	97.93	109.37
2	X	319	TYR	CB-CA-C	-6.25	97.94	109.37
2	F	77	GLU	CB-CG-CD	6.25	123.22	112.60
2	Q	220	GLU	CB-CG-CD	6.24	123.22	112.60
2	E	180	ALA	CA-C-N	-6.24	111.59	121.02
2	E	180	ALA	C-N-CA	-6.24	111.59	121.02
2	U	367	ASP	CB-CA-C	6.24	120.16	109.24
2	O	319	TYR	CB-CA-C	-6.24	97.95	109.37
2	E	90	GLU	CB-CG-CD	6.24	123.20	112.60
2	S	370	LYS	CB-CG-CD	6.23	125.64	111.30
2	I	220	GLU	CB-CG-CD	6.23	123.20	112.60
2	I	319	TYR	CB-CA-C	-6.23	97.96	109.37
2	C	180	ALA	CA-C-N	-6.23	111.61	121.02
2	C	180	ALA	C-N-CA	-6.23	111.61	121.02
2	Q	319	TYR	CB-CA-C	-6.23	97.97	109.37
2	H	319	TYR	CB-CA-C	-6.23	97.98	109.37
2	L	319	TYR	CB-CA-C	-6.22	97.99	109.37
2	D	319	TYR	CB-CA-C	-6.22	97.99	109.37
2	T	319	TYR	CB-CA-C	-6.21	98.00	109.37
2	V	296	PHE	CA-CB-CG	-6.21	107.59	113.80
1	x	222	TYR	CB-CG-CD1	6.21	130.11	120.80
2	W	319	TYR	CB-CA-C	-6.20	98.02	109.37
2	L	220	GLU	CB-CG-CD	6.20	123.14	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	319	TYR	CB-CA-C	-6.20	98.02	109.37
2	T	367	ASP	CB-CA-C	6.20	120.09	109.24
2	N	319	TYR	CB-CA-C	-6.20	98.03	109.37
1	u	257	MET	CA-C-N	-6.20	116.43	123.25
1	u	257	MET	C-N-CA	-6.20	116.43	123.25
1	d	257	MET	CA-C-N	-6.20	116.44	123.25
1	d	257	MET	C-N-CA	-6.20	116.44	123.25
2	D	296	PHE	CA-CB-CG	-6.20	107.61	113.80
2	F	220	GLU	CB-CG-CD	6.20	123.13	112.60
2	J	224	TYR	CA-CB-CG	6.19	125.04	113.90
2	D	282	TYR	CA-C-N	-6.19	113.22	122.07
2	D	282	TYR	C-N-CA	-6.19	113.22	122.07
2	J	220	GLU	CB-CG-CD	6.19	123.12	112.60
1	a	257	MET	CA-C-N	-6.18	116.45	123.25
1	a	257	MET	C-N-CA	-6.18	116.45	123.25
2	V	319	TYR	CB-CA-C	-6.18	98.05	109.37
2	X	370	LYS	CB-CG-CD	6.18	125.52	111.30
1	h	178	THR	CB-CA-C	-6.17	98.14	110.42
2	Y	220	GLU	CB-CG-CD	6.17	123.09	112.60
2	S	220	GLU	CB-CG-CD	6.17	123.09	112.60
1	k	257	MET	CA-C-N	-6.16	116.47	123.25
1	k	257	MET	C-N-CA	-6.16	116.47	123.25
1	s	60	VAL	CA-C-O	6.16	123.20	119.19
2	M	319	TYR	CB-CA-C	-6.16	98.10	109.37
1	n	222	TYR	CB-CG-CD1	6.16	130.04	120.80
1	y	60	VAL	CA-C-O	6.16	123.19	119.19
2	Q	370	LYS	CB-CG-CD	6.15	125.45	111.30
1	t	60	VAL	CA-C-O	6.15	123.19	119.19
2	Z	296	PHE	CA-CB-CG	-6.15	107.65	113.80
2	G	220	GLU	CB-CG-CD	6.15	123.06	112.60
2	T	296	PHE	CA-CB-CG	-6.15	107.65	113.80
2	N	296	PHE	CA-CB-CG	-6.15	107.65	113.80
1	b	276	ARG	CB-CG-CD	6.14	125.43	111.30
2	K	220	GLU	CB-CG-CD	6.14	123.05	112.60
1	k	140	GLY	CA-C-N	6.14	128.63	122.30
1	k	140	GLY	C-N-CA	6.14	128.63	122.30
2	U	319	TYR	CB-CA-C	-6.14	98.13	109.37
1	g	178	THR	CB-CA-C	-6.14	98.20	110.42
2	N	220	GLU	CB-CG-CD	6.14	123.04	112.60
1	d	276	ARG	CB-CG-CD	6.13	125.41	111.30
1	e	60	VAL	CA-C-O	6.13	123.18	119.19
1	h	60	VAL	CA-C-O	6.13	123.18	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	220	GLU	CB-CG-CD	6.13	123.02	112.60
1	e	257	MET	CA-C-N	-6.13	116.51	123.25
1	e	257	MET	C-N-CA	-6.13	116.51	123.25
2	Y	370	LYS	CB-CG-CD	6.13	125.39	111.30
2	W	220	GLU	CB-CG-CD	6.12	123.01	112.60
1	r	60	VAL	CA-C-O	6.12	123.17	119.19
2	W	296	PHE	CA-CB-CG	-6.12	107.68	113.80
1	p	257	MET	CA-C-N	-6.12	116.52	123.25
1	p	257	MET	C-N-CA	-6.12	116.52	123.25
1	q	241	ARG	CB-CA-C	-6.12	98.26	109.15
2	T	370	LYS	CB-CG-CD	6.12	125.37	111.30
2	F	319	TYR	CB-CA-C	-6.12	98.18	109.37
1	o	60	VAL	CA-C-O	6.12	123.17	119.19
2	E	220	GLU	CB-CG-CD	6.11	122.99	112.60
1	q	257	MET	CA-C-N	-6.11	116.53	123.25
1	q	257	MET	C-N-CA	-6.11	116.53	123.25
1	m	257	MET	CA-C-N	-6.11	116.53	123.25
1	m	257	MET	C-N-CA	-6.11	116.53	123.25
1	j	323	MET	N-CA-C	-6.11	106.47	114.04
2	C	229	ARG	CB-CA-C	-6.11	98.94	110.67
1	w	222	TYR	CB-CG-CD1	6.11	129.96	120.80
1	d	241	ARG	CB-CA-C	-6.11	98.28	109.15
2	M	220	GLU	CB-CG-CD	6.10	122.97	112.60
1	p	241	ARG	CB-CG-CD	-6.10	97.27	111.30
2	P	220	GLU	CB-CG-CD	6.09	122.96	112.60
2	Z	180	ALA	CA-C-N	-6.09	111.82	121.02
2	Z	180	ALA	C-N-CA	-6.09	111.82	121.02
2	V	220	GLU	CB-CG-CD	6.09	122.96	112.60
2	C	220	GLU	CB-CG-CD	6.09	122.96	112.60
1	p	60	VAL	CA-C-O	6.09	123.15	119.19
2	T	220	GLU	CB-CG-CD	6.09	122.95	112.60
2	O	220	GLU	CB-CG-CD	6.08	122.94	112.60
1	f	178	THR	CB-CA-C	-6.08	98.32	110.42
2	U	220	GLU	CB-CG-CD	6.08	122.94	112.60
1	n	60	VAL	CA-C-O	6.08	123.14	119.19
1	u	60	VAL	CA-C-O	6.08	123.14	119.19
2	Q	296	PHE	CA-CB-CG	-6.08	107.72	113.80
2	U	180	ALA	CA-C-N	-6.08	111.85	121.02
2	U	180	ALA	C-N-CA	-6.08	111.85	121.02
2	H	370	LYS	CB-CG-CD	6.08	125.28	111.30
2	Z	89	PRO	N-CD-CG	-6.07	94.09	103.20
1	u	241	ARG	CB-CA-C	-6.07	98.34	109.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	z	60	VAL	CA-C-O	6.07	123.14	119.19
2	X	296	PHE	CA-CB-CG	-6.07	107.73	113.80
2	Y	296	PHE	CA-CB-CG	-6.07	107.73	113.80
2	Z	220	GLU	CB-CG-CD	6.07	122.91	112.60
1	x	60	VAL	CA-C-O	6.07	123.13	119.19
2	D	121	ARG	NE-CZ-NH2	6.07	124.66	119.20
1	m	323	MET	N-CA-C	-6.06	106.49	114.31
1	q	178	THR	CB-CA-C	-6.06	98.35	110.42
1	w	241	ARG	CB-CA-C	-6.06	98.36	109.15
1	h	257	MET	CA-C-N	-6.06	116.58	123.25
1	h	257	MET	C-N-CA	-6.06	116.58	123.25
1	q	60	VAL	CA-C-O	6.06	123.13	119.19
2	E	370	LYS	CB-CG-CD	6.06	125.24	111.30
2	L	370	LYS	CB-CG-CD	6.06	125.24	111.30
2	C	296	PHE	CA-CB-CG	-6.06	107.74	113.80
1	z	222	TYR	CB-CG-CD1	6.06	129.89	120.80
1	d	241	ARG	CB-CG-CD	-6.06	97.37	111.30
1	o	241	ARG	CB-CA-C	-6.06	98.37	109.15
1	t	257	MET	CA-C-N	-6.05	116.59	123.25
1	t	257	MET	C-N-CA	-6.05	116.59	123.25
2	A	220	GLU	CB-CG-CD	6.05	122.88	112.60
1	s	257	MET	CA-C-N	-6.05	116.60	123.25
1	s	257	MET	C-N-CA	-6.05	116.60	123.25
1	b	257	MET	CA-C-N	-6.05	116.60	123.25
1	b	257	MET	C-N-CA	-6.05	116.60	123.25
1	l	178	THR	CB-CA-C	-6.05	98.38	110.42
2	B	220	GLU	CB-CG-CD	6.05	122.88	112.60
1	c	257	MET	CA-C-N	-6.04	116.60	123.25
1	c	257	MET	C-N-CA	-6.04	116.60	123.25
1	g	257	MET	CA-C-N	-6.04	116.60	123.25
1	g	257	MET	C-N-CA	-6.04	116.60	123.25
2	U	296	PHE	CA-CB-CG	-6.04	107.76	113.80
2	D	220	GLU	CB-CG-CD	6.04	122.87	112.60
1	w	60	VAL	CA-C-O	6.04	123.12	119.19
2	D	224	TYR	CA-CB-CG	6.04	124.77	113.90
1	c	323	MET	N-CA-C	-6.04	106.52	114.31
1	m	178	THR	CB-CA-C	-6.04	98.41	110.42
2	T	308	ARG	N-CA-C	-6.04	105.68	113.16
1	w	241	ARG	CB-CG-CD	-6.04	97.42	111.30
1	g	323	MET	N-CA-C	-6.03	106.53	114.31
2	U	308	ARG	N-CA-C	-6.03	105.68	113.16
1	i	285	THR	CA-C-N	6.03	124.04	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	i	285	THR	C-N-CA	6.03	124.04	120.24
2	B	308	ARG	N-CA-C	-6.03	105.68	113.16
2	C	89	PRO	N-CD-CG	-6.03	94.16	103.20
1	s	178	THR	CB-CA-C	-6.03	98.42	110.42
1	c	241	ARG	CB-CA-C	-6.03	98.42	109.15
1	q	241	ARG	CB-CG-CD	-6.03	97.43	111.30
1	j	257	MET	CA-C-N	-6.03	116.62	123.25
1	j	257	MET	C-N-CA	-6.03	116.62	123.25
2	W	180	ALA	CA-C-N	-6.03	111.92	121.02
2	W	180	ALA	C-N-CA	-6.03	111.92	121.02
2	M	180	ALA	CA-C-N	-6.03	111.92	121.02
2	M	180	ALA	C-N-CA	-6.03	111.92	121.02
1	b	60	VAL	CA-C-O	6.03	123.11	119.19
1	c	60	VAL	CA-C-O	6.03	123.11	119.19
2	O	180	ALA	CA-C-N	-6.03	111.92	121.02
2	O	180	ALA	C-N-CA	-6.03	111.92	121.02
1	v	257	MET	CA-C-N	-6.03	116.62	123.25
1	v	257	MET	C-N-CA	-6.03	116.62	123.25
2	Q	180	ALA	CA-C-N	-6.02	111.92	121.02
2	Q	180	ALA	C-N-CA	-6.02	111.92	121.02
2	W	308	ARG	N-CA-C	-6.02	105.69	113.16
2	J	370	LYS	CB-CG-CD	6.02	125.15	111.30
1	p	178	THR	CB-CA-C	-6.02	98.44	110.42
1	a	241	ARG	CB-CA-C	-6.02	98.44	109.15
1	f	257	MET	CA-C-N	-6.02	116.63	123.25
1	f	257	MET	C-N-CA	-6.02	116.63	123.25
1	b	241	ARG	CB-CG-CD	-6.02	97.46	111.30
1	l	87	PRO	N-CA-CB	6.02	109.57	103.25
2	S	308	ARG	N-CA-C	-6.02	105.70	113.16
2	Z	308	ARG	N-CA-C	-6.02	105.70	113.16
2	X	220	GLU	CB-CG-CD	6.01	122.82	112.60
2	O	296	PHE	CA-CB-CG	-6.01	107.79	113.80
2	O	308	ARG	N-CA-C	-6.01	105.70	113.16
1	i	178	THR	CB-CA-C	-6.01	98.46	110.42
2	A	180	ALA	CA-C-N	-6.01	111.94	121.02
2	A	180	ALA	C-N-CA	-6.01	111.94	121.02
2	C	308	ARG	N-CA-C	-6.01	105.71	113.16
1	x	178	THR	CB-CA-C	-6.01	98.46	110.42
1	g	285	THR	CA-C-N	6.01	124.03	120.24
1	g	285	THR	C-N-CA	6.01	124.03	120.24
2	V	308	ARG	N-CA-C	-6.01	105.71	113.16
2	N	308	ARG	N-CA-C	-6.00	105.72	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	296	PHE	CA-CB-CG	-6.00	107.80	113.80
2	K	308	ARG	N-CA-C	-6.00	105.72	113.16
1	p	276	ARG	CB-CG-CD	6.00	125.10	111.30
1	m	60	VAL	CA-C-O	6.00	123.09	119.19
2	D	213	CYS	CA-CB-SG	-6.00	100.60	114.40
2	I	308	ARG	N-CA-C	-6.00	105.72	113.16
1	r	178	THR	CB-CA-C	-6.00	98.48	110.42
1	i	257	MET	CA-C-N	-6.00	116.65	123.25
1	i	257	MET	C-N-CA	-6.00	116.65	123.25
1	h	285	THR	CA-C-N	5.99	124.02	120.24
1	h	285	THR	C-N-CA	5.99	124.02	120.24
1	e	241	ARG	CB-CA-C	-5.99	98.48	109.15
2	Y	308	ARG	N-CA-C	-5.99	105.73	113.16
1	l	60	VAL	CA-C-O	5.99	123.08	119.19
1	l	241	ARG	CB-CA-C	-5.99	98.49	109.15
2	A	308	ARG	N-CA-C	-5.99	105.73	113.16
2	J	308	ARG	N-CA-C	-5.99	105.73	113.16
1	e	241	ARG	CB-CG-CD	-5.99	97.53	111.30
2	R	296	PHE	CA-CB-CG	-5.99	107.81	113.80
2	E	296	PHE	CA-CB-CG	-5.99	107.81	113.80
1	h	323	MET	N-CA-C	-5.99	106.59	114.31
1	n	241	ARG	CB-CA-C	-5.99	98.50	109.15
2	M	224	TYR	CA-CB-CG	5.98	124.67	113.90
1	u	178	THR	CB-CA-C	-5.98	98.52	110.42
2	P	308	ARG	N-CA-C	-5.98	105.75	113.16
2	G	308	ARG	N-CA-C	-5.98	105.75	113.16
1	w	178	THR	CB-CA-C	-5.98	98.52	110.42
1	c	241	ARG	CB-CG-CD	-5.97	97.56	111.30
2	R	308	ARG	N-CA-C	-5.97	105.76	113.16
1	x	241	ARG	CB-CA-C	-5.97	98.52	109.15
2	L	308	ARG	N-CA-C	-5.97	105.76	113.16
2	Q	308	ARG	N-CA-C	-5.97	105.76	113.16
2	R	220	GLU	CB-CG-CD	5.97	122.74	112.60
2	U	370	LYS	CB-CG-CD	5.97	125.02	111.30
2	V	180	ALA	CA-C-N	-5.97	112.01	121.02
2	V	180	ALA	C-N-CA	-5.97	112.01	121.02
2	F	308	ARG	N-CA-C	-5.97	105.76	113.16
1	i	60	VAL	CA-C-O	5.96	123.07	119.19
2	X	308	ARG	N-CA-C	-5.96	105.77	113.16
2	B	180	ALA	CA-C-N	-5.96	112.02	121.02
2	B	180	ALA	C-N-CA	-5.96	112.02	121.02
2	H	308	ARG	N-CA-C	-5.96	105.77	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	s	241	ARG	CB-CG-CD	-5.96	97.59	111.30
1	w	257	MET	CA-C-N	-5.96	116.69	123.25
1	w	257	MET	C-N-CA	-5.96	116.69	123.25
2	N	180	ALA	CA-C-N	-5.96	112.02	121.02
2	N	180	ALA	C-N-CA	-5.96	112.02	121.02
2	Z	370	LYS	CB-CG-CD	5.96	125.00	111.30
2	C	370	LYS	CB-CG-CD	5.96	125.01	111.30
2	E	308	ARG	N-CA-C	-5.96	105.77	113.16
1	i	323	MET	N-CA-C	-5.96	106.62	114.31
2	M	308	ARG	N-CA-C	-5.96	105.77	113.16
1	k	241	ARG	CB-CA-C	-5.95	98.56	109.15
2	H	274	PRO	N-CA-C	5.95	120.51	112.48
1	t	241	ARG	CB-CG-CD	-5.95	97.62	111.30
1	j	178	THR	CB-CA-C	-5.95	98.58	110.42
2	S	180	ALA	CA-C-N	-5.95	112.04	121.02
2	S	180	ALA	C-N-CA	-5.95	112.04	121.02
2	K	370	LYS	CB-CG-CD	5.95	124.98	111.30
1	u	241	ARG	CB-CG-CD	-5.95	97.63	111.30
2	P	296	PHE	CA-CB-CG	-5.94	107.86	113.80
1	a	60	VAL	CA-C-O	5.94	123.05	119.19
1	a	241	ARG	CB-CG-CD	-5.94	97.64	111.30
1	k	323	MET	N-CA-C	-5.94	106.65	114.31
1	r	241	ARG	CB-CG-CD	-5.94	97.65	111.30
2	L	180	ALA	CA-C-N	-5.93	112.06	121.02
2	L	180	ALA	C-N-CA	-5.93	112.06	121.02
1	b	241	ARG	CB-CA-C	-5.93	98.59	109.15
1	f	323	MET	N-CA-C	-5.93	106.69	114.04
2	M	274	PRO	N-CA-C	5.93	120.49	112.48
1	m	241	ARG	CB-CA-C	-5.93	98.59	109.15
2	P	180	ALA	CA-C-N	-5.93	112.07	121.02
2	P	180	ALA	C-N-CA	-5.93	112.07	121.02
2	T	271	THR	CA-CB-OG1	5.92	118.49	109.60
1	y	241	ARG	CB-CA-C	-5.92	98.61	109.15
2	O	370	LYS	CB-CG-CD	5.92	124.91	111.30
1	v	178	THR	CB-CA-C	-5.92	98.64	110.42
1	z	323	MET	N-CA-C	-5.92	106.67	114.31
1	t	227	HIS	CA-CB-CG	-5.92	107.89	113.80
1	i	241	ARG	CB-CA-C	-5.91	98.62	109.15
2	D	308	ARG	N-CA-C	-5.91	105.83	113.16
1	b	178	THR	CB-CA-C	-5.91	98.66	110.42
2	Y	180	ALA	CA-C-N	-5.91	112.10	121.02
2	Y	180	ALA	C-N-CA	-5.91	112.10	121.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	v	241	ARG	CB-CA-C	-5.91	98.63	109.15
1	y	222	TYR	CB-CG-CD1	5.91	129.66	120.80
1	t	178	THR	CB-CA-C	-5.91	98.67	110.42
1	k	178	THR	CB-CA-C	-5.91	98.67	110.42
2	N	370	LYS	CB-CG-CD	5.91	124.88	111.30
2	Q	89	PRO	N-CD-CG	-5.91	94.34	103.20
2	I	274	PRO	N-CA-C	5.90	120.45	112.48
2	R	274	PRO	N-CA-C	5.90	120.45	112.48
1	z	241	ARG	CB-CA-C	-5.90	98.64	109.15
1	j	60	VAL	CA-C-O	5.90	123.03	119.19
2	O	229	ARG	CB-CA-C	-5.90	97.98	110.31
2	G	274	PRO	N-CA-C	5.90	120.45	112.48
2	A	274	PRO	N-CA-C	5.90	120.44	112.48
2	I	77	GLU	CB-CG-CD	5.90	122.62	112.60
1	a	178	THR	CB-CA-C	-5.90	98.69	110.42
2	W	370	LYS	CB-CG-CD	5.89	124.86	111.30
2	F	274	PRO	N-CA-C	5.89	120.44	112.48
2	G	370	LYS	CB-CG-CD	5.89	124.85	111.30
1	x	257	MET	CA-C-N	-5.89	116.77	123.25
1	x	257	MET	C-N-CA	-5.89	116.77	123.25
1	q	119	VAL	CA-CB-CG1	-5.89	100.39	110.40
2	W	77	GLU	CB-CG-CD	5.89	122.61	112.60
2	O	271	THR	CA-CB-OG1	5.88	118.42	109.60
2	B	274	PRO	N-CA-C	5.88	120.42	112.48
2	K	274	PRO	N-CA-C	5.88	120.42	112.48
1	h	280	GLN	N-CA-C	-5.88	105.87	113.16
2	G	77	GLU	CB-CG-CD	5.88	122.59	112.60
2	R	180	ALA	CA-C-N	-5.87	112.16	121.02
2	R	180	ALA	C-N-CA	-5.87	112.16	121.02
1	n	276	ARG	CB-CG-CD	5.87	124.80	111.30
1	v	60	VAL	CA-C-O	5.87	123.00	119.19
2	L	77	GLU	CB-CG-CD	5.86	122.56	112.60
1	j	241	ARG	CB-CA-C	-5.86	98.73	109.15
1	k	60	VAL	CA-C-O	5.86	123.00	119.19
1	m	285	THR	CA-C-N	5.86	123.93	120.24
1	m	285	THR	C-N-CA	5.86	123.93	120.24
1	x	241	ARG	CB-CG-CD	-5.86	97.83	111.30
1	a	323	MET	N-CA-C	-5.85	106.76	114.31
1	f	60	VAL	CA-C-O	5.85	122.99	119.19
2	T	180	ALA	CA-C-N	-5.85	112.19	121.02
2	T	180	ALA	C-N-CA	-5.85	112.19	121.02
1	j	285	THR	CA-C-N	5.85	123.92	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	j	285	THR	C-N-CA	5.85	123.92	120.24
1	l	241	ARG	CB-CG-CD	-5.84	97.86	111.30
1	o	241	ARG	CB-CG-CD	-5.84	97.86	111.30
2	R	370	LYS	CB-CG-CD	5.84	124.73	111.30
2	X	180	ALA	CA-C-N	-5.84	112.20	121.02
2	X	180	ALA	C-N-CA	-5.84	112.20	121.02
1	v	241	ARG	CB-CG-CD	-5.84	97.87	111.30
2	T	167	LEU	CB-CG-CD1	5.84	128.21	110.70
1	l	323	MET	N-CA-C	-5.84	106.78	114.31
2	J	274	PRO	N-CA-C	5.83	120.36	112.48
1	z	257	MET	CA-C-N	-5.83	116.83	123.25
1	z	257	MET	C-N-CA	-5.83	116.83	123.25
1	c	363	MET	CB-CG-SD	5.83	130.20	112.70
2	W	89	PRO	N-CD-CG	-5.83	94.45	103.20
2	L	274	PRO	N-CA-C	5.83	120.35	112.48
1	e	323	MET	N-CA-C	-5.83	106.80	114.31
1	j	241	ARG	CB-CG-CD	-5.83	97.90	111.30
1	r	392	LYS	CB-CG-CD	5.83	124.70	111.30
1	k	285	THR	CA-C-N	5.82	123.91	120.24
1	k	285	THR	C-N-CA	5.82	123.91	120.24
1	d	323	MET	N-CA-C	-5.82	106.81	114.31
1	u	359	ARG	CB-CA-C	5.82	119.00	111.50
1	v	222	TYR	CB-CG-CD1	5.82	129.53	120.80
2	Q	5	ILE	CA-CB-CG2	-5.82	100.61	110.50
1	b	323	MET	N-CA-C	-5.81	106.81	114.31
2	J	296	PHE	CA-CB-CG	-5.81	107.99	113.80
2	N	89	PRO	N-CD-CG	-5.81	94.49	103.20
1	o	222	TYR	CB-CG-CD1	5.80	129.51	120.80
2	R	282	TYR	N-CA-C	-5.80	101.37	110.36
2	K	282	TYR	CA-C-N	-5.80	113.77	122.07
2	K	282	TYR	C-N-CA	-5.80	113.77	122.07
1	n	241	ARG	CB-CG-CD	-5.80	97.96	111.30
1	s	276	ARG	CB-CG-CD	5.80	124.64	111.30
1	c	392	LYS	CB-CG-CD	5.80	124.63	111.30
1	n	323	MET	N-CA-C	-5.79	106.84	114.31
1	r	257	MET	CA-C-N	-5.79	116.88	123.25
1	r	257	MET	C-N-CA	-5.79	116.88	123.25
1	e	46	ARG	CG-CD-NE	5.79	124.74	112.00
2	Z	271	THR	CA-CB-OG1	5.79	118.28	109.60
2	A	296	PHE	CA-CB-CG	-5.79	108.01	113.80
1	n	257	MET	CA-C-N	-5.79	116.88	123.25
1	n	257	MET	C-N-CA	-5.79	116.88	123.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	89	PRO	N-CD-CG	-5.79	94.52	103.20
1	o	276	ARG	CB-CG-CD	5.79	124.61	111.30
1	x	323	MET	N-CA-C	-5.78	106.85	114.31
1	o	257	MET	CA-C-N	-5.78	116.90	123.25
1	o	257	MET	C-N-CA	-5.78	116.90	123.25
1	k	241	ARG	CB-CG-CD	-5.77	98.02	111.30
2	L	282	TYR	CA-C-N	-5.77	113.82	122.07
2	L	282	TYR	C-N-CA	-5.77	113.82	122.07
1	f	241	ARG	CB-CG-CD	-5.77	98.03	111.30
2	S	271	THR	CA-CB-OG1	5.77	118.26	109.60
2	F	296	PHE	CA-CB-CG	-5.77	108.03	113.80
1	v	276	ARG	CB-CG-CD	5.77	124.56	111.30
1	y	276	ARG	CB-CG-CD	5.77	124.56	111.30
2	X	169	PHE	CA-CB-CG	-5.77	108.03	113.80
1	x	276	ARG	CB-CG-CD	5.77	124.56	111.30
1	v	280	GLN	N-CA-C	-5.76	106.01	113.16
1	v	323	MET	N-CA-C	-5.76	106.87	114.31
2	G	282	TYR	CA-C-N	-5.76	113.83	122.07
2	G	282	TYR	C-N-CA	-5.76	113.83	122.07
1	y	257	MET	CA-C-N	-5.76	116.91	123.25
1	y	257	MET	C-N-CA	-5.76	116.91	123.25
2	D	274	PRO	N-CA-C	5.76	120.26	112.48
1	p	323	MET	N-CA-C	-5.76	106.88	114.31
1	z	221	THR	CA-C-O	-5.76	113.95	121.73
1	t	323	MET	N-CA-C	-5.76	106.89	114.31
2	M	296	PHE	CA-CB-CG	-5.75	108.05	113.80
1	g	241	ARG	CB-CA-C	-5.75	98.91	109.15
2	A	370	LYS	CB-CG-CD	5.75	124.53	111.30
1	f	285	THR	CA-C-N	5.75	123.86	120.24
1	f	285	THR	C-N-CA	5.75	123.86	120.24
2	Y	282	TYR	N-CA-C	-5.75	101.45	110.36
1	d	285	THR	CA-C-N	5.75	123.86	120.24
1	d	285	THR	C-N-CA	5.75	123.86	120.24
2	J	180	ALA	CA-C-N	-5.74	112.35	121.02
2	J	180	ALA	C-N-CA	-5.74	112.35	121.02
1	h	241	ARG	CB-CA-C	-5.74	98.93	109.15
1	u	276	ARG	CB-CG-CD	5.74	124.50	111.30
1	w	323	MET	N-CA-C	-5.74	106.91	114.31
2	B	370	LYS	CB-CG-CD	5.74	124.50	111.30
2	W	274	PRO	N-CA-C	5.74	120.22	112.48
1	s	323	MET	N-CA-C	-5.74	106.91	114.31
2	P	274	PRO	N-CA-C	5.73	120.22	112.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	l	285	THR	CA-C-N	5.73	123.85	120.24
1	l	285	THR	C-N-CA	5.73	123.85	120.24
1	r	285	THR	CA-C-N	5.73	123.85	120.24
1	r	285	THR	C-N-CA	5.73	123.85	120.24
1	g	60	VAL	CA-C-O	5.73	122.91	119.19
2	Y	271	THR	CA-CB-OG1	5.73	118.19	109.60
1	y	323	MET	N-CA-C	-5.73	106.92	114.31
1	u	323	MET	N-CA-C	-5.72	106.93	114.31
2	Y	229	ARG	CB-CA-C	-5.72	98.36	110.31
2	H	121	ARG	NE-CZ-NH2	5.72	124.34	119.20
1	d	46	ARG	CG-CD-NE	5.71	124.57	112.00
2	K	296	PHE	CA-CB-CG	-5.71	108.09	113.80
2	M	282	TYR	CA-C-N	-5.71	113.90	122.07
2	M	282	TYR	C-N-CA	-5.71	113.90	122.07
1	r	323	MET	N-CA-C	-5.71	106.94	114.31
1	f	241	ARG	CB-CA-C	-5.71	98.98	109.15
1	b	285	THR	CA-C-N	5.71	123.84	120.24
1	b	285	THR	C-N-CA	5.71	123.84	120.24
1	c	285	THR	CA-C-N	5.71	123.84	120.24
1	c	285	THR	C-N-CA	5.71	123.84	120.24
2	E	274	PRO	N-CA-C	5.71	120.18	112.48
1	q	323	MET	N-CA-C	-5.71	106.95	114.31
2	O	169	PHE	CA-CB-CG	-5.71	108.09	113.80
2	G	296	PHE	CA-CB-CG	-5.70	108.10	113.80
2	U	271	THR	CA-CB-OG1	5.70	118.15	109.60
2	L	296	PHE	CA-CB-CG	-5.70	108.10	113.80
1	q	125	GLU	CB-CG-CD	5.70	122.29	112.60
1	m	241	ARG	CB-CG-CD	-5.70	98.20	111.30
2	Z	169	PHE	CA-CB-CG	-5.70	108.10	113.80
2	N	169	PHE	CA-CB-CG	-5.69	108.11	113.80
2	Q	274	PRO	N-CA-C	5.69	120.16	112.48
2	E	282	TYR	CA-C-N	-5.69	113.94	122.07
2	E	282	TYR	C-N-CA	-5.69	113.94	122.07
1	b	222	TYR	CB-CG-CD1	5.68	129.33	120.80
2	V	89	PRO	N-CD-CG	-5.68	94.67	103.20
2	C	271	THR	CA-CB-OG1	5.68	118.13	109.60
1	o	323	MET	N-CA-C	-5.68	106.98	114.31
2	X	282	TYR	N-CA-C	-5.68	101.55	110.36
2	I	296	PHE	CA-CB-CG	-5.68	108.12	113.80
2	Y	5	ILE	CA-CB-CG2	-5.68	100.85	110.50
2	N	282	TYR	N-CA-C	-5.67	101.57	110.36
2	T	229	ARG	CB-CA-C	-5.67	98.46	110.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	296	PHE	CA-CB-CG	-5.67	108.13	113.80
2	V	229	ARG	CB-CA-C	-5.67	98.47	110.31
1	a	125	GLU	CB-CG-CD	5.66	122.23	112.60
1	z	276	ARG	CB-CG-CD	5.66	124.32	111.30
2	V	271	THR	CA-CB-OG1	5.66	118.09	109.60
1	z	280	GLN	N-CA-C	-5.66	106.14	113.16
1	a	285	THR	CA-C-N	5.66	123.81	120.24
1	a	285	THR	C-N-CA	5.66	123.81	120.24
1	k	46	ARG	CG-CD-NE	5.66	124.45	112.00
1	n	221	THR	CA-C-O	-5.66	114.10	121.73
2	Z	229	ARG	CB-CA-C	-5.65	98.50	110.31
2	J	282	TYR	CA-C-N	-5.65	113.99	122.07
2	J	282	TYR	C-N-CA	-5.65	113.99	122.07
1	d	363	MET	CB-CG-SD	5.65	129.65	112.70
2	N	5	ILE	CA-CB-CG2	-5.65	100.90	110.50
1	s	285	THR	CA-C-N	5.65	123.80	120.24
1	s	285	THR	C-N-CA	5.65	123.80	120.24
2	Q	282	TYR	N-CA-C	-5.64	101.61	110.36
2	Z	282	TYR	N-CA-C	-5.64	101.61	110.36
1	r	125	GLU	CB-CG-CD	5.64	122.19	112.60
1	z	241	ARG	CB-CG-CD	-5.64	98.33	111.30
2	P	169	PHE	CA-CB-CG	-5.64	108.16	113.80
1	n	125	GLU	CB-CG-CD	5.64	122.18	112.60
1	c	125	GLU	CB-CG-CD	5.63	122.18	112.60
2	X	229	ARG	CB-CA-C	-5.63	98.54	110.31
1	f	46	ARG	CG-CD-NE	5.63	124.39	112.00
1	i	280	GLN	N-CA-C	-5.63	106.18	113.16
1	p	125	GLU	CB-CG-CD	5.63	122.17	112.60
1	x	221	THR	CA-C-O	-5.63	114.13	121.73
2	W	282	TYR	N-CA-C	-5.63	101.63	110.36
2	W	271	THR	CA-CB-OG1	5.63	118.04	109.60
2	T	282	TYR	N-CA-C	-5.62	101.64	110.36
2	W	229	ARG	CB-CA-C	-5.62	98.56	110.31
2	T	169	PHE	CA-CB-CG	-5.62	108.18	113.80
1	l	125	GLU	CB-CG-CD	5.61	122.14	112.60
2	V	274	PRO	N-CA-C	5.61	120.06	112.48
2	R	369	ALA	CA-C-N	-5.61	115.05	122.85
2	R	369	ALA	C-N-CA	-5.61	115.05	122.85
1	w	276	ARG	CB-CG-CD	5.61	124.21	111.30
1	d	125	GLU	CB-CG-CD	5.61	122.14	112.60
2	R	229	ARG	CB-CA-C	-5.61	98.58	110.31
2	S	274	PRO	N-CA-C	5.61	120.05	112.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	o	221	THR	CA-C-O	-5.61	114.16	121.73
2	V	169	PHE	CA-CB-CG	-5.61	108.19	113.80
2	C	169	PHE	CA-CB-CG	-5.61	108.19	113.80
1	y	125	GLU	CB-CG-CD	5.61	122.13	112.60
2	N	271	THR	CA-CB-OG1	5.61	118.01	109.60
2	U	229	ARG	CB-CA-C	-5.61	98.59	110.31
2	U	282	TYR	N-CA-C	-5.60	101.67	110.36
2	E	169	PHE	CA-CB-CG	-5.60	108.20	113.80
2	I	235	VAL	CA-CB-CG1	5.60	119.92	110.40
2	R	169	PHE	CA-CB-CG	-5.60	108.20	113.80
1	e	125	GLU	CB-CG-CD	5.60	122.12	112.60
2	C	282	TYR	N-CA-C	-5.59	101.69	110.36
1	m	280	GLN	N-CA-C	-5.59	106.22	113.16
2	B	296	PHE	CA-CB-CG	-5.59	108.21	113.80
1	i	241	ARG	CB-CG-CD	-5.59	98.45	111.30
2	L	169	PHE	CA-CB-CG	-5.59	108.21	113.80
2	X	271	THR	CA-CB-OG1	5.58	117.98	109.60
2	D	169	PHE	CA-CB-CG	-5.58	108.22	113.80
2	S	77	GLU	CB-CG-CD	5.58	122.09	112.60
1	b	280	GLN	N-CA-C	-5.58	106.24	113.16
2	O	282	TYR	N-CA-C	-5.58	101.71	110.36
1	p	280	GLN	N-CA-C	-5.58	106.24	113.16
1	t	280	GLN	N-CA-C	-5.58	106.24	113.16
1	y	221	THR	CA-C-O	-5.58	114.20	121.73
1	k	280	GLN	N-CA-C	-5.57	106.25	113.16
1	q	276	ARG	CB-CG-CD	5.57	124.12	111.30
2	T	274	PRO	N-CA-C	5.57	120.00	112.48
2	A	169	PHE	CA-CB-CG	-5.57	108.23	113.80
2	N	229	ARG	CB-CA-C	-5.57	98.67	110.31
2	Q	169	PHE	CA-CB-CG	-5.57	108.23	113.80
2	V	282	TYR	N-CA-C	-5.57	101.73	110.36
2	X	274	PRO	N-CA-C	5.57	120.00	112.48
2	I	282	TYR	CA-C-N	-5.57	114.10	122.07
2	I	282	TYR	C-N-CA	-5.57	114.10	122.07
2	K	77	GLU	CB-CG-CD	5.57	122.07	112.60
2	W	169	PHE	CA-CB-CG	-5.57	108.23	113.80
2	Y	169	PHE	CA-CB-CG	-5.57	108.23	113.80
1	b	125	GLU	CB-CG-CD	5.57	122.06	112.60
1	h	241	ARG	CB-CG-CD	-5.57	98.50	111.30
2	M	169	PHE	CA-CB-CG	-5.56	108.24	113.80
1	v	125	GLU	CB-CG-CD	5.56	122.05	112.60
2	Q	229	ARG	CB-CA-C	-5.56	98.69	110.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	r	99	ASN	OD1-CG-ND2	-5.56	117.04	122.60
1	o	125	GLU	CB-CG-CD	5.55	122.04	112.60
2	N	274	PRO	N-CA-C	5.55	119.97	112.48
2	N	192	HIS	CB-CA-C	5.55	119.59	110.88
2	G	192	HIS	CB-CA-C	5.55	119.59	110.88
2	K	169	PHE	CA-CB-CG	-5.55	108.25	113.80
2	B	169	PHE	CA-CB-CG	-5.55	108.25	113.80
2	U	192	HIS	CB-CA-C	5.55	119.59	110.88
2	Y	77	GLU	CB-CG-CD	5.55	122.03	112.60
2	C	274	PRO	N-CA-C	5.55	119.97	112.48
2	D	192	HIS	CB-CA-C	5.55	119.59	110.88
2	L	192	HIS	CB-CA-C	5.54	119.58	110.88
1	f	11	GLN	CA-C-N	5.54	127.70	120.28
1	f	11	GLN	C-N-CA	5.54	127.70	120.28
2	F	192	HIS	CB-CA-C	5.54	119.58	110.88
1	x	125	GLU	CB-CG-CD	5.54	122.01	112.60
1	z	125	GLU	CB-CG-CD	5.54	122.01	112.60
2	S	192	HIS	CB-CA-C	5.53	119.57	110.88
2	J	192	HIS	CB-CA-C	5.53	119.57	110.88
1	q	280	GLN	N-CA-C	-5.53	106.30	113.16
1	m	125	GLU	CB-CG-CD	5.53	122.00	112.60
1	g	241	ARG	CB-CG-CD	-5.53	98.58	111.30
2	X	283	HIS	CB-CA-C	5.53	119.87	111.80
2	M	192	HIS	CB-CA-C	5.53	119.56	110.88
2	F	169	PHE	CA-CB-CG	-5.53	108.27	113.80
2	R	271	THR	CA-CB-OG1	5.53	117.89	109.60
2	H	231	ILE	N-CA-C	-5.53	104.98	110.62
1	s	46	ARG	CG-CD-NE	5.53	124.16	112.00
2	S	229	ARG	CB-CA-C	-5.53	98.76	110.31
2	U	169	PHE	CA-CB-CG	-5.53	108.28	113.80
2	Z	192	HIS	CB-CA-C	5.53	119.55	110.88
2	T	192	HIS	CB-CA-C	5.52	119.55	110.88
2	J	169	PHE	CA-CB-CG	-5.52	108.28	113.80
2	W	238	ILE	CA-C-N	-5.52	113.84	122.73
2	W	238	ILE	C-N-CA	-5.52	113.84	122.73
2	H	192	HIS	CB-CA-C	5.52	119.55	110.88
1	u	125	GLU	CB-CG-CD	5.52	121.98	112.60
1	g	11	GLN	CA-C-N	5.52	127.67	120.28
1	g	11	GLN	C-N-CA	5.52	127.67	120.28
2	Y	192	HIS	CB-CA-C	5.52	119.54	110.88
1	c	221	THR	CA-C-O	-5.51	114.28	121.73
1	l	222	TYR	CB-CG-CD1	5.51	129.07	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	169	PHE	CA-CB-CG	-5.51	108.29	113.80
1	q	285	THR	CA-C-N	5.51	123.71	120.24
1	q	285	THR	C-N-CA	5.51	123.71	120.24
2	D	283	HIS	CA-C-O	5.51	127.94	121.54
1	s	280	GLN	N-CA-C	-5.51	106.33	113.16
1	a	280	GLN	N-CA-C	-5.51	106.33	113.16
1	u	280	GLN	N-CA-C	-5.51	106.33	113.16
1	a	222	TYR	CB-CG-CD1	5.50	129.06	120.80
1	h	125	GLU	CB-CG-CD	5.50	121.96	112.60
1	f	125	GLU	CB-CG-CD	5.50	121.96	112.60
1	w	125	GLU	CB-CG-CD	5.50	121.96	112.60
2	F	282	TYR	N-CA-C	-5.50	101.83	110.36
2	I	169	PHE	CA-CB-CG	-5.50	108.30	113.80
1	i	125	GLU	CB-CG-CD	5.50	121.95	112.60
1	q	46	ARG	CG-CD-NE	5.50	124.10	112.00
2	A	271	THR	CA-CB-OG1	5.50	117.85	109.60
2	H	169	PHE	CA-CB-CG	-5.50	108.30	113.80
1	t	276	ARG	CB-CG-CD	5.50	123.95	111.30
2	V	192	HIS	CB-CA-C	5.50	119.51	110.88
1	n	280	GLN	N-CA-C	-5.50	106.34	113.16
2	C	192	HIS	CB-CA-C	5.49	119.50	110.88
2	R	192	HIS	CB-CA-C	5.49	119.50	110.88
2	I	192	HIS	CB-CA-C	5.49	119.50	110.88
2	O	274	PRO	N-CA-C	5.49	119.89	112.48
2	O	192	HIS	CB-CA-C	5.49	119.50	110.88
2	W	5	ILE	CA-CB-CG2	-5.49	101.17	110.50
2	S	167	LEU	CB-CG-CD1	5.49	127.16	110.70
2	S	282	TYR	N-CA-C	-5.49	101.86	110.36
2	U	5	ILE	CA-CB-CG2	-5.49	101.18	110.50
2	F	271	THR	CA-CB-OG1	5.49	117.83	109.60
1	k	125	GLU	CB-CG-CD	5.48	121.92	112.60
2	X	192	HIS	CB-CA-C	5.48	119.49	110.88
2	X	238	ILE	CA-C-N	-5.48	113.91	122.73
2	X	238	ILE	C-N-CA	-5.48	113.91	122.73
2	O	238	ILE	CA-C-N	-5.48	113.91	122.73
2	O	238	ILE	C-N-CA	-5.48	113.91	122.73
2	K	192	HIS	CB-CA-C	5.48	119.48	110.88
1	t	221	THR	CA-C-O	-5.48	114.34	121.73
1	m	46	ARG	CG-CD-NE	5.48	124.05	112.00
2	V	238	ILE	CA-C-N	-5.48	113.91	122.73
2	V	238	ILE	C-N-CA	-5.48	113.91	122.73
1	v	221	THR	CA-C-O	-5.48	114.34	121.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	t	222	TYR	CB-CG-CD1	5.47	129.01	120.80
2	X	77	GLU	CB-CG-CD	5.47	121.90	112.60
1	u	221	THR	CA-C-O	-5.47	114.34	121.73
1	w	280	GLN	N-CA-C	-5.47	106.38	113.16
1	z	285	THR	CA-C-N	5.47	123.69	120.24
1	z	285	THR	C-N-CA	5.47	123.69	120.24
2	Z	5	ILE	CA-CB-CG2	-5.47	101.20	110.50
2	W	192	HIS	CB-CA-C	5.47	119.47	110.88
1	i	46	ARG	CG-CD-NE	5.47	124.03	112.00
2	P	192	HIS	CB-CA-C	5.47	119.46	110.88
2	X	5	ILE	CA-CB-CG2	-5.47	101.21	110.50
2	F	231	ILE	N-CA-C	-5.47	105.04	110.62
1	j	280	GLN	N-CA-C	-5.46	106.39	113.16
2	Q	192	HIS	CB-CA-C	5.46	119.45	110.88
2	Y	274	PRO	N-CA-C	5.46	119.85	112.48
2	E	192	HIS	CB-CA-C	5.46	119.46	110.88
2	F	238	ILE	CA-C-N	-5.46	113.94	122.73
2	F	238	ILE	C-N-CA	-5.46	113.94	122.73
2	H	224	TYR	N-CA-CB	5.46	118.63	110.22
2	K	89	PRO	N-CD-CG	-5.46	95.01	103.20
1	i	11	GLN	CA-C-N	5.46	127.60	120.28
1	i	11	GLN	C-N-CA	5.46	127.60	120.28
1	g	222	TYR	CA-CB-CG	5.46	123.72	113.90
2	P	229	ARG	CB-CA-C	-5.46	98.90	110.31
2	J	178	SER	CA-C-N	5.46	130.33	121.98
2	J	178	SER	C-N-CA	5.46	130.33	121.98
2	A	229	ARG	CB-CA-C	-5.46	98.91	110.31
1	k	11	GLN	CA-C-N	5.46	127.59	120.28
1	k	11	GLN	C-N-CA	5.46	127.59	120.28
1	f	280	GLN	N-CA-C	-5.45	106.40	113.16
1	a	221	THR	CA-C-O	-5.45	114.37	121.73
2	T	77	GLU	CB-CG-CD	5.45	121.87	112.60
2	B	229	ARG	CB-CA-C	-5.45	98.92	110.31
2	G	169	PHE	CA-CB-CG	-5.45	108.35	113.80
1	x	285	THR	CA-C-N	5.45	123.67	120.24
1	x	285	THR	C-N-CA	5.45	123.67	120.24
1	s	221	THR	CA-C-O	-5.45	114.37	121.73
1	y	241	ARG	CB-CG-CD	-5.45	98.77	111.30
2	S	5	ILE	CA-CB-CG2	-5.45	101.24	110.50
2	S	238	ILE	CA-C-N	-5.44	113.97	122.73
2	S	238	ILE	C-N-CA	-5.44	113.97	122.73
2	C	238	ILE	CA-C-N	-5.44	113.97	122.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	238	ILE	C-N-CA	-5.44	113.97	122.73
1	n	358	PRO	N-CA-CB	5.44	108.51	103.39
1	g	125	GLU	CB-CG-CD	5.44	121.85	112.60
2	O	102	ASN	CB-CA-C	5.44	118.35	110.79
1	w	285	THR	CA-C-N	5.44	123.67	120.24
1	w	285	THR	C-N-CA	5.44	123.67	120.24
2	P	238	ILE	CA-C-N	-5.44	113.97	122.73
2	P	238	ILE	C-N-CA	-5.44	113.97	122.73
2	Q	271	THR	CA-CB-OG1	5.44	117.76	109.60
2	J	229	ARG	CB-CA-C	-5.44	98.95	110.31
2	X	89	PRO	CA-CB-CG	-5.43	94.18	104.50
1	y	280	GLN	N-CA-C	-5.43	106.42	113.16
2	E	102	ASN	CB-CA-C	5.43	118.34	110.79
1	u	222	TYR	CB-CG-CD1	5.43	128.95	120.80
1	y	285	THR	CA-C-N	5.43	123.66	120.24
1	y	285	THR	C-N-CA	5.43	123.66	120.24
2	V	5	ILE	CA-CB-CG2	-5.43	101.27	110.50
1	p	221	THR	CA-C-O	-5.43	114.40	121.73
2	B	192	HIS	CB-CA-C	5.43	119.41	110.88
1	l	280	GLN	N-CA-C	-5.43	106.43	113.16
2	Z	238	ILE	CA-C-N	-5.43	113.99	122.73
2	Z	238	ILE	C-N-CA	-5.43	113.99	122.73
2	U	369	ALA	CA-C-N	-5.42	115.31	122.85
2	U	369	ALA	C-N-CA	-5.42	115.31	122.85
1	w	221	THR	CA-C-O	-5.42	114.41	121.73
2	G	235	VAL	CA-CB-CG1	5.42	119.61	110.40
2	I	271	THR	CA-CB-OG1	5.42	117.73	109.60
2	K	271	THR	CA-CB-OG1	5.42	117.73	109.60
2	U	274	PRO	N-CA-C	5.42	119.80	112.48
2	A	192	HIS	CB-CA-C	5.42	119.39	110.88
2	I	231	ILE	N-CA-C	-5.42	105.09	110.62
1	q	221	THR	CA-C-O	-5.42	114.42	121.73
2	T	238	ILE	CA-C-N	-5.41	114.01	122.73
2	T	238	ILE	C-N-CA	-5.41	114.01	122.73
2	X	102	ASN	CB-CA-C	5.41	118.31	110.79
2	N	102	ASN	CB-CA-C	5.41	118.31	110.79
2	T	5	ILE	CA-CB-CG2	-5.41	101.30	110.50
2	E	229	ARG	CB-CA-C	-5.41	99.00	110.31
2	G	231	ILE	N-CA-C	-5.41	105.10	110.62
2	H	271	THR	CA-CB-OG1	5.41	117.72	109.60
1	x	304	ASP	CB-CA-C	5.41	116.37	110.15
2	U	238	ILE	CA-C-N	-5.41	114.02	122.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	U	238	ILE	C-N-CA	-5.41	114.02	122.73
1	r	221	THR	CA-C-O	-5.41	114.43	121.73
2	Y	238	ILE	CA-C-N	-5.41	114.03	122.73
2	Y	238	ILE	C-N-CA	-5.41	114.03	122.73
2	Z	102	ASN	CB-CA-C	5.41	118.30	110.79
2	E	238	ILE	CA-C-N	-5.40	114.03	122.73
2	E	238	ILE	C-N-CA	-5.40	114.03	122.73
1	v	46	ARG	CG-CD-NE	5.40	123.88	112.00
2	R	5	ILE	CA-CB-CG2	-5.40	101.32	110.50
1	e	366	THR	CB-CA-C	-5.40	100.20	109.65
1	j	11	GLN	CA-C-N	5.40	127.51	120.28
1	j	11	GLN	C-N-CA	5.40	127.51	120.28
2	N	238	ILE	CA-C-N	-5.40	114.04	122.73
2	N	238	ILE	C-N-CA	-5.40	114.04	122.73
2	H	235	VAL	CA-CB-CG1	5.40	119.58	110.40
1	h	11	GLN	CA-C-N	5.39	127.51	120.28
1	h	11	GLN	C-N-CA	5.39	127.51	120.28
2	H	238	ILE	CA-C-N	-5.39	114.05	122.73
2	H	238	ILE	C-N-CA	-5.39	114.05	122.73
1	s	304	ASP	CB-CA-C	5.39	116.35	110.15
1	i	304	ASP	CB-CA-C	5.39	116.35	110.15
1	p	46	ARG	CG-CD-NE	5.39	123.86	112.00
1	c	280	GLN	N-CA-C	-5.39	106.47	113.16
2	E	127	ASP	CA-CB-CG	5.39	117.99	112.60
1	w	304	ASP	CB-CA-C	5.39	116.35	110.15
2	R	238	ILE	CA-C-N	-5.39	114.05	122.73
2	R	238	ILE	C-N-CA	-5.39	114.05	122.73
2	K	229	ARG	CB-CA-C	-5.39	99.05	110.31
1	d	221	THR	CA-C-O	-5.39	114.46	121.73
2	Q	238	ILE	CA-C-N	-5.38	114.06	122.73
2	Q	238	ILE	C-N-CA	-5.38	114.06	122.73
1	n	285	THR	CA-C-N	5.38	123.63	120.24
1	n	285	THR	C-N-CA	5.38	123.63	120.24
1	n	392	LYS	CB-CG-CD	5.38	123.69	111.30
2	M	238	ILE	CA-C-N	-5.38	114.06	122.73
2	M	238	ILE	C-N-CA	-5.38	114.06	122.73
1	v	304	ASP	CB-CA-C	5.38	116.34	110.15
1	g	280	GLN	N-CA-C	-5.38	106.49	113.16
2	P	271	THR	CA-CB-OG1	5.38	117.67	109.60
2	E	271	THR	CA-CB-OG1	5.38	117.67	109.60
2	M	102	ASN	CB-CA-C	5.38	118.27	110.79
2	B	102	ASN	CB-CA-C	5.38	118.27	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	v	285	THR	CA-C-N	5.38	123.63	120.24
1	v	285	THR	C-N-CA	5.38	123.63	120.24
2	V	102	ASN	CB-CA-C	5.38	118.26	110.79
2	J	277	SER	CA-C-N	5.38	127.75	120.38
2	J	277	SER	C-N-CA	5.38	127.75	120.38
2	H	282	TYR	CA-C-N	-5.38	114.38	122.07
2	H	282	TYR	C-N-CA	-5.38	114.38	122.07
1	u	304	ASP	CB-CA-C	5.37	116.33	110.15
1	x	392	LYS	CB-CG-CD	5.37	123.66	111.30
1	m	11	GLN	CA-C-N	5.37	127.48	120.28
1	m	11	GLN	C-N-CA	5.37	127.48	120.28
2	N	238	ILE	CA-C-O	5.37	126.86	121.17
2	D	127	ASP	CA-CB-CG	5.37	117.97	112.60
2	A	102	ASN	CB-CA-C	5.37	118.25	110.79
1	b	46	ARG	CG-CD-NE	5.37	123.81	112.00
1	l	304	ASP	CB-CA-C	5.37	116.32	110.15
1	m	304	ASP	CB-CA-C	5.37	116.32	110.15
2	U	102	ASN	CB-CA-C	5.37	118.25	110.79
2	Y	102	ASN	CB-CA-C	5.37	118.25	110.79
2	I	229	ARG	CB-CA-C	-5.37	99.09	110.31
2	L	229	ARG	CB-CA-C	-5.37	99.09	110.31
1	k	304	ASP	CB-CA-C	5.36	116.32	110.15
2	B	238	ILE	CA-C-N	-5.36	114.10	122.73
2	B	238	ILE	C-N-CA	-5.36	114.10	122.73
2	D	102	ASN	CB-CA-C	5.36	118.25	110.79
1	b	221	THR	CA-C-O	-5.36	114.49	121.73
2	P	102	ASN	CB-CA-C	5.36	118.24	110.79
2	A	238	ILE	CA-C-N	-5.36	114.10	122.73
2	A	238	ILE	C-N-CA	-5.36	114.10	122.73
2	L	231	ILE	N-CA-C	-5.36	105.15	110.62
1	z	304	ASP	CB-CA-C	5.36	116.31	110.15
1	d	222	TYR	CB-CG-CD1	5.36	128.84	120.80
1	g	304	ASP	CB-CA-C	5.36	116.31	110.15
1	j	304	ASP	CB-CA-C	5.36	116.31	110.15
1	o	304	ASP	CB-CA-C	5.36	116.31	110.15
1	d	304	ASP	CB-CA-C	5.36	116.31	110.15
2	P	127	ASP	CA-CB-CG	5.36	117.96	112.60
2	S	102	ASN	CB-CA-C	5.36	118.24	110.79
2	Z	238	ILE	N-CA-C	-5.36	105.28	110.42
2	C	102	ASN	CB-CA-C	5.36	118.24	110.79
2	E	231	ILE	N-CA-C	-5.36	105.16	110.62
2	K	238	ILE	N-CA-C	-5.36	105.28	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	l	11	GLN	CA-C-N	5.36	127.46	120.28
1	l	11	GLN	C-N-CA	5.36	127.46	120.28
2	P	238	ILE	N-CA-C	-5.36	105.28	110.42
2	D	277	SER	CA-C-N	5.36	127.72	120.38
2	D	277	SER	C-N-CA	5.36	127.72	120.38
1	n	304	ASP	CB-CA-C	5.36	116.31	110.15
1	o	280	GLN	N-CA-C	-5.36	106.52	113.16
1	q	304	ASP	CB-CA-C	5.36	116.31	110.15
2	R	102	ASN	CB-CA-C	5.35	118.23	110.79
1	e	221	THR	CA-C-O	-5.35	114.51	121.73
2	Y	369	ALA	CA-C-N	-5.35	115.41	122.85
2	Y	369	ALA	C-N-CA	-5.35	115.41	122.85
2	J	102	ASN	CB-CA-C	5.35	118.23	110.79
2	D	238	ILE	CA-C-N	-5.35	114.12	122.73
2	D	238	ILE	C-N-CA	-5.35	114.12	122.73
2	I	127	ASP	CA-CB-CG	5.35	117.95	112.60
2	C	231	ILE	N-CA-C	-5.35	105.17	110.62
2	I	238	ILE	CA-C-N	-5.35	114.12	122.73
2	I	238	ILE	C-N-CA	-5.35	114.12	122.73
2	T	102	ASN	CB-CA-C	5.35	118.22	110.79
1	h	304	ASP	CB-CA-C	5.34	116.30	110.15
2	Q	102	ASN	CB-CA-C	5.34	118.22	110.79
2	R	127	ASP	CA-CB-CG	5.34	117.94	112.60
1	r	304	ASP	CB-CA-C	5.34	116.30	110.15
1	c	304	ASP	CB-CA-C	5.34	116.29	110.15
2	J	271	THR	CA-CB-OG1	5.34	117.61	109.60
2	K	102	ASN	CB-CA-C	5.34	118.22	110.79
1	w	291	GLN	CB-CG-CD	5.34	121.68	112.60
1	f	221	THR	CA-C-O	-5.34	114.52	121.73
2	R	393	HIS	CA-CB-CG	-5.34	108.46	113.80
2	O	127	ASP	CA-CB-CG	5.34	117.94	112.60
2	M	229	ARG	CB-CA-C	-5.34	99.15	110.31
1	u	46	ARG	CG-CD-NE	5.34	123.75	112.00
1	b	304	ASP	CB-CA-C	5.34	116.29	110.15
2	O	369	ALA	CA-C-N	-5.34	115.43	122.85
2	O	369	ALA	C-N-CA	-5.34	115.43	122.85
2	C	238	ILE	N-CA-C	-5.34	105.30	110.42
1	t	46	ARG	CG-CD-NE	5.33	123.74	112.00
1	x	280	GLN	N-CA-C	-5.33	106.54	113.16
1	g	87	PRO	CB-CA-C	5.33	120.36	111.56
2	L	102	ASN	CB-CA-C	5.33	118.20	110.79
1	f	304	ASP	CB-CA-C	5.33	116.28	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	127	ASP	CA-CB-CG	5.33	117.93	112.60
1	e	280	GLN	N-CA-C	-5.33	106.55	113.16
2	Y	238	ILE	CA-C-O	5.33	126.82	121.17
2	G	326	LYS	N-CA-C	-5.33	106.04	112.54
1	y	11	GLN	CA-C-N	5.33	127.42	120.28
1	y	11	GLN	C-N-CA	5.33	127.42	120.28
2	Q	238	ILE	CA-C-O	5.33	126.81	121.17
2	S	127	ASP	CA-CB-CG	5.33	117.92	112.60
2	Z	19	ALA	CB-CA-C	5.33	121.12	109.99
1	y	304	ASP	CB-CA-C	5.33	116.27	110.15
1	l	221	THR	CA-C-O	-5.32	114.54	121.73
2	H	127	ASP	CA-CB-CG	5.32	117.92	112.60
1	r	280	GLN	N-CA-C	-5.32	106.56	113.16
1	p	99	ASN	N-CA-CB	-5.32	104.10	112.13
1	a	304	ASP	CB-CA-C	5.32	116.27	110.15
2	Z	274	PRO	N-CA-C	5.32	119.66	112.48
2	I	102	ASN	CB-CA-C	5.32	118.18	110.79
1	m	221	THR	CA-C-O	-5.32	114.55	121.73
2	E	5	ILE	CA-CB-CG2	-5.32	101.46	110.50
2	H	229	ARG	CB-CA-C	-5.32	99.20	110.31
1	t	304	ASP	CB-CA-C	5.32	116.27	110.15
1	j	46	ARG	CG-CD-NE	5.32	123.70	112.00
2	G	238	ILE	CA-C-N	-5.32	114.17	122.73
2	G	238	ILE	C-N-CA	-5.32	114.17	122.73
1	j	125	GLU	CB-CG-CD	5.31	121.63	112.60
2	I	277	SER	CA-C-N	5.31	127.66	120.38
2	I	277	SER	C-N-CA	5.31	127.66	120.38
2	Q	127	ASP	CA-CB-CG	5.31	117.91	112.60
2	F	326	LYS	N-CA-C	-5.31	106.06	112.54
2	K	127	ASP	CA-CB-CG	5.31	117.91	112.60
2	M	127	ASP	CA-CB-CG	5.31	117.91	112.60
2	D	231	ILE	N-CA-C	-5.30	105.21	110.62
1	r	46	ARG	CG-CD-NE	5.30	123.67	112.00
2	Y	127	ASP	CA-CB-CG	5.30	117.90	112.60
2	C	127	ASP	CA-CB-CG	5.30	117.90	112.60
2	K	231	ILE	N-CA-C	-5.30	105.21	110.62
1	p	304	ASP	CB-CA-C	5.30	116.25	110.15
1	z	11	GLN	CA-C-N	5.30	127.38	120.28
1	z	11	GLN	C-N-CA	5.30	127.38	120.28
2	U	127	ASP	CA-CB-CG	5.30	117.90	112.60
2	F	127	ASP	CA-CB-CG	5.30	117.90	112.60
2	D	5	ILE	CA-CB-CG2	-5.29	101.50	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	277	SER	CA-C-N	5.29	127.63	120.38
2	E	277	SER	C-N-CA	5.29	127.63	120.38
2	K	326	LYS	N-CA-C	-5.29	106.08	112.54
2	W	102	ASN	CB-CA-C	5.29	118.14	110.79
2	A	277	SER	CA-C-N	5.29	127.63	120.38
2	A	277	SER	C-N-CA	5.29	127.63	120.38
2	Z	127	ASP	CA-CB-CG	5.29	117.89	112.60
2	J	127	ASP	CA-CB-CG	5.29	117.89	112.60
2	K	238	ILE	CA-C-N	-5.29	114.22	122.73
2	K	238	ILE	C-N-CA	-5.29	114.22	122.73
2	L	271	THR	CA-CB-OG1	5.29	117.53	109.60
1	k	221	THR	CA-C-O	-5.28	114.60	121.73
2	G	271	THR	CA-CB-OG1	5.28	117.53	109.60
1	o	285	THR	CA-C-N	5.28	123.57	120.24
1	o	285	THR	C-N-CA	5.28	123.57	120.24
2	L	238	ILE	CA-C-N	-5.28	114.23	122.73
2	L	238	ILE	C-N-CA	-5.28	114.23	122.73
1	d	11	GLN	CA-C-N	5.28	127.36	120.28
1	d	11	GLN	C-N-CA	5.28	127.36	120.28
2	V	77	GLU	CB-CG-CD	5.28	121.58	112.60
2	O	5	ILE	CA-CB-CG2	-5.28	101.53	110.50
2	M	271	THR	CA-CB-OG1	5.28	117.52	109.60
1	j	221	THR	CA-C-O	-5.28	114.61	121.73
2	N	127	ASP	CA-CB-CG	5.28	117.88	112.60
2	H	277	SER	CA-C-N	5.28	127.61	120.38
2	H	277	SER	C-N-CA	5.28	127.61	120.38
2	L	277	SER	CA-C-N	5.28	127.61	120.38
2	L	277	SER	C-N-CA	5.28	127.61	120.38
2	L	127	ASP	CA-CB-CG	5.28	117.88	112.60
2	R	238	ILE	N-CA-C	-5.27	105.36	110.42
1	e	304	ASP	CB-CA-C	5.27	116.21	110.15
1	c	291	GLN	CB-CG-CD	5.27	121.56	112.60
2	J	231	ILE	N-CA-C	-5.27	105.25	110.62
1	g	291	GLN	CB-CG-CD	5.27	121.55	112.60
2	V	238	ILE	CA-C-O	5.27	126.75	121.17
1	e	11	GLN	CA-C-N	5.27	127.34	120.28
1	e	11	GLN	C-N-CA	5.27	127.34	120.28
2	X	127	ASP	CA-CB-CG	5.27	117.87	112.60
2	D	238	ILE	N-CA-C	-5.26	105.37	110.42
2	X	238	ILE	CA-C-O	5.26	126.75	121.17
2	D	271	THR	CA-CB-OG1	5.26	117.49	109.60
2	H	238	ILE	N-CA-C	-5.26	105.37	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	p	241	ARG	CB-CA-C	-5.26	99.78	109.15
1	s	241	ARG	CB-CA-C	-5.26	99.78	109.15
1	t	241	ARG	CB-CA-C	-5.26	99.78	109.15
1	c	46	ARG	CG-CD-NE	5.26	123.58	112.00
1	e	284	LEU	CA-C-N	-5.26	114.44	122.23
1	e	284	LEU	C-N-CA	-5.26	114.44	122.23
2	V	127	ASP	CA-CB-CG	5.26	117.86	112.60
2	D	282	TYR	N-CA-C	-5.26	102.21	110.36
2	T	369	ALA	CA-C-N	-5.26	115.54	122.85
2	T	369	ALA	C-N-CA	-5.26	115.54	122.85
2	Y	326	LYS	N-CA-C	-5.25	106.13	112.54
2	G	102	ASN	CB-CA-C	5.25	118.09	110.79
1	o	11	GLN	CB-CA-C	5.25	119.62	110.79
1	i	221	THR	CA-C-O	-5.25	114.64	121.73
1	x	11	GLN	CA-C-N	5.25	127.32	120.28
1	x	11	GLN	C-N-CA	5.25	127.32	120.28
2	W	127	ASP	CA-CB-CG	5.25	117.85	112.60
2	F	102	ASN	CB-CA-C	5.25	118.08	110.79
1	x	46	ARG	CG-CD-NE	5.25	123.55	112.00
2	A	127	ASP	CA-CB-CG	5.25	117.85	112.60
2	J	238	ILE	CA-C-N	-5.25	114.28	122.73
2	J	238	ILE	C-N-CA	-5.25	114.28	122.73
1	l	46	ARG	CG-CD-NE	5.24	123.54	112.00
2	O	238	ILE	CA-C-O	5.24	126.73	121.17
2	Z	369	ALA	CA-C-N	-5.24	115.56	122.85
2	Z	369	ALA	C-N-CA	-5.24	115.56	122.85
2	J	326	LYS	N-CA-C	-5.24	106.14	112.54
2	M	231	ILE	N-CA-C	-5.24	105.27	110.62
1	n	350	LYS	CB-CG-CD	5.24	123.36	111.30
1	i	227	HIS	CA-CB-CG	-5.24	108.56	113.80
2	F	229	ARG	CB-CA-C	-5.24	99.36	110.31
1	c	11	GLN	CA-C-N	5.24	127.30	120.28
1	c	11	GLN	C-N-CA	5.24	127.30	120.28
2	X	326	LYS	N-CA-C	-5.24	106.15	112.54
2	F	369	ALA	CA-C-N	-5.24	115.57	122.85
2	F	369	ALA	C-N-CA	-5.24	115.57	122.85
2	H	102	ASN	CB-CA-C	5.24	118.07	110.79
2	F	238	ILE	N-CA-C	-5.24	105.39	110.42
2	Q	369	ALA	CA-C-N	-5.24	115.57	122.85
2	Q	369	ALA	C-N-CA	-5.24	115.57	122.85
2	A	326	LYS	N-CA-C	-5.24	106.15	112.54
2	J	238	ILE	N-CA-C	-5.24	105.39	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	y	11	GLN	CB-CG-CD	5.24	121.50	112.60
2	P	5	ILE	CA-CB-CG2	-5.23	101.61	110.50
2	Y	283	HIS	CB-CA-C	5.23	119.44	111.80
2	M	277	SER	CA-C-N	5.23	127.55	120.38
2	M	277	SER	C-N-CA	5.23	127.55	120.38
2	Z	77	GLU	CB-CG-CD	5.23	121.49	112.60
2	S	238	ILE	CA-C-O	5.23	126.71	121.17
2	T	127	ASP	CA-CB-CG	5.23	117.83	112.60
2	V	369	ALA	CA-C-N	-5.23	115.58	122.85
2	V	369	ALA	C-N-CA	-5.23	115.58	122.85
1	z	46	ARG	CG-CD-NE	5.23	123.50	112.00
2	G	238	ILE	N-CA-C	-5.23	105.40	110.42
2	D	238	ILE	CA-C-O	5.22	126.71	121.17
2	G	229	ARG	CB-CA-C	-5.22	99.39	110.31
2	I	326	LYS	N-CA-C	-5.22	106.17	112.54
2	L	238	ILE	N-CA-C	-5.22	105.40	110.42
2	N	369	ALA	CA-C-N	-5.22	115.59	122.85
2	N	369	ALA	C-N-CA	-5.22	115.59	122.85
2	P	277	SER	CA-C-N	5.22	127.53	120.38
2	P	277	SER	C-N-CA	5.22	127.53	120.38
2	E	238	ILE	N-CA-C	-5.22	105.41	110.42
2	E	326	LYS	N-CA-C	-5.22	106.17	112.54
2	R	238	ILE	CA-C-O	5.22	126.70	121.17
2	W	238	ILE	CA-C-O	5.22	126.70	121.17
2	W	238	ILE	N-CA-C	-5.22	105.41	110.42
2	C	363	VAL	CA-CB-CG2	5.22	119.27	110.40
2	C	369	ALA	CA-C-N	-5.22	115.60	122.85
2	C	369	ALA	C-N-CA	-5.22	115.60	122.85
2	I	238	ILE	N-CA-C	-5.22	105.41	110.42
2	U	238	ILE	CA-C-O	5.21	126.70	121.17
2	M	326	LYS	N-CA-C	-5.21	106.18	112.54
2	L	326	LYS	N-CA-C	-5.21	106.18	112.54
2	O	238	ILE	N-CA-C	-5.21	105.42	110.42
2	W	326	LYS	N-CA-C	-5.21	106.18	112.54
1	z	11	GLN	CB-CA-C	5.21	119.54	110.79
2	Q	393	HIS	CA-CB-CG	-5.21	108.59	113.80
2	K	277	SER	CA-C-N	5.21	127.52	120.38
2	K	277	SER	C-N-CA	5.21	127.52	120.38
2	B	277	SER	CA-C-N	5.21	127.51	120.38
2	B	277	SER	C-N-CA	5.21	127.51	120.38
1	v	11	GLN	CA-C-N	5.21	127.26	120.28
1	v	11	GLN	C-N-CA	5.21	127.26	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	326	LYS	N-CA-C	-5.21	106.19	112.54
2	W	283	HIS	CB-CA-C	5.20	119.40	111.80
2	Y	238	ILE	N-CA-C	-5.20	105.42	110.42
2	W	369	ALA	CA-C-N	-5.20	115.62	122.85
2	W	369	ALA	C-N-CA	-5.20	115.62	122.85
2	S	277	SER	CA-C-N	5.20	127.50	120.38
2	S	277	SER	C-N-CA	5.20	127.50	120.38
2	Z	326	LYS	N-CA-C	-5.20	106.20	112.54
1	x	283	ALA	CB-CA-C	5.20	118.21	109.89
2	W	235	VAL	CA-CB-CG1	5.20	119.24	110.40
1	a	90	PHE	CB-CA-C	-5.20	104.38	112.07
2	D	369	ALA	CA-C-N	-5.20	115.63	122.85
2	D	369	ALA	C-N-CA	-5.20	115.63	122.85
2	F	5	ILE	CA-CB-CG2	-5.20	101.67	110.50
1	n	11	GLN	CB-CA-C	5.20	119.52	110.79
1	n	291	GLN	CB-CG-CD	5.20	121.43	112.60
2	O	326	LYS	N-CA-C	-5.20	106.20	112.54
2	B	231	ILE	N-CA-C	-5.20	105.32	110.62
2	K	282	TYR	N-CA-C	-5.20	102.31	110.36
2	G	238	ILE	CA-C-O	5.19	126.67	121.17
2	G	127	ASP	CA-CB-CG	5.19	117.79	112.60
1	a	11	GLN	CA-C-N	5.19	127.23	120.28
1	a	11	GLN	C-N-CA	5.19	127.23	120.28
1	c	90	PHE	CB-CA-C	-5.19	104.17	112.05
1	f	366	THR	CB-CA-C	-5.18	100.58	109.65
2	A	231	ILE	N-CA-C	-5.18	105.33	110.62
2	B	51	THR	N-CA-C	-5.18	107.33	113.97
2	I	121	ARG	NE-CZ-NH2	5.18	123.86	119.20
2	K	5	ILE	CA-CB-CG2	-5.18	101.69	110.50
1	t	358	PRO	N-CA-CB	5.18	108.26	103.39
1	d	280	GLN	N-CA-C	-5.18	106.73	113.16
1	y	11	GLN	CB-CA-C	5.18	119.49	110.79
2	T	238	ILE	CA-C-O	5.18	126.66	121.17
2	C	326	LYS	N-CA-C	-5.18	106.22	112.54
2	E	238	ILE	CA-C-O	5.18	126.66	121.17
1	x	11	GLN	CB-CA-C	5.18	119.49	110.79
2	G	277	SER	CA-C-N	5.18	127.47	120.38
2	G	277	SER	C-N-CA	5.18	127.47	120.38
2	P	393	HIS	CA-CB-CG	-5.18	108.62	113.80
2	Q	326	LYS	N-CA-C	-5.18	106.22	112.54
2	U	277	SER	CA-C-N	5.18	127.47	120.38
2	U	277	SER	C-N-CA	5.18	127.47	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	326	LYS	N-CA-C	-5.17	106.23	112.54
2	H	5	ILE	CA-CB-CG2	-5.17	101.70	110.50
1	y	46	ARG	CG-CD-NE	5.17	123.38	112.00
2	N	326	LYS	N-CA-C	-5.17	106.23	112.54
1	r	11	GLN	CB-CA-C	5.17	119.47	110.79
1	j	366	THR	CB-CA-C	-5.17	100.60	109.65
2	F	277	SER	CA-C-N	5.16	127.45	120.38
2	F	277	SER	C-N-CA	5.16	127.45	120.38
2	L	5	ILE	CA-CB-CG2	-5.16	101.72	110.50
1	q	291	GLN	CB-CG-CD	5.16	121.38	112.60
1	g	221	THR	CA-C-O	-5.16	114.76	121.73
2	U	238	ILE	N-CA-C	-5.16	105.47	110.42
2	I	238	ILE	CA-C-O	5.16	126.64	121.17
2	B	271	THR	CA-CB-OG1	5.16	117.34	109.60
2	F	329	ASN	CA-CB-CG	5.16	117.76	112.60
2	G	5	ILE	CA-CB-CG2	-5.16	101.73	110.50
1	s	11	GLN	CA-C-N	5.16	127.19	120.28
1	s	11	GLN	C-N-CA	5.16	127.19	120.28
1	d	366	THR	CB-CA-C	-5.16	100.62	109.65
2	K	329	ASN	CA-CB-CG	5.16	117.76	112.60
2	T	283	HIS	CB-CA-C	5.15	119.32	111.80
1	w	46	ARG	CG-CD-NE	5.15	123.34	112.00
2	A	51	THR	N-CA-C	-5.15	107.38	113.97
2	D	326	LYS	N-CA-C	-5.15	106.25	112.54
2	X	393	HIS	CA-CB-CG	-5.15	108.65	113.80
2	M	238	ILE	N-CA-C	-5.15	105.48	110.42
2	M	238	ILE	CA-C-O	5.15	126.63	121.17
2	B	238	ILE	CA-C-O	5.15	126.62	121.17
2	B	238	ILE	N-CA-C	-5.15	105.48	110.42
1	n	11	GLN	CA-C-N	5.15	127.17	120.28
1	n	11	GLN	C-N-CA	5.15	127.17	120.28
1	v	242	PHE	CB-CA-C	5.15	116.56	108.63
2	G	233	GLN	CB-CG-CD	5.14	121.34	112.60
1	j	242	PHE	CB-CA-C	5.14	116.54	108.63
1	k	366	THR	CB-CA-C	-5.14	100.66	109.65
1	e	90	PHE	CB-CA-C	-5.14	104.24	112.05
2	H	238	ILE	CA-C-O	5.14	126.61	121.17
2	K	51	THR	N-CA-C	-5.14	107.39	113.97
1	r	366	THR	CB-CA-C	-5.14	100.66	109.65
1	i	366	THR	CB-CA-C	-5.13	100.66	109.65
2	S	51	THR	N-CA-C	-5.13	107.40	113.97
1	n	90	PHE	CB-CA-C	-5.13	104.25	112.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	326	LYS	N-CA-C	-5.13	106.28	112.54
1	w	11	GLN	CB-CA-C	5.13	119.41	110.79
2	N	238	ILE	N-CA-C	-5.13	105.49	110.42
1	t	11	GLN	CB-CA-C	5.13	119.41	110.79
1	k	242	PHE	CB-CA-C	5.13	116.52	108.63
2	W	163	LYS	CB-CG-CD	5.13	123.09	111.30
1	o	242	PHE	CB-CA-C	5.13	116.53	108.63
1	u	11	GLN	CB-CA-C	5.13	119.40	110.79
1	w	90	PHE	CB-CA-C	-5.13	104.26	112.05
1	g	11	GLN	CB-CA-C	5.12	119.40	110.79
1	w	366	THR	CB-CA-C	-5.12	100.68	109.65
2	Q	238	ILE	N-CA-C	-5.12	105.50	110.42
2	U	51	THR	N-CA-C	-5.12	107.41	113.97
2	A	238	ILE	N-CA-C	-5.12	105.50	110.42
2	C	121	ARG	NE-CZ-NH2	5.12	123.81	119.20
2	L	51	THR	N-CA-C	-5.12	107.41	113.97
1	z	392	LYS	CB-CG-CD	5.12	123.08	111.30
1	d	90	PHE	CB-CA-C	-5.12	104.27	112.05
2	T	238	ILE	N-CA-C	-5.12	105.50	110.42
2	Y	51	THR	N-CA-C	-5.12	107.41	113.97
1	q	11	GLN	CB-CA-C	5.12	119.40	110.79
1	r	90	PHE	CB-CA-C	-5.12	104.27	112.05
2	V	277	SER	CA-C-N	5.12	127.39	120.38
2	V	277	SER	C-N-CA	5.12	127.39	120.38
2	L	329	ASN	CA-CB-CG	5.12	117.72	112.60
1	d	242	PHE	CB-CA-C	5.12	116.51	108.63
2	O	393	HIS	CA-CB-CG	-5.12	108.68	113.80
2	W	51	THR	N-CA-C	-5.12	107.42	113.97
2	X	238	ILE	N-CA-C	-5.12	105.51	110.42
1	c	366	THR	CB-CA-C	-5.12	100.70	109.65
2	Z	238	ILE	CA-C-O	5.12	126.59	121.17
1	t	125	GLU	CB-CG-CD	5.12	121.30	112.60
2	U	326	LYS	N-CA-C	-5.12	106.30	112.54
2	V	393	HIS	CA-CB-CG	-5.12	108.69	113.80
2	C	5	ILE	CA-CB-CG2	-5.12	101.80	110.50
2	V	51	THR	N-CA-C	-5.11	107.43	113.97
1	x	358	PRO	N-CA-CB	5.11	108.20	103.39
2	R	283	HIS	CB-CA-C	5.11	119.26	111.80
2	K	283	HIS	CA-C-O	5.11	127.47	121.54
2	X	231	ILE	N-CA-C	-5.11	105.41	110.62
1	u	366	THR	CB-CA-C	-5.11	100.71	109.65
1	p	366	THR	CB-CA-C	-5.11	100.71	109.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	366	THR	CB-CA-C	-5.11	100.71	109.65
1	g	366	THR	CB-CA-C	-5.11	100.71	109.65
1	h	366	THR	CB-CA-C	-5.11	100.71	109.65
1	l	366	THR	CB-CA-C	-5.11	100.71	109.65
2	I	5	ILE	CA-CB-CG2	-5.11	101.82	110.50
1	p	11	GLN	CB-CA-C	5.11	119.37	110.79
1	s	222	TYR	CB-CG-CD1	5.11	128.46	120.80
2	P	326	LYS	N-CA-C	-5.11	106.31	112.54
2	S	369	ALA	CA-C-N	-5.11	115.75	122.85
2	S	369	ALA	C-N-CA	-5.11	115.75	122.85
2	Y	231	ILE	N-CA-C	-5.10	105.41	110.62
1	l	242	PHE	CB-CA-C	5.10	116.49	108.63
2	B	326	LYS	N-CA-C	-5.10	106.31	112.54
1	v	291	GLN	CB-CG-CD	5.10	121.27	112.60
1	z	366	THR	CB-CA-C	-5.10	100.72	109.65
1	g	227	HIS	CA-CB-CG	-5.10	108.70	113.80
2	F	51	THR	N-CA-C	-5.10	107.44	113.97
1	c	11	GLN	CB-CA-C	5.10	119.36	110.79
1	v	358	PRO	N-CA-CB	5.10	108.18	103.39
1	v	366	THR	CB-CA-C	-5.10	100.73	109.65
1	t	366	THR	CB-CA-C	-5.10	100.73	109.65
2	C	277	SER	CA-C-N	5.10	127.36	120.38
2	C	277	SER	C-N-CA	5.10	127.36	120.38
2	G	51	THR	N-CA-C	-5.10	107.45	113.97
1	v	11	GLN	CB-CA-C	5.10	119.35	110.79
1	b	366	THR	CB-CA-C	-5.09	100.73	109.65
1	h	221	THR	CA-C-O	-5.09	114.85	121.73
2	V	238	ILE	N-CA-C	-5.09	105.53	110.42
2	C	393	HIS	CA-CB-CG	-5.09	108.71	113.80
2	I	393	HIS	CA-CB-CG	-5.09	108.71	113.80
2	M	51	THR	N-CA-C	-5.09	107.45	113.97
1	q	242	PHE	CB-CA-C	5.09	116.48	108.63
1	w	11	GLN	CA-C-N	5.09	127.11	120.28
1	w	11	GLN	C-N-CA	5.09	127.11	120.28
2	X	51	THR	N-CA-C	-5.09	107.45	113.97
1	f	11	GLN	CB-CA-C	5.09	119.34	110.79
2	P	51	THR	N-CA-C	-5.09	107.45	113.97
2	R	326	LYS	N-CA-C	-5.09	106.33	112.54
2	H	51	THR	N-CA-C	-5.09	107.45	113.97
1	z	358	PRO	N-CA-CB	5.09	108.17	103.39
2	Q	224	TYR	N-CA-CB	5.09	118.18	110.14
1	a	358	PRO	N-CA-CB	5.09	108.17	103.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	f	90	PHE	CB-CA-C	-5.09	104.32	112.05
1	h	358	PRO	N-CA-CB	5.09	108.17	103.39
2	E	233	GLN	CB-CG-CD	5.09	121.25	112.60
2	F	393	HIS	CA-CB-CG	-5.09	108.71	113.80
1	o	291	GLN	CB-CG-CD	5.09	121.25	112.60
1	r	11	GLN	CA-C-N	5.09	127.09	120.28
1	r	11	GLN	C-N-CA	5.09	127.09	120.28
2	C	51	THR	N-CA-C	-5.08	107.46	113.97
2	C	77	GLU	CB-CG-CD	5.08	121.24	112.60
1	q	11	GLN	CA-C-N	5.08	127.09	120.28
1	q	11	GLN	C-N-CA	5.08	127.09	120.28
1	d	227	HIS	CA-CB-CG	-5.08	108.72	113.80
2	A	329	ASN	CA-CB-CG	5.08	117.68	112.60
2	G	329	ASN	CA-CB-CG	5.08	117.68	112.60
2	L	235	VAL	CA-CB-CG1	5.08	119.04	110.40
2	P	282	TYR	N-CA-C	-5.08	101.98	109.86
2	E	51	THR	N-CA-C	-5.08	107.47	113.97
1	h	46	ARG	CG-CD-NE	5.08	123.18	112.00
2	N	51	THR	N-CA-C	-5.08	107.47	113.97
1	q	363	MET	CB-CG-SD	5.08	127.94	112.70
2	F	238	ILE	CA-C-O	5.08	126.55	121.17
2	J	233	GLN	CB-CG-CD	5.08	121.23	112.60
2	P	238	ILE	CA-C-O	5.08	126.55	121.17
1	e	291	GLN	CB-CG-CD	5.08	121.23	112.60
2	W	231	ILE	N-CA-C	-5.08	105.44	110.62
1	u	291	GLN	OE1-CD-NE2	-5.08	117.53	122.60
1	x	366	THR	CB-CA-C	-5.08	100.77	109.65
2	S	326	LYS	N-CA-C	-5.07	106.35	112.54
2	I	51	THR	N-CA-C	-5.07	107.47	113.97
1	o	194	GLU	CB-CG-CD	5.07	121.22	112.60
2	H	233	GLN	CB-CG-CD	5.07	121.22	112.60
1	s	227	HIS	CA-CB-CG	-5.07	108.73	113.80
2	N	277	SER	CA-C-N	5.07	127.33	120.38
2	N	277	SER	C-N-CA	5.07	127.33	120.38
2	E	393	HIS	CA-CB-CG	-5.07	108.73	113.80
2	K	393	HIS	CA-CB-CG	-5.07	108.73	113.80
1	y	392	LYS	CB-CG-CD	5.07	122.96	111.30
2	T	51	THR	N-CA-C	-5.07	107.48	113.97
1	h	242	PHE	CB-CA-C	5.07	116.43	108.63
2	Z	51	THR	N-CA-C	-5.07	107.48	113.97
1	o	11	GLN	CA-C-N	5.07	127.07	120.28
1	o	11	GLN	C-N-CA	5.07	127.07	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	v	363	MET	CB-CG-SD	5.07	127.90	112.70
2	N	329	ASN	CA-CB-CG	5.07	117.67	112.60
2	D	51	THR	N-CA-C	-5.07	107.49	113.97
2	F	233	GLN	CB-CG-CD	5.07	121.21	112.60
1	p	358	PRO	N-CA-CB	5.07	108.15	103.39
1	q	366	THR	CB-CA-C	-5.07	100.79	109.65
2	P	171	ILE	CB-CG1-CD1	5.06	124.44	113.80
2	Q	51	THR	N-CA-C	-5.06	107.49	113.97
2	T	231	ILE	N-CA-C	-5.06	105.45	110.62
2	K	121	ARG	NE-CZ-NH2	5.06	123.76	119.20
2	F	235	VAL	CA-CB-CG1	5.06	119.01	110.40
1	a	46	ARG	CG-CD-NE	5.06	123.14	112.00
1	b	11	GLN	CA-C-N	5.06	127.06	120.28
1	b	11	GLN	C-N-CA	5.06	127.06	120.28
2	O	283	HIS	CB-CA-C	5.06	119.19	111.80
1	s	366	THR	CB-CA-C	-5.06	100.79	109.65
2	U	393	HIS	CA-CB-CG	-5.06	108.74	113.80
1	u	11	GLN	CA-C-N	5.06	127.06	120.28
1	u	11	GLN	C-N-CA	5.06	127.06	120.28
1	v	90	PHE	CB-CA-C	-5.06	104.36	112.05
1	d	194	GLU	CB-CG-CD	5.06	121.20	112.60
1	n	366	THR	CB-CA-C	-5.06	100.80	109.65
2	N	393	HIS	CA-CB-CG	-5.06	108.74	113.80
2	C	283	HIS	CA-C-O	5.06	127.41	121.54
1	x	242	PHE	CB-CA-C	5.06	116.42	108.63
1	h	11	GLN	CB-CA-C	5.05	119.28	110.79
2	D	393	HIS	CA-CB-CG	-5.05	108.75	113.80
2	J	283	HIS	CA-C-O	5.05	127.40	121.54
1	q	90	PHE	CB-CA-C	-5.05	104.37	112.05
2	G	282	TYR	N-CA-C	-5.05	102.53	110.36
1	n	99	ASN	N-CA-C	-5.05	104.42	111.39
1	o	366	THR	CB-CA-C	-5.05	100.81	109.65
1	p	90	PHE	CB-CA-C	-5.05	104.37	112.05
1	x	291	GLN	CB-CG-CD	5.05	121.19	112.60
2	A	238	ILE	CA-C-O	5.05	126.52	121.17
2	A	285	GLN	N-CA-C	-5.05	104.38	110.44
1	s	125	GLU	CB-CG-CD	5.05	121.19	112.60
1	y	366	THR	CB-CA-C	-5.05	100.81	109.65
1	w	358	PRO	N-CA-CB	5.05	108.14	103.39
2	Q	329	ASN	CA-CB-CG	5.05	117.65	112.60
2	A	5	ILE	CA-CB-CG2	-5.05	101.92	110.50
1	e	11	GLN	CB-CA-C	5.04	119.26	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	51	THR	N-CA-C	-5.04	107.51	113.97
2	R	77	GLU	CB-CG-CD	5.04	121.17	112.60
2	T	277	SER	CA-C-N	5.04	127.29	120.38
2	T	277	SER	C-N-CA	5.04	127.29	120.38
1	z	99	ASN	N-CA-C	-5.04	104.43	111.39
1	a	242	PHE	CB-CA-C	5.04	116.39	108.63
1	d	11	GLN	CB-CA-C	5.04	119.26	110.79
1	m	366	THR	CB-CA-C	-5.04	100.83	109.65
2	S	231	ILE	N-CA-C	-5.04	105.48	110.62
1	u	358	PRO	N-CA-CB	5.04	108.13	103.39
2	I	233	GLN	CB-CG-CD	5.04	121.17	112.60
2	K	238	ILE	CA-C-O	5.04	126.51	121.17
1	l	194	GLU	CB-CG-CD	5.04	121.17	112.60
2	O	231	ILE	N-CA-C	-5.04	105.48	110.62
2	I	329	ASN	CA-CB-CG	5.04	117.64	112.60
2	J	238	ILE	CA-C-O	5.04	126.51	121.17
2	J	51	THR	N-CA-C	-5.04	107.53	113.97
2	J	329	ASN	CA-CB-CG	5.04	117.64	112.60
1	y	90	PHE	CB-CA-C	-5.04	104.40	112.05
1	s	11	GLN	CB-CA-C	5.03	119.25	110.79
2	P	231	ILE	N-CA-C	-5.03	105.49	110.62
1	c	242	PHE	CB-CA-C	5.03	116.38	108.63
1	z	194	GLU	CB-CG-CD	5.03	121.15	112.60
2	Y	315	CYS	CA-C-N	-5.03	111.93	121.54
2	Y	315	CYS	C-N-CA	-5.03	111.93	121.54
1	x	90	PHE	CB-CA-C	-5.03	104.41	112.05
2	G	393	HIS	CA-CB-CG	-5.03	108.77	113.80
1	o	99	ASN	N-CA-C	-5.03	104.45	111.39
1	d	291	GLN	CB-CG-CD	5.03	121.14	112.60
1	i	242	PHE	CB-CA-C	5.03	116.37	108.63
2	N	231	ILE	N-CA-C	-5.03	105.49	110.62
1	o	325	GLU	CA-C-N	-5.03	114.13	120.56
1	o	325	GLU	C-N-CA	-5.03	114.13	120.56
2	L	238	ILE	CA-C-O	5.02	126.50	121.17
1	j	291	GLN	CB-CG-CD	5.02	121.14	112.60
2	Z	277	SER	CA-C-N	5.02	127.26	120.38
2	Z	277	SER	C-N-CA	5.02	127.26	120.38
2	J	393	HIS	CA-CB-CG	-5.02	108.78	113.80
1	q	99	ASN	N-CA-C	-5.02	104.46	111.39
1	z	90	PHE	CB-CA-C	-5.02	104.42	112.05
1	i	291	GLN	CB-CG-CD	5.02	121.13	112.60
1	j	11	GLN	CB-CA-C	5.02	119.22	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Z	231	ILE	N-CA-C	-5.02	105.50	110.62
1	u	242	PHE	CB-CA-C	5.02	116.36	108.63
2	W	393	HIS	CA-CB-CG	-5.02	108.78	113.80
2	Y	393	HIS	CA-CB-CG	-5.02	108.78	113.80
2	R	231	ILE	N-CA-C	-5.01	105.51	110.62
2	B	329	ASN	CA-CB-CG	5.01	117.61	112.60
2	D	315	CYS	CA-C-N	-5.01	111.97	121.54
2	D	315	CYS	C-N-CA	-5.01	111.97	121.54
1	p	11	GLN	CA-C-N	5.01	127.00	120.28
1	p	11	GLN	C-N-CA	5.01	127.00	120.28
1	k	99	ASN	N-CA-C	-5.01	104.48	111.39
1	b	291	GLN	CB-CG-CD	5.01	121.11	112.60
1	f	227	HIS	CA-CB-CG	-5.01	108.79	113.80
1	f	291	GLN	CB-CG-CD	5.01	121.11	112.60
2	Q	231	ILE	N-CA-C	-5.01	105.51	110.62
2	H	393	HIS	CA-CB-CG	-5.01	108.79	113.80
1	g	99	ASN	N-CA-C	-5.00	104.48	111.39
2	I	369	ALA	CA-C-N	-5.00	115.89	122.85
2	I	369	ALA	C-N-CA	-5.00	115.89	122.85
1	o	90	PHE	CB-CA-C	-5.00	104.44	112.05
1	j	90	PHE	CB-CA-C	-5.00	104.45	112.05
1	m	194	GLU	CB-CG-CD	5.00	121.10	112.60

There are no chirality outliers.

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	347	CYS	Peptide
2	B	347	CYS	Peptide
2	C	347	CYS	Peptide
2	D	347	CYS	Peptide
2	E	347	CYS	Peptide
2	F	347	CYS	Peptide
2	G	347	CYS	Peptide
2	H	347	CYS	Peptide
2	I	347	CYS	Peptide
2	J	347	CYS	Peptide
2	K	347	CYS	Peptide
2	L	347	CYS	Peptide
2	M	347	CYS	Peptide
2	N	347	CYS	Peptide
2	O	347	CYS	Peptide

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Mol	Chain	Res	Type	Group
2	P	347	CYS	Peptide
2	Q	347	CYS	Peptide
2	R	347	CYS	Peptide
2	S	347	CYS	Peptide
2	T	347	CYS	Peptide
2	U	347	CYS	Peptide
2	V	347	CYS	Peptide
2	W	347	CYS	Peptide
2	X	347	CYS	Peptide
2	Y	347	CYS	Peptide
2	Z	347	CYS	Peptide
1	e	285	THR	Mainchain
1	h	222	TYR	Sidechain
1	i	310	TYR	Sidechain

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	a	3376	0	3257	111	0
1	b	3376	0	3256	148	0
1	c	3376	0	3256	136	0
1	d	3376	0	3257	129	0
1	e	3376	0	3256	133	0
1	f	3376	0	3257	121	0
1	g	3376	0	3257	111	0
1	h	3376	0	3256	112	0
1	i	3376	0	3257	105	0
1	j	3376	0	3257	104	0
1	k	3376	0	3257	101	0
1	l	3376	0	3257	105	0
1	m	3376	0	3257	114	0
1	n	3376	0	3257	76	0
1	o	3376	0	3257	72	0
1	p	3376	0	3257	68	0
1	q	3376	0	3257	81	0
1	r	3376	0	3257	80	0
1	s	3376	0	3257	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	t	3376	0	3257	88	0
1	u	3376	0	3257	76	0
1	v	3376	0	3257	79	0
1	w	3376	0	3257	82	0
1	x	3376	0	3257	77	0
1	y	3376	0	3257	74	0
1	z	3376	0	3257	72	0
2	A	3446	0	3355	110	0
2	B	3446	0	3355	104	0
2	C	3446	0	3355	89	0
2	D	3446	0	3355	97	0
2	E	3446	0	3355	83	0
2	F	3446	0	3355	106	0
2	G	3446	0	3355	119	0
2	H	3446	0	3355	108	0
2	I	3446	0	3355	103	0
2	J	3446	0	3355	104	0
2	K	3446	0	3355	100	0
2	L	3446	0	3355	106	0
2	M	3446	0	3355	101	0
2	N	3446	0	3355	116	0
2	O	3446	0	3355	113	0
2	P	3446	0	3355	109	0
2	Q	3446	0	3355	115	0
2	R	3446	0	3354	117	0
2	S	3446	0	3355	132	0
2	T	3446	0	3355	126	0
2	U	3446	0	3355	121	0
2	V	3446	0	3355	110	0
2	W	3446	0	3355	116	0
2	X	3446	0	3355	115	0
2	Y	3446	0	3355	118	0
2	Z	3446	0	3355	117	0
3	a	62	0	51	18	0
3	b	62	0	51	11	0
3	c	62	0	51	23	0
3	d	62	0	51	19	0
3	e	62	0	51	19	0
3	f	62	0	51	10	0
3	g	62	0	50	18	0
3	h	62	0	51	18	0
3	i	62	0	51	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	j	62	0	51	14	0
3	k	62	0	51	16	0
3	l	62	0	51	17	0
3	m	62	0	51	15	0
4	a	28	0	12	19	0
4	b	28	0	10	61	0
4	c	28	0	12	40	0
4	d	28	0	12	35	0
4	e	28	0	12	33	0
4	f	28	0	12	31	0
4	g	28	0	12	15	0
4	h	28	0	12	29	0
4	i	28	0	12	12	0
4	j	28	0	12	15	0
4	k	28	0	12	13	0
4	l	28	0	12	16	0
4	m	28	0	12	30	0
5	N	1	0	0	0	0
5	O	1	0	0	0	0
5	P	1	0	0	0	0
5	Q	1	0	0	0	0
5	R	1	0	0	0	0
5	S	1	0	0	0	0
5	T	1	0	0	0	0
5	U	1	0	0	0	0
5	V	1	0	0	0	0
5	W	1	0	0	0	0
5	X	1	0	0	0	0
5	Y	1	0	0	0	0
5	Z	1	0	0	0	0
6	N	32	0	12	30	0
6	O	32	0	12	27	0
6	P	32	0	12	17	0
6	Q	32	0	12	23	0
6	R	32	0	12	19	0
6	S	32	0	12	31	0
6	T	32	0	11	31	0
6	U	32	0	12	38	0
6	V	32	0	12	28	0
6	W	32	0	12	28	0
6	X	32	0	12	29	0
6	Y	32	0	12	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Z	32	0	12	30	0
All	All	178971	0	172878	4628	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 13.

All (4628) 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)
2:K:88:HIS:CD2	2:L:283:HIS:CB	1.77	1.62
1:e:222:TYR:CE1	4:e:602:GDP:C2	1.86	1.62
1:e:222:TYR:HE1	4:e:602:GDP:C2	1.13	1.60
1:f:222:TYR:HE1	4:f:602:GDP:C2	0.98	1.59
1:f:222:TYR:CE1	4:f:602:GDP:C2	1.87	1.59
2:A:89:PRO:HD3	2:B:283:HIS:CE1	1.38	1.59
2:F:88:HIS:CD2	2:G:283:HIS:CB	1.87	1.58
2:L:88:HIS:CD2	2:M:283:HIS:CB	1.80	1.58
1:t:87:PRO:HD3	1:u:281:TYR:CE2	1.36	1.56
2:G:88:HIS:CD2	2:H:283:HIS:CB	1.85	1.55
2:I:88:HIS:CD2	2:J:283:HIS:CB	1.87	1.55
2:P:12:ALA:HB2	6:P:502:GTP:C8	1.40	1.55
1:w:87:PRO:HD3	1:x:281:TYR:CE2	1.40	1.54
2:H:88:HIS:CD2	2:I:283:HIS:CB	1.85	1.54
2:L:88:HIS:CD2	2:M:283:HIS:HB2	1.34	1.54
1:c:222:TYR:CE1	4:c:602:GDP:N1	1.73	1.52
1:b:12:CYS:CB	4:b:602:GDP:H1'	1.32	1.52
2:P:12:ALA:CB	6:P:502:GTP:N7	1.73	1.51
1:b:12:CYS:HB3	4:b:602:GDP:C1'	1.08	1.51
1:f:222:TYR:CE1	4:f:602:GDP:N1	1.78	1.51
1:q:87:PRO:HD3	1:r:281:TYR:CE2	1.41	1.50
2:G:88:HIS:CD2	2:H:283:HIS:HB2	1.42	1.50
1:c:12:CYS:SG	4:c:602:GDP:C2	2.05	1.50
1:s:87:PRO:HD3	1:t:281:TYR:CE2	1.49	1.48
2:K:88:HIS:CD2	2:L:283:HIS:HB2	1.36	1.48
2:J:88:HIS:CD2	2:K:283:HIS:HB2	1.44	1.47
2:X:224:TYR:CE2	6:X:502:GTP:C2	2.05	1.45
2:A:88:HIS:HA	2:B:283:HIS:CD2	1.52	1.45
2:A:283:HIS:CE1	2:M:89:PRO:HD3	1.51	1.44
1:s:87:PRO:CD	1:t:281:TYR:CD2	1.99	1.44
1:y:87:PRO:HD3	1:z:281:TYR:CE2	1.54	1.43
2:F:88:HIS:CD2	2:G:283:HIS:HB2	1.45	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:88:HIS:CD2	2:J:283:HIS:HB2	1.48	1.39
1:t:87:PRO:CD	1:u:281:TYR:CE2	2.03	1.39
1:c:222:TYR:CE1	4:c:602:GDP:C2	2.08	1.39
2:H:88:HIS:CD2	2:I:283:HIS:HB3	1.44	1.38
1:s:87:PRO:CD	1:t:281:TYR:CE2	2.07	1.37
2:C:88:HIS:CD2	2:D:283:HIS:CB	2.08	1.37
2:A:283:HIS:CD2	2:M:88:HIS:HA	1.58	1.36
1:x:87:PRO:HD3	1:y:281:TYR:CE2	1.62	1.35
1:t:87:PRO:CD	1:u:281:TYR:CD2	2.07	1.35
1:n:281:TYR:CE2	1:z:87:PRO:HD3	1.60	1.35
1:e:55:THR:CB	2:F:284:GLU:OE2	1.74	1.34
1:e:294:PHE:C	1:e:295:ASP:N	1.83	1.34
1:f:222:TYR:CE1	4:f:602:GDP:C6	2.14	1.34
2:C:88:HIS:CD2	2:D:283:HIS:HB2	1.63	1.34
2:L:88:HIS:HD2	2:M:283:HIS:CB	1.16	1.34
1:n:87:PRO:HD3	1:o:281:TYR:CE2	1.60	1.34
1:c:347:ASN:O	2:P:181:VAL:HG22	1.27	1.33
2:J:88:HIS:CD2	2:K:283:HIS:CB	2.07	1.33
1:s:87:PRO:HD2	1:t:281:TYR:CD2	1.59	1.33
1:e:222:TYR:CE1	4:e:602:GDP:N1	1.96	1.32
2:K:88:HIS:HD2	2:L:283:HIS:CB	1.15	1.32
1:g:347:ASN:O	2:T:181:VAL:CG2	1.76	1.32
1:a:347:ASN:O	2:N:181:VAL:HG22	1.27	1.31
1:q:87:PRO:CD	1:r:281:TYR:CE2	2.12	1.31
2:X:224:TYR:CD2	6:X:502:GTP:N1	2.00	1.30
2:F:88:HIS:CD2	2:G:283:HIS:HB3	1.56	1.30
1:g:347:ASN:O	2:T:181:VAL:HG22	1.19	1.30
1:m:222:TYR:CE1	4:m:602:GDP:C2	2.20	1.30
2:I:88:HIS:CD2	2:J:283:HIS:HB3	1.53	1.29
2:V:224:TYR:CE2	6:V:502:GTP:C2	2.21	1.29
1:m:12:CYS:SG	4:m:602:GDP:C2	2.25	1.29
1:l:347:ASN:O	2:Y:181:VAL:HG22	1.31	1.29
1:h:347:ASN:O	2:U:181:VAL:HG22	1.26	1.28
1:c:222:TYR:HE1	4:c:602:GDP:C2	1.48	1.28
2:J:88:HIS:HD2	2:K:283:HIS:CB	1.38	1.27
2:P:12:ALA:HB1	6:P:502:GTP:N7	1.38	1.27
1:f:347:ASN:O	2:S:181:VAL:HG22	1.30	1.27
1:k:347:ASN:O	2:X:181:VAL:HG22	1.28	1.27
1:b:347:ASN:O	2:O:181:VAL:HG22	1.30	1.26
1:c:222:TYR:OH	4:c:602:GDP:C4	1.87	1.26
2:U:224:TYR:CE2	6:U:502:GTP:C4	2.24	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:11:GLN:HB3	6:Y:502:GTP:O2A	1.34	1.26
1:u:87:PRO:HD3	1:v:281:TYR:CE2	1.69	1.26
1:m:347:ASN:O	2:Z:181:VAL:HG22	1.32	1.26
1:c:222:TYR:CE1	4:c:602:GDP:C6	2.24	1.26
1:j:347:ASN:O	2:W:181:VAL:HG22	1.25	1.26
1:q:87:PRO:CD	1:r:281:TYR:CD2	2.19	1.26
1:d:347:ASN:O	2:Q:181:VAL:HG22	1.27	1.26
1:e:347:ASN:O	2:R:181:VAL:HG22	1.21	1.26
2:S:224:TYR:CE2	6:S:502:GTP:C2	2.23	1.25
1:v:87:PRO:HD3	1:w:281:TYR:CE2	1.69	1.25
2:S:224:TYR:CD2	6:S:502:GTP:N1	2.04	1.25
2:T:224:TYR:CD2	6:T:502:GTP:N1	2.03	1.25
2:T:224:TYR:CD2	6:T:502:GTP:C6	2.24	1.25
2:P:12:ALA:CB	6:P:502:GTP:C8	2.13	1.24
1:e:55:THR:HB	2:F:284:GLU:OE2	1.27	1.24
1:i:347:ASN:O	2:V:181:VAL:HG22	1.31	1.24
2:G:88:HIS:CD2	2:H:283:HIS:HB3	1.58	1.24
2:F:88:HIS:HA	2:G:283:HIS:CD2	1.73	1.24
1:e:347:ASN:O	2:R:181:VAL:CG2	1.87	1.23
2:Z:224:TYR:CE2	6:Z:502:GTP:C2	2.25	1.23
2:G:88:HIS:HA	2:H:283:HIS:CD2	1.72	1.23
2:G:89:PRO:HD3	2:H:283:HIS:CE1	1.72	1.23
1:h:347:ASN:O	2:U:181:VAL:CG2	1.88	1.22
1:l:347:ASN:O	2:Y:181:VAL:CG2	1.86	1.22
1:d:350:LYS:HG3	2:Q:179:THR:O	1.40	1.22
2:Z:224:TYR:HE2	6:Z:502:GTP:C2	1.57	1.22
2:H:88:HIS:CD2	2:I:283:HIS:HB2	1.55	1.22
1:j:347:ASN:O	2:W:181:VAL:CG2	1.88	1.21
2:R:43:GLY:C	2:R:44:GLY:N	1.98	1.21
2:D:88:HIS:HA	2:E:283:HIS:CD2	1.74	1.21
1:w:87:PRO:CD	1:x:281:TYR:CE2	2.23	1.21
1:w:87:PRO:HD3	1:x:281:TYR:CD2	1.74	1.21
1:a:350:LYS:HG3	2:N:179:THR:O	1.41	1.21
1:e:222:TYR:CD1	4:e:602:GDP:N1	2.09	1.21
1:m:12:CYS:SG	4:m:602:GDP:N3	2.12	1.21
2:F:88:HIS:HD2	2:G:283:HIS:CB	1.36	1.21
1:k:347:ASN:O	2:X:181:VAL:CG2	1.88	1.21
2:S:326:LYS:CG	1:s:220:PRO:HD2	1.71	1.21
2:V:224:TYR:CD2	6:V:502:GTP:N1	2.07	1.21
1:w:87:PRO:CD	1:x:281:TYR:CD2	2.24	1.21
1:a:347:ASN:O	2:N:181:VAL:CG2	1.88	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:88:HIS:HA	2:M:283:HIS:CD2	1.76	1.20
1:f:222:TYR:CZ	4:f:602:GDP:C4	2.28	1.20
1:m:350:LYS:HG3	2:Z:179:THR:O	1.40	1.20
1:t:87:PRO:HD3	1:u:281:TYR:CD2	1.69	1.20
1:d:222:TYR:CE1	4:d:602:GDP:C2	2.28	1.20
1:i:55:THR:OG1	1:j:283:ALA:HA	1.39	1.20
1:q:87:PRO:HD2	1:r:281:TYR:CD2	1.77	1.20
2:S:284:GLU:OE2	1:r:55:THR:CB	1.89	1.20
1:b:12:CYS:CB	4:b:602:GDP:C1'	1.99	1.19
1:b:347:ASN:O	2:O:181:VAL:CG2	1.90	1.19
1:f:347:ASN:O	2:S:181:VAL:CG2	1.90	1.19
2:Y:171:ILE:CD1	6:Y:502:GTP:HN22	1.55	1.19
2:K:88:HIS:CD2	2:L:283:HIS:HB3	1.50	1.19
2:N:224:TYR:CE2	6:N:502:GTP:C2	2.29	1.19
1:v:87:PRO:HD3	1:w:281:TYR:CD2	1.77	1.19
1:f:222:TYR:CD1	4:f:602:GDP:N1	2.09	1.18
2:O:224:TYR:CE2	6:O:502:GTP:C2	2.31	1.18
2:U:224:TYR:CD2	6:U:502:GTP:N1	2.12	1.18
1:c:350:LYS:HG3	2:P:179:THR:O	1.40	1.18
2:C:88:HIS:HD2	2:D:283:HIS:CB	1.46	1.18
1:c:347:ASN:O	2:P:181:VAL:CG2	1.90	1.17
2:T:224:TYR:CE2	6:T:502:GTP:C4	2.30	1.17
2:U:224:TYR:CE2	6:U:502:GTP:C2	2.32	1.17
1:b:350:LYS:HG3	2:O:179:THR:O	1.41	1.17
1:e:350:LYS:HG3	2:R:179:THR:O	1.44	1.17
1:m:347:ASN:O	2:Z:181:VAL:CG2	1.92	1.17
2:Z:224:TYR:CD2	6:Z:502:GTP:C6	2.33	1.17
1:d:347:ASN:O	2:Q:181:VAL:CG2	1.92	1.17
2:D:89:PRO:HD3	2:E:283:HIS:CE1	1.80	1.17
2:H:88:HIS:HA	2:I:283:HIS:CD2	1.78	1.16
2:I:88:HIS:HA	2:J:283:HIS:CD2	1.80	1.16
2:K:88:HIS:HA	2:L:283:HIS:CD2	1.80	1.16
2:W:224:TYR:CD2	6:W:502:GTP:N1	2.12	1.16
1:i:347:ASN:O	2:V:181:VAL:CG2	1.91	1.16
2:W:224:TYR:CE2	6:W:502:GTP:C4	2.33	1.16
1:y:87:PRO:CD	1:z:281:TYR:CE2	2.29	1.16
1:k:55:THR:OG1	1:l:283:ALA:HA	1.46	1.15
2:Z:224:TYR:CE2	6:Z:502:GTP:C4	2.32	1.15
1:t:87:PRO:HD2	1:u:281:TYR:CD2	1.70	1.15
2:Z:224:TYR:CD2	6:Z:502:GTP:N1	2.15	1.15
2:I:88:HIS:HD2	2:J:283:HIS:CB	1.33	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:222:TYR:CZ	4:e:602:GDP:C4	2.35	1.15
2:X:11:GLN:HB3	6:X:502:GTP:O2A	1.47	1.15
2:Y:224:TYR:CE2	6:Y:502:GTP:C2	2.34	1.15
1:s:87:PRO:HD3	1:t:281:TYR:CD2	1.71	1.15
1:c:222:TYR:CZ	4:c:602:GDP:C5	2.35	1.14
1:e:12:CYS:SG	4:e:602:GDP:C2	2.40	1.14
2:L:88:HIS:CD2	2:M:283:HIS:HB3	1.57	1.14
2:N:326:LYS:HE2	1:n:219:THR:HA	1.28	1.14
1:f:222:TYR:CD1	4:f:602:GDP:C6	2.36	1.14
2:R:326:LYS:HG2	1:r:220:PRO:HD2	1.22	1.14
1:f:281:TYR:CD2	2:R:89:PRO:HD3	1.82	1.14
1:l:350:LYS:HG3	2:Y:179:THR:O	1.48	1.14
1:v:87:PRO:CD	1:w:281:TYR:CD2	2.29	1.14
2:Y:326:LYS:HG2	1:y:220:PRO:HD2	1.26	1.13
1:d:220:PRO:HD2	2:D:326:LYS:HG2	1.27	1.13
1:j:55:THR:OG1	1:k:283:ALA:HA	1.46	1.13
1:l:55:THR:OG1	1:m:283:ALA:HA	1.47	1.13
2:T:224:TYR:CE2	6:T:502:GTP:C2	2.36	1.13
2:L:89:PRO:HD3	2:M:283:HIS:CE1	1.81	1.13
1:e:220:PRO:HD2	2:E:326:LYS:HG2	1.28	1.13
1:u:87:PRO:CD	1:v:281:TYR:CE2	2.32	1.13
1:b:220:PRO:HD2	2:B:326:LYS:HG2	1.23	1.13
1:d:222:TYR:CE1	4:d:602:GDP:N1	2.17	1.13
1:i:350:LYS:HG3	2:V:179:THR:O	1.48	1.13
1:b:10:GLY:HA3	4:b:602:GDP:H4'	1.27	1.12
1:f:222:TYR:OH	4:f:602:GDP:C4	2.02	1.12
2:O:326:LYS:HE2	1:o:219:THR:HA	1.31	1.12
2:A:89:PRO:CD	2:B:283:HIS:CE1	2.31	1.12
1:a:220:PRO:HD2	2:A:326:LYS:HG2	1.21	1.12
2:Z:11:GLN:HB3	6:Z:502:GTP:O2A	1.46	1.12
1:j:350:LYS:HG3	2:W:179:THR:O	1.50	1.12
2:S:326:LYS:HG2	1:s:220:PRO:CD	1.79	1.12
1:q:87:PRO:HD3	1:r:281:TYR:CD2	1.82	1.12
2:V:326:LYS:HG2	1:v:220:PRO:HD2	1.23	1.11
2:A:88:HIS:CA	2:B:283:HIS:CD2	2.32	1.11
1:m:11:GLN:HB3	4:m:602:GDP:O1A	1.51	1.11
1:b:169:VAL:HG21	4:b:602:GDP:N2	1.65	1.11
2:X:224:TYR:HE2	6:X:502:GTP:C2	1.55	1.11
2:F:89:PRO:HD3	2:G:283:HIS:CE1	1.84	1.11
1:h:222:TYR:CE2	4:h:602:GDP:C5	2.38	1.11
1:k:350:LYS:HG3	2:X:179:THR:O	1.48	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:224:TYR:CZ	6:T:502:GTP:C4	2.37	1.11
2:Y:171:ILE:HD11	6:Y:502:GTP:N2	1.66	1.11
2:Z:224:TYR:HE2	6:Z:502:GTP:N3	1.48	1.11
1:x:87:PRO:HD3	1:y:281:TYR:CD2	1.85	1.11
1:c:12:CYS:SG	4:c:602:GDP:N1	2.23	1.10
1:i:220:PRO:HD2	2:I:326:LYS:HG2	1.31	1.10
2:T:224:TYR:CD2	6:T:502:GTP:C2	2.39	1.10
2:K:89:PRO:HD3	2:L:283:HIS:CE1	1.87	1.10
2:X:224:TYR:CZ	6:X:502:GTP:C4	2.40	1.10
2:G:88:HIS:HD2	2:H:283:HIS:CB	1.32	1.10
2:U:326:LYS:HG2	1:u:220:PRO:HD2	1.18	1.10
1:y:87:PRO:HD3	1:z:281:TYR:CD2	1.87	1.10
1:e:234:SER:HB3	3:e:601:TA1:H401	1.34	1.09
1:h:220:PRO:HD2	2:H:326:LYS:HG2	1.34	1.09
2:R:326:LYS:HE2	1:r:219:THR:HA	1.30	1.09
1:l:220:PRO:HD2	2:L:326:LYS:HG2	1.33	1.09
2:C:88:HIS:CD2	2:D:283:HIS:HB3	1.76	1.09
1:n:281:TYR:CD2	1:z:87:PRO:HD3	1.88	1.09
1:f:350:LYS:HG3	2:S:179:THR:O	1.51	1.09
2:W:326:LYS:HE2	1:w:219:THR:HA	1.34	1.09
2:T:224:TYR:CE2	6:T:502:GTP:N3	2.21	1.09
2:Q:326:LYS:HE2	1:q:219:THR:HA	1.29	1.09
1:b:10:GLY:CA	4:b:602:GDP:H4'	1.81	1.08
1:h:350:LYS:HG3	2:U:179:THR:O	1.53	1.08
2:Q:326:LYS:HG2	1:q:220:PRO:HD2	1.15	1.08
2:Y:326:LYS:HE2	1:y:219:THR:HA	1.35	1.08
2:Z:326:LYS:HG2	1:z:220:PRO:HD2	1.31	1.08
1:s:87:PRO:CG	1:t:281:TYR:HE2	1.66	1.08
2:N:326:LYS:HG2	1:n:220:PRO:HD2	1.28	1.08
2:W:326:LYS:HG2	1:w:220:PRO:HD2	1.25	1.08
1:x:87:PRO:CD	1:y:281:TYR:CD2	2.36	1.08
1:b:10:GLY:HA3	4:b:602:GDP:C4'	1.84	1.08
2:H:89:PRO:HD3	2:I:283:HIS:CE1	1.88	1.08
1:m:222:TYR:CZ	4:m:602:GDP:N3	2.21	1.08
2:U:224:TYR:CZ	6:U:502:GTP:C4	2.41	1.08
2:A:88:HIS:HA	2:B:283:HIS:NE2	1.68	1.08
1:h:12:CYS:SG	4:h:602:GDP:C2	2.47	1.07
2:U:326:LYS:HE2	1:u:219:THR:HA	1.31	1.07
2:W:224:TYR:CE2	6:W:502:GTP:C2	2.41	1.07
2:Y:171:ILE:CD1	6:Y:502:GTP:N2	2.16	1.07
1:e:222:TYR:CE1	4:e:602:GDP:N3	2.23	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:88:HIS:HD2	2:I:283:HIS:CB	1.36	1.07
2:I:89:PRO:HD3	2:J:283:HIS:CE1	1.88	1.07
1:n:281:TYR:CE2	1:z:87:PRO:CD	2.38	1.07
1:c:222:TYR:CZ	4:c:602:GDP:C4	2.42	1.07
1:k:220:PRO:HD2	2:K:326:LYS:HG2	1.35	1.07
2:X:326:LYS:HG2	1:x:220:PRO:HD2	1.32	1.07
2:Y:224:TYR:CD2	6:Y:502:GTP:N1	2.22	1.07
2:J:88:HIS:HD2	2:K:283:HIS:HB3	1.14	1.07
1:f:220:PRO:HD2	2:F:326:LYS:HG2	1.34	1.07
2:U:224:TYR:CE2	6:U:502:GTP:N3	2.21	1.07
2:Z:326:LYS:HE2	1:z:219:THR:HA	1.30	1.07
1:x:87:PRO:CD	1:y:281:TYR:CE2	2.37	1.07
2:S:224:TYR:CE2	6:S:502:GTP:C4	2.43	1.07
1:n:87:PRO:CD	1:o:281:TYR:CE2	2.38	1.07
1:y:87:PRO:CD	1:z:281:TYR:CD2	2.36	1.06
1:q:87:PRO:HD2	1:r:281:TYR:HD2	1.10	1.06
1:a:141:GLY:HA3	4:a:602:GDP:H2'	1.33	1.06
1:f:222:TYR:CZ	4:f:602:GDP:C5	2.42	1.06
2:S:224:TYR:CZ	6:S:502:GTP:C4	2.43	1.06
1:b:179:VAL:H	2:B:258:ASN:ND2	1.51	1.06
1:e:222:TYR:CE1	4:e:602:GDP:C6	2.43	1.06
2:O:326:LYS:HG2	1:o:220:PRO:HD2	1.32	1.06
1:u:87:PRO:CD	1:v:281:TYR:CD2	2.38	1.05
1:d:12:CYS:SG	4:d:602:GDP:C2	2.49	1.05
2:T:326:LYS:HE2	1:t:219:THR:HA	1.35	1.05
1:c:222:TYR:CZ	4:c:602:GDP:C6	2.44	1.05
1:j:220:PRO:HD2	2:J:326:LYS:HG2	1.38	1.05
1:c:220:PRO:HD2	2:C:326:LYS:HG2	1.34	1.05
2:S:284:GLU:OE2	1:r:55:THR:HB	1.53	1.05
2:X:326:LYS:HE2	1:x:219:THR:HA	1.36	1.05
2:C:88:HIS:HD2	2:D:283:HIS:HB3	0.92	1.04
1:d:219:THR:HA	2:D:326:LYS:HE2	1.35	1.04
2:X:224:TYR:CE2	6:X:502:GTP:N3	2.25	1.04
2:Z:224:TYR:CE2	6:Z:502:GTP:C5	2.44	1.04
2:N:11:GLN:HB3	6:N:502:GTP:O2A	1.56	1.04
1:g:23:VAL:HG13	3:g:601:TA1:H421	1.39	1.04
1:h:55:THR:OG1	1:i:283:ALA:HA	1.57	1.04
2:X:224:TYR:CD2	6:X:502:GTP:C6	2.46	1.03
2:N:224:TYR:CZ	6:N:502:GTP:C4	2.45	1.03
2:S:326:LYS:HE2	1:s:219:THR:HA	1.35	1.03
2:A:283:HIS:CE1	2:M:89:PRO:CD	2.41	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:55:THR:OG1	1:e:283:ALA:HA	1.54	1.03
1:m:220:PRO:HD2	2:M:326:LYS:HG2	1.37	1.03
1:v:87:PRO:HD2	1:w:281:TYR:HD2	1.23	1.03
1:w:87:PRO:HD2	1:x:281:TYR:HD2	1.18	1.03
1:f:281:TYR:HE1	2:R:60:LYS:NZ	1.57	1.03
2:O:11:GLN:HB3	6:O:502:GTP:O2A	1.59	1.03
2:V:224:TYR:CZ	6:V:502:GTP:C4	2.46	1.03
1:n:281:TYR:CD2	1:z:87:PRO:CD	2.41	1.03
1:e:219:THR:HA	2:E:326:LYS:HE2	1.38	1.02
2:W:224:TYR:CD2	6:W:502:GTP:C6	2.47	1.02
1:v:87:PRO:CD	1:w:281:TYR:CE2	2.42	1.02
1:e:12:CYS:SG	4:e:602:GDP:N3	2.32	1.02
2:W:224:TYR:CZ	6:W:502:GTP:C4	2.47	1.02
2:Y:224:TYR:CD2	6:Y:502:GTP:C6	2.47	1.02
1:g:220:PRO:HD2	2:G:326:LYS:HG2	1.38	1.02
2:V:326:LYS:HE2	1:v:219:THR:HA	1.40	1.01
2:H:88:HIS:NE2	2:I:283:HIS:HB2	1.75	1.01
1:t:87:PRO:HD2	1:u:281:TYR:HD2	1.03	1.01
1:f:222:TYR:CE1	4:f:602:GDP:N3	2.28	1.01
1:b:138:SER:HB3	4:b:602:GDP:H2'	1.38	1.01
2:T:326:LYS:HG2	1:t:220:PRO:HD2	1.05	1.01
2:W:224:TYR:CE2	6:W:502:GTP:N3	2.29	1.01
1:b:138:SER:HB2	4:b:602:GDP:C4	1.95	1.00
1:b:222:TYR:OH	4:b:602:GDP:C6	2.14	1.00
2:P:326:LYS:CG	1:p:220:PRO:HD2	1.91	1.00
1:t:87:PRO:CG	1:u:281:TYR:HE2	1.73	1.00
1:e:222:TYR:CD1	4:e:602:GDP:C6	2.48	1.00
2:V:224:TYR:CE2	6:V:502:GTP:C4	2.50	1.00
2:Y:171:ILE:HD13	6:Y:502:GTP:HN22	1.25	1.00
2:K:88:HIS:NE2	2:L:283:HIS:HB2	1.75	1.00
1:n:87:PRO:HD3	1:o:281:TYR:CD2	1.96	1.00
1:a:283:ALA:HA	1:m:55:THR:OG1	1.60	1.00
1:f:55:THR:OG1	1:g:283:ALA:HA	1.60	1.00
2:S:224:TYR:CD2	6:S:502:GTP:C2	2.48	0.99
1:g:55:THR:OG1	1:h:283:ALA:HA	1.62	0.99
1:g:350:LYS:HG3	2:T:179:THR:O	1.60	0.99
1:n:87:PRO:CD	1:o:281:TYR:CD2	2.45	0.99
1:f:12:CYS:SG	4:f:602:GDP:C2	2.55	0.99
2:W:11:GLN:HB3	6:W:502:GTP:O2A	1.61	0.99
1:c:360:GLY:HA3	3:c:601:TA1:H443	1.44	0.99
2:P:12:ALA:HB2	6:P:502:GTP:N7	1.51	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:222:TYR:CE1	4:l:602:GDP:C2	2.51	0.99
1:d:222:TYR:CD1	4:d:602:GDP:N1	2.29	0.99
2:X:224:TYR:CE2	6:X:502:GTP:C4	2.50	0.98
1:u:87:PRO:HD3	1:v:281:TYR:CD2	1.95	0.98
2:S:224:TYR:CE2	6:S:502:GTP:N3	2.31	0.98
1:b:138:SER:CB	4:b:602:GDP:N9	2.25	0.98
1:h:227:HIS:HB3	3:h:601:TA1:HC71	1.45	0.98
2:U:224:TYR:CD2	6:U:502:GTP:C6	2.51	0.98
2:Z:224:TYR:CE2	6:Z:502:GTP:N3	2.28	0.98
2:G:88:HIS:HD2	2:H:283:HIS:HB3	0.82	0.98
1:f:222:TYR:CE1	4:f:602:GDP:C4	2.51	0.98
1:h:222:TYR:CE1	4:h:602:GDP:C2	2.52	0.98
1:t:87:PRO:CD	1:u:281:TYR:HE2	1.64	0.98
2:N:224:TYR:CE2	6:N:502:GTP:N3	2.31	0.98
2:N:171:ILE:HD11	6:N:502:GTP:HN22	1.29	0.98
2:P:326:LYS:HG2	1:p:220:PRO:CD	1.94	0.98
2:U:224:TYR:CD2	6:U:502:GTP:C2	2.51	0.98
1:c:219:THR:HA	2:C:326:LYS:HE2	1.43	0.97
2:U:171:ILE:CD1	6:U:502:GTP:HN22	1.76	0.97
1:x:87:PRO:HD2	1:y:281:TYR:HD2	1.29	0.97
2:N:224:TYR:OH	6:N:502:GTP:C4	2.16	0.97
2:P:326:LYS:HG2	1:p:220:PRO:HD2	0.99	0.97
2:P:326:LYS:HE2	1:p:219:THR:HA	1.45	0.97
2:J:88:HIS:HA	2:K:283:HIS:CD2	2.00	0.97
2:T:326:LYS:CG	1:t:220:PRO:HD2	1.93	0.97
1:f:222:TYR:CE1	4:f:602:GDP:C5	2.51	0.97
1:d:222:TYR:CE1	4:d:602:GDP:C6	2.53	0.97
1:m:12:CYS:SG	4:m:602:GDP:N2	2.37	0.97
2:S:284:GLU:OE2	1:r:55:THR:OG1	1.82	0.97
2:X:224:TYR:CE2	6:X:502:GTP:N1	2.20	0.97
2:A:283:HIS:CD2	2:M:88:HIS:CA	2.47	0.96
1:d:222:TYR:CD1	4:d:602:GDP:C6	2.52	0.96
1:u:87:PRO:HD2	1:v:281:TYR:CD2	1.99	0.96
2:V:224:TYR:CD2	6:V:502:GTP:C2	2.51	0.96
1:n:281:TYR:HE2	1:z:87:PRO:HD3	1.30	0.96
2:Z:224:TYR:CZ	6:Z:502:GTP:C4	2.53	0.96
2:I:88:HIS:NE2	2:J:283:HIS:HB2	1.80	0.96
1:a:10:GLY:HA3	4:a:602:GDP:O3'	1.65	0.96
1:b:10:GLY:C	4:b:602:GDP:H4'	1.91	0.96
2:J:89:PRO:HD3	2:K:283:HIS:CE1	2.00	0.95
2:T:224:TYR:CZ	6:T:502:GTP:C5	2.54	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:262:TYR:HB3	2:U:263:PRO:HD2	1.48	0.95
2:N:224:TYR:HE2	6:N:502:GTP:C2	1.77	0.95
2:F:88:HIS:HD2	2:G:283:HIS:HB3	0.85	0.95
2:L:88:HIS:NE2	2:M:283:HIS:HB2	1.79	0.95
1:e:360:GLY:HA3	3:e:601:TA1:H443	1.48	0.95
2:S:262:TYR:HB3	2:S:263:PRO:HD2	1.48	0.95
2:Z:224:TYR:CE2	6:Z:502:GTP:C6	2.53	0.95
2:O:224:TYR:CD2	6:O:502:GTP:N1	2.34	0.95
2:R:224:TYR:CE2	6:R:502:GTP:C4	2.53	0.95
2:T:224:TYR:CE2	6:T:502:GTP:C5	2.54	0.95
2:V:262:TYR:HB3	2:V:263:PRO:HD2	1.48	0.95
2:H:262:TYR:HB3	2:H:263:PRO:HD2	1.49	0.95
2:N:224:TYR:CE2	6:N:502:GTP:C4	2.54	0.95
2:U:11:GLN:HB3	6:U:502:GTP:O2A	1.67	0.95
1:f:179:VAL:H	2:F:258:ASN:ND2	1.64	0.95
2:S:258:ASN:ND2	1:s:179:VAL:H	1.65	0.95
2:Y:224:TYR:CZ	6:Y:502:GTP:C4	2.55	0.95
2:T:262:TYR:HB3	2:T:263:PRO:HD2	1.48	0.95
1:c:222:TYR:CD1	4:c:602:GDP:N1	2.33	0.94
2:W:262:TYR:HB3	2:W:263:PRO:HD2	1.48	0.94
1:a:179:VAL:H	2:A:258:ASN:ND2	1.65	0.94
1:b:138:SER:CB	4:b:602:GDP:C4	2.49	0.94
2:E:262:TYR:HB3	2:E:263:PRO:HD2	1.48	0.94
2:I:262:TYR:HB3	2:I:263:PRO:HD2	1.49	0.94
2:J:262:TYR:HB3	2:J:263:PRO:HD2	1.49	0.94
2:P:12:ALA:HB2	6:P:502:GTP:H8	1.14	0.94
2:R:262:TYR:HB3	2:R:263:PRO:HD2	1.48	0.94
2:X:224:TYR:CZ	6:X:502:GTP:C5	2.55	0.94
1:m:222:TYR:CZ	4:m:602:GDP:C4	2.56	0.94
1:m:12:CYS:HB2	4:m:602:GDP:C4	2.03	0.94
2:D:262:TYR:HB3	2:D:263:PRO:HD2	1.48	0.94
2:F:262:TYR:HB3	2:F:263:PRO:HD2	1.50	0.94
1:y:87:PRO:HD2	1:z:281:TYR:HD2	1.32	0.94
1:y:87:PRO:HD2	1:z:281:TYR:CD2	2.03	0.94
2:Q:262:TYR:HB3	2:Q:263:PRO:HD2	1.48	0.94
2:V:224:TYR:CE2	6:V:502:GTP:N3	2.35	0.94
1:m:222:TYR:CE1	4:m:602:GDP:N2	2.34	0.94
2:U:224:TYR:HE2	6:U:502:GTP:N3	1.66	0.94
1:e:55:THR:OG1	2:F:284:GLU:OE2	1.85	0.93
2:Y:224:TYR:HE2	6:Y:502:GTP:C2	1.86	0.93
1:n:87:PRO:HD3	1:o:281:TYR:HE2	1.23	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:224:TYR:CZ	6:S:502:GTP:C5	2.55	0.93
2:Z:262:TYR:HB3	2:Z:263:PRO:HD2	1.48	0.93
2:B:262:TYR:HB3	2:B:263:PRO:HD2	1.48	0.93
2:G:262:TYR:HB3	2:G:263:PRO:HD2	1.50	0.93
2:O:224:TYR:CZ	6:O:502:GTP:C4	2.55	0.93
2:K:262:TYR:HB3	2:K:263:PRO:HD2	1.49	0.93
2:N:262:TYR:HB3	2:N:263:PRO:HD2	1.48	0.93
2:T:224:TYR:CG	6:T:502:GTP:C6	2.55	0.93
2:V:224:TYR:CZ	6:V:502:GTP:C5	2.56	0.93
2:O:262:TYR:HB3	2:O:263:PRO:HD2	1.48	0.93
2:R:224:TYR:CD2	6:R:502:GTP:N1	2.36	0.93
2:G:88:HIS:NE2	2:H:283:HIS:HB2	1.83	0.93
1:s:87:PRO:CG	1:t:281:TYR:CE2	2.45	0.93
1:w:87:PRO:HD2	1:x:281:TYR:CD2	1.94	0.93
2:X:171:ILE:HD11	6:X:502:GTP:HN22	1.32	0.93
2:F:89:PRO:HD3	2:G:283:HIS:ND1	1.82	0.93
1:s:87:PRO:HD2	1:t:281:TYR:HD2	1.00	0.93
2:Y:262:TYR:HB3	2:Y:263:PRO:HD2	1.48	0.93
2:C:262:TYR:HB3	2:C:263:PRO:HD2	1.48	0.93
1:y:87:PRO:HD3	1:z:281:TYR:HE2	1.26	0.93
2:X:262:TYR:HB3	2:X:263:PRO:HD2	1.48	0.92
2:S:224:TYR:CD2	6:S:502:GTP:C6	2.57	0.92
2:V:224:TYR:CD2	6:V:502:GTP:C6	2.57	0.92
2:A:262:TYR:HB3	2:A:263:PRO:HD2	1.48	0.92
2:L:262:TYR:HB3	2:L:263:PRO:HD2	1.49	0.92
2:V:224:TYR:HE2	6:V:502:GTP:C2	1.86	0.92
1:e:179:VAL:H	2:E:258:ASN:ND2	1.66	0.92
2:P:262:TYR:HB3	2:P:263:PRO:HD2	1.48	0.92
2:J:88:HIS:CD2	2:K:283:HIS:HB3	1.93	0.92
2:M:262:TYR:HB3	2:M:263:PRO:HD2	1.49	0.92
2:O:88:HIS:CD2	2:C:283:HIS:HB2	2.05	0.92
1:c:12:CYS:SG	4:c:602:GDP:N3	2.43	0.92
2:X:224:TYR:CD2	6:X:502:GTP:C2	2.54	0.92
2:A:128:GLN:NE2	2:B:285:GLN:HG3	1.84	0.92
2:W:224:TYR:CD2	6:W:502:GTP:C2	2.58	0.91
2:Y:258:ASN:ND2	1:y:179:VAL:H	1.67	0.91
1:c:222:TYR:CD1	4:c:602:GDP:C6	2.58	0.91
2:T:326:LYS:HG2	1:t:220:PRO:CD	1.99	0.91
1:c:83:GLN:O	1:d:281:TYR:OH	1.89	0.91
1:d:331:LEU:HD13	2:Q:176:GLN:HB3	1.51	0.91
1:m:222:TYR:CZ	4:m:602:GDP:C2	2.57	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:179:VAL:H	2:L:258:ASN:ND2	1.68	0.91
1:e:222:TYR:CE1	4:e:602:GDP:C4	2.58	0.91
2:W:224:TYR:CZ	6:W:502:GTP:C5	2.59	0.91
2:G:89:PRO:HD3	2:H:283:HIS:ND1	1.85	0.91
1:b:138:SER:HB3	4:b:602:GDP:C2'	2.00	0.91
1:c:179:VAL:H	2:C:258:ASN:ND2	1.68	0.91
1:d:222:TYR:CZ	4:d:602:GDP:C4	2.57	0.91
2:N:224:TYR:CD2	6:N:502:GTP:N1	2.39	0.91
2:L:88:HIS:HD2	2:M:283:HIS:HB3	0.75	0.91
1:c:23:VAL:CG1	3:c:601:TA1:H411	2.01	0.91
2:W:224:TYR:HE2	6:W:502:GTP:N3	1.68	0.90
1:b:138:SER:CB	4:b:602:GDP:C2'	2.50	0.90
2:P:324:VAL:HG11	1:p:219:THR:HB	1.51	0.90
1:a:55:THR:OG1	1:b:283:ALA:HA	1.70	0.90
1:f:281:TYR:HD2	2:R:89:PRO:HD3	1.30	0.90
2:I:88:HIS:HD2	2:J:283:HIS:HB3	0.74	0.90
2:A:283:HIS:ND1	2:M:89:PRO:HD3	1.85	0.90
1:b:179:VAL:H	2:B:258:ASN:HD22	1.20	0.90
2:S:324:VAL:HG11	1:s:219:THR:HB	1.54	0.90
1:w:87:PRO:HD3	1:x:281:TYR:HE2	1.09	0.90
1:e:222:TYR:OH	4:e:602:GDP:C4	2.24	0.90
2:A:128:GLN:CD	2:B:285:GLN:HG3	1.95	0.90
1:q:87:PRO:CD	1:r:281:TYR:HE2	1.71	0.90
1:x:87:PRO:HD2	1:y:281:TYR:CD2	2.05	0.90
1:i:227:HIS:HB3	3:i:601:TA1:HC71	1.54	0.90
2:O:224:TYR:CE2	6:O:502:GTP:N3	2.39	0.89
2:P:258:ASN:ND2	1:p:179:VAL:H	1.70	0.89
1:d:12:CYS:SG	4:d:602:GDP:N3	2.45	0.89
1:b:10:GLY:HA3	4:b:602:GDP:C5'	2.01	0.89
1:m:179:VAL:H	2:M:258:ASN:ND2	1.69	0.89
2:G:128:GLN:NE2	2:H:285:GLN:HG3	1.86	0.89
1:m:360:GLY:HA3	3:m:601:TA1:H443	1.54	0.89
2:W:258:ASN:ND2	1:w:179:VAL:H	1.69	0.89
2:X:258:ASN:ND2	1:x:179:VAL:H	1.70	0.89
2:T:258:ASN:ND2	1:t:179:VAL:H	1.70	0.89
2:F:128:GLN:NE2	2:G:285:GLN:HG3	1.88	0.89
1:h:179:VAL:H	2:H:258:ASN:ND2	1.68	0.89
2:Y:171:ILE:HD11	6:Y:502:GTP:HN22	1.28	0.89
2:X:171:ILE:CD1	6:X:502:GTP:HN22	1.85	0.89
2:F:88:HIS:NE2	2:G:283:HIS:HB2	1.87	0.89
1:n:87:PRO:HD2	1:o:281:TYR:HD2	1.37	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:331:LEU:HD13	2:P:176:GLN:HB3	1.53	0.89
1:i:179:VAL:H	2:I:258:ASN:ND2	1.71	0.89
1:a:141:GLY:HA3	4:a:602:GDP:C2'	2.02	0.88
1:k:179:VAL:H	2:K:258:ASN:ND2	1.71	0.88
2:P:206:ASN:OD1	6:P:502:GTP:N2	2.06	0.88
2:U:224:TYR:OH	6:U:502:GTP:N9	2.05	0.88
1:u:87:PRO:HD2	1:v:281:TYR:HD2	1.35	0.88
1:d:231:ALA:HB1	3:d:601:TA1:H391	1.55	0.88
2:X:224:TYR:CE2	6:X:502:GTP:C6	2.62	0.88
2:Y:224:TYR:CZ	6:Y:502:GTP:C5	2.62	0.88
1:n:281:TYR:HD2	1:z:87:PRO:HD2	1.38	0.88
2:T:224:TYR:HD2	6:T:502:GTP:N1	1.71	0.88
2:W:224:TYR:CE2	6:W:502:GTP:C5	2.61	0.88
1:c:222:TYR:CZ	4:c:602:GDP:C2	2.61	0.88
1:f:281:TYR:CE1	2:R:60:LYS:NZ	2.38	0.88
1:d:222:TYR:HE1	4:d:602:GDP:C2	1.78	0.88
2:Y:224:TYR:CE2	6:Y:502:GTP:N1	2.40	0.88
1:b:138:SER:CB	4:b:602:GDP:H2'	2.03	0.88
1:h:12:CYS:SG	4:h:602:GDP:N3	2.45	0.87
1:e:222:TYR:CZ	4:e:602:GDP:C5	2.62	0.87
1:j:179:VAL:H	2:J:258:ASN:ND2	1.72	0.87
1:n:87:PRO:HD2	1:o:281:TYR:CD2	2.09	0.87
1:x:87:PRO:HD3	1:y:281:TYR:HE2	1.36	0.87
1:y:87:PRO:CD	1:z:281:TYR:HE2	1.80	0.87
1:e:294:PHE:C	1:e:295:ASP:CA	2.47	0.87
1:g:179:VAL:H	2:G:258:ASN:ND2	1.71	0.87
2:U:224:TYR:CE2	6:U:502:GTP:C5	2.62	0.87
2:D:89:PRO:HD3	2:E:283:HIS:ND1	1.90	0.87
2:S:224:TYR:HE2	6:S:502:GTP:C2	1.90	0.87
2:C:88:HIS:HA	2:D:283:HIS:CD2	2.08	0.87
2:A:285:GLN:HG3	2:M:128:GLN:NE2	1.88	0.87
1:l:222:TYR:CD1	4:l:602:GDP:N1	2.42	0.86
1:b:144:GLY:N	4:b:602:GDP:H5'	1.91	0.86
2:O:171:ILE:HD11	6:O:502:GTP:HN22	1.38	0.86
2:U:258:ASN:ND2	1:u:179:VAL:H	1.71	0.86
1:j:55:THR:HG1	1:k:283:ALA:HA	1.36	0.86
1:b:12:CYS:HB3	4:b:602:GDP:N9	1.73	0.86
1:d:222:TYR:CZ	4:d:602:GDP:C5	2.63	0.86
1:m:331:LEU:HD13	2:Z:176:GLN:HB3	1.58	0.86
2:O:88:HIS:CD2	2:C:283:HIS:CB	2.58	0.86
2:K:89:PRO:HD3	2:L:283:HIS:ND1	1.91	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:224:TYR:OH	6:N:502:GTP:N9	2.09	0.86
2:P:258:ASN:HD22	1:p:179:VAL:H	1.23	0.86
2:S:258:ASN:HD22	1:s:179:VAL:H	1.19	0.86
2:A:89:PRO:HD3	2:B:283:HIS:ND1	1.89	0.86
1:j:54:ALA:HA	1:k:283:ALA:HB2	1.58	0.85
2:D:128:GLN:NE2	2:E:285:GLN:HG3	1.91	0.85
1:a:358:PRO:HB2	3:a:601:TA1:H281	1.58	0.85
1:d:179:VAL:H	2:D:258:ASN:ND2	1.75	0.85
2:V:224:TYR:CE2	6:V:502:GTP:N1	2.37	0.85
1:m:99:ASN:OD1	4:m:602:GDP:H5'	1.75	0.85
2:G:89:PRO:CD	2:H:283:HIS:CE1	2.58	0.85
2:S:224:TYR:CE2	6:S:502:GTP:N1	2.38	0.85
2:U:326:LYS:CG	1:u:220:PRO:HD2	2.06	0.85
2:R:224:TYR:CE2	6:R:502:GTP:C2	2.65	0.85
2:A:88:HIS:HA	2:B:283:HIS:CG	2.10	0.85
1:j:331:LEU:HD13	2:W:176:GLN:HB3	1.59	0.84
1:h:12:CYS:SG	4:h:602:GDP:C4	2.70	0.84
1:k:219:THR:HA	2:K:326:LYS:HE2	1.58	0.84
2:Q:326:LYS:CG	1:q:220:PRO:HD2	2.05	0.84
1:n:281:TYR:CD2	1:z:87:PRO:HD2	2.12	0.84
1:c:350:LYS:CG	2:P:179:THR:O	2.25	0.84
2:T:224:TYR:HE2	6:T:502:GTP:N3	1.76	0.84
2:U:224:TYR:CZ	6:U:502:GTP:C5	2.65	0.84
2:Z:224:TYR:CE2	6:Z:502:GTP:N1	2.39	0.84
2:N:258:ASN:ND2	1:n:179:VAL:H	1.74	0.84
2:Y:224:TYR:CE2	6:Y:502:GTP:C4	2.65	0.84
1:e:331:LEU:HD13	2:R:176:GLN:HB3	1.60	0.84
2:O:224:TYR:CE2	6:O:502:GTP:C4	2.66	0.84
1:m:350:LYS:CG	2:Z:179:THR:O	2.25	0.84
1:f:281:TYR:HE1	2:R:60:LYS:HZ1	0.84	0.83
1:c:87:PRO:HD3	1:d:281:TYR:CD2	2.13	0.83
2:V:258:ASN:ND2	1:v:179:VAL:H	1.74	0.83
2:O:224:TYR:CD2	6:O:502:GTP:C2	2.65	0.83
2:K:88:HIS:HD2	2:L:283:HIS:HB3	0.67	0.83
2:T:324:VAL:HG11	1:t:219:THR:HB	1.60	0.83
2:X:224:TYR:HE2	6:X:502:GTP:N3	1.71	0.83
1:q:87:PRO:CG	1:r:281:TYR:HE2	1.92	0.83
2:S:326:LYS:NZ	1:s:218:THR:O	2.11	0.83
1:j:361:LEU:HD23	3:j:601:TA1:H442	1.60	0.83
2:D:209:ILE:O	2:D:213:CYS:SG	2.37	0.83
1:q:87:PRO:HD3	1:r:281:TYR:HE2	1.22	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:224:TYR:CG	6:X:502:GTP:C6	2.66	0.82
2:O:258:ASN:ND2	1:o:179:VAL:H	1.77	0.82
2:U:171:ILE:HD11	6:U:502:GTP:HN22	1.43	0.82
1:l:219:THR:HA	2:L:326:LYS:HE2	1.61	0.82
2:N:224:TYR:CZ	6:N:502:GTP:C5	2.67	0.82
2:Q:324:VAL:HG11	1:q:219:THR:HB	1.60	0.82
2:H:88:HIS:HD2	2:I:283:HIS:HB3	0.67	0.82
2:O:88:HIS:HD2	2:C:283:HIS:CB	1.92	0.82
2:T:258:ASN:HD22	1:t:179:VAL:H	1.26	0.82
1:j:219:THR:HA	2:J:326:LYS:HE2	1.59	0.82
2:Y:224:TYR:CE2	6:Y:502:GTP:C6	2.67	0.82
1:b:138:SER:HB3	4:b:602:GDP:N9	1.95	0.82
1:b:169:VAL:HG21	4:b:602:GDP:HN22	1.38	0.82
1:b:331:LEU:HD13	2:O:176:GLN:HB3	1.60	0.82
1:h:219:THR:HA	2:H:326:LYS:HE2	1.62	0.82
2:S:326:LYS:HG2	1:s:220:PRO:HD2	0.85	0.82
2:X:224:TYR:CE2	6:X:502:GTP:C5	2.68	0.82
1:i:219:THR:HA	2:I:326:LYS:HE2	1.61	0.82
2:A:283:HIS:CG	2:M:88:HIS:HA	2.15	0.82
2:U:224:TYR:HE2	6:U:502:GTP:C2	1.92	0.81
1:a:331:LEU:HD13	2:N:176:GLN:HB3	1.62	0.81
2:R:224:TYR:CD2	6:R:502:GTP:C6	2.69	0.81
2:N:171:ILE:HD11	6:N:502:GTP:N2	1.95	0.81
1:c:222:TYR:OH	4:c:602:GDP:N3	2.09	0.81
1:v:87:PRO:HD2	1:w:281:TYR:CD2	2.04	0.81
1:a:361:LEU:HD23	3:a:601:TA1:H442	1.61	0.81
2:Q:258:ASN:ND2	1:q:179:VAL:H	1.78	0.81
1:d:222:TYR:OH	4:d:602:GDP:C4	2.34	0.81
2:P:224:TYR:CE2	6:P:502:GTP:C5	2.68	0.81
1:u:87:PRO:CD	1:v:281:TYR:HE2	1.91	0.81
1:c:54:ALA:HA	1:d:283:ALA:HB2	1.62	0.81
1:f:331:LEU:HD13	2:S:176:GLN:HB3	1.63	0.81
1:a:99:ASN:ND2	4:a:602:GDP:O2A	2.13	0.80
1:a:179:VAL:H	2:A:258:ASN:HD22	1.26	0.80
1:b:12:CYS:HB2	4:b:602:GDP:N9	1.89	0.80
1:i:331:LEU:HD13	2:V:176:GLN:HB3	1.62	0.80
2:J:89:PRO:HD3	2:K:283:HIS:ND1	1.96	0.80
1:e:294:PHE:CA	1:e:295:ASP:N	2.44	0.80
2:T:224:TYR:OH	6:T:502:GTP:N9	2.14	0.80
2:V:11:GLN:HB3	6:V:502:GTP:O2A	1.82	0.80
1:k:331:LEU:HD13	2:X:176:GLN:HB3	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:222:TYR:OH	4:f:602:GDP:N9	2.14	0.80
2:W:224:TYR:HE2	6:W:502:GTP:C2	1.97	0.80
1:h:222:TYR:CE1	4:h:602:GDP:N1	2.50	0.80
1:l:222:TYR:CD1	4:l:602:GDP:C2	2.70	0.80
1:m:219:THR:HA	2:M:326:LYS:HE2	1.63	0.80
1:m:222:TYR:OH	4:m:602:GDP:O2'	2.00	0.80
2:S:326:LYS:HE2	1:s:218:THR:O	1.81	0.80
2:H:128:GLN:NE2	2:I:285:GLN:HG3	1.96	0.80
2:L:89:PRO:HD3	2:M:283:HIS:ND1	1.95	0.80
1:p:86:ARG:HG3	1:q:281:TYR:CD2	2.17	0.80
2:R:224:TYR:CE2	6:R:502:GTP:C5	2.70	0.79
2:X:171:ILE:HD11	6:X:502:GTP:N2	1.97	0.79
1:w:87:PRO:CD	1:x:281:TYR:HE2	1.76	0.79
2:U:324:VAL:HG11	1:u:219:THR:HB	1.63	0.79
1:g:331:LEU:HD13	2:T:176:GLN:HB3	1.62	0.79
1:l:331:LEU:HD13	2:Y:176:GLN:HB3	1.64	0.79
2:Z:258:ASN:ND2	1:z:179:VAL:H	1.80	0.79
2:I:128:GLN:NE2	2:J:285:GLN:HG3	1.96	0.79
1:a:11:GLN:H	4:a:602:GDP:H4'	1.47	0.79
1:d:12:CYS:HB2	4:d:602:GDP:C4	2.17	0.79
1:d:331:LEU:CD1	2:Q:176:GLN:HB3	2.12	0.79
1:d:350:LYS:CG	2:Q:179:THR:O	2.25	0.79
2:O:88:HIS:HD2	2:C:283:HIS:HB3	1.46	0.79
2:P:326:LYS:HE2	1:p:218:THR:O	1.83	0.79
2:K:128:GLN:NE2	2:L:285:GLN:HG3	1.97	0.79
1:e:285:THR:O	1:e:289:LEU:HG	1.83	0.79
2:R:324:VAL:HG11	1:r:219:THR:HB	1.63	0.79
2:W:324:VAL:HG11	1:w:219:THR:HB	1.65	0.79
1:b:179:VAL:N	2:B:258:ASN:ND2	2.31	0.79
1:f:219:THR:HA	2:F:326:LYS:HE2	1.64	0.78
2:H:89:PRO:HD3	2:I:283:HIS:ND1	1.98	0.78
1:n:87:PRO:CD	1:o:281:TYR:HE2	1.87	0.78
1:k:23:VAL:CG1	3:k:601:TA1:H411	2.13	0.78
2:S:224:TYR:CG	6:S:502:GTP:C6	2.71	0.78
1:d:30:ILE:HD11	1:d:47:ILE:HD11	1.66	0.78
1:m:30:ILE:HD11	1:m:47:ILE:HD11	1.65	0.78
2:Y:224:TYR:CE2	6:Y:502:GTP:C5	2.71	0.78
1:a:219:THR:HA	2:A:326:LYS:HE2	1.64	0.78
1:g:222:TYR:OH	4:g:602:GDP:C4	2.36	0.78
2:Z:224:TYR:CZ	6:Z:502:GTP:C5	2.71	0.78
2:N:224:TYR:CE2	6:N:502:GTP:N1	2.51	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:224:TYR:OH	6:V:502:GTP:N9	2.17	0.78
1:i:55:THR:HG1	1:j:283:ALA:HA	1.49	0.78
1:j:30:ILE:HD11	1:j:47:ILE:HD11	1.65	0.78
1:l:179:VAL:H	2:L:258:ASN:HD22	1.31	0.78
2:Q:171:ILE:HD13	6:Q:502:GTP:N3	1.99	0.78
2:I:89:PRO:HD3	2:J:283:HIS:ND1	1.98	0.78
1:b:138:SER:HB2	4:b:602:GDP:N9	1.96	0.78
1:c:12:CYS:SG	4:c:602:GDP:C6	2.76	0.78
2:V:100:ALA:N	6:V:502:GTP:O2G	2.16	0.78
1:f:281:TYR:HB3	2:R:88:HIS:CD2	2.20	0.77
1:g:219:THR:HA	2:G:326:LYS:HE2	1.66	0.77
1:h:331:LEU:HD13	2:U:176:GLN:HB3	1.65	0.77
1:d:231:ALA:HB1	3:d:601:TA1:C39	2.14	0.77
1:f:30:ILE:HD11	1:f:47:ILE:HD11	1.66	0.77
2:Q:224:TYR:CE2	6:Q:502:GTP:C4	2.72	0.77
2:C:88:HIS:NE2	2:D:283:HIS:HB2	1.99	0.77
1:e:12:CYS:SG	4:e:602:GDP:C4	2.77	0.77
2:U:224:TYR:CG	6:U:502:GTP:C6	2.73	0.77
2:V:224:TYR:CE2	6:V:502:GTP:C6	2.73	0.77
2:Z:171:ILE:HD13	6:Z:502:GTP:N3	2.00	0.77
2:W:224:TYR:CE2	6:W:502:GTP:C6	2.72	0.77
2:A:283:HIS:ND1	2:M:89:PRO:CD	2.46	0.77
2:L:128:GLN:NE2	2:M:285:GLN:HG3	2.00	0.77
1:b:144:GLY:H	4:b:602:GDP:H5'	1.46	0.77
1:d:11:GLN:HB2	4:d:602:GDP:O2B	1.84	0.77
2:V:224:TYR:OH	6:V:502:GTP:C4	2.38	0.77
2:C:89:PRO:HD3	2:D:283:HIS:CE1	2.20	0.77
1:b:30:ILE:HD11	1:b:47:ILE:HD11	1.67	0.77
1:e:350:LYS:CG	2:R:179:THR:O	2.29	0.77
2:V:324:VAL:HG11	1:v:219:THR:HB	1.67	0.77
1:s:30:ILE:HD11	1:s:47:ILE:HD11	1.67	0.77
1:c:169:VAL:HG21	4:c:602:GDP:N2	2.00	0.77
2:W:224:TYR:OH	6:W:502:GTP:N9	2.18	0.77
1:k:30:ILE:HD11	1:k:47:ILE:HD11	1.66	0.77
1:a:350:LYS:CG	2:N:179:THR:O	2.27	0.76
1:f:216:LYS:NZ	2:R:90:GLU:OE2	2.17	0.76
2:R:224:TYR:CD2	6:R:502:GTP:C2	2.73	0.76
1:q:30:ILE:HD11	1:q:47:ILE:HD11	1.67	0.76
1:c:169:VAL:HG21	4:c:602:GDP:HN22	1.50	0.76
2:T:224:TYR:CE2	6:T:502:GTP:C6	2.72	0.76
2:U:258:ASN:HD22	1:u:179:VAL:H	1.32	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:224:TYR:OH	6:X:502:GTP:C4	2.38	0.76
2:Y:224:TYR:CE2	6:Y:502:GTP:N3	2.52	0.76
1:t:87:PRO:CG	1:u:281:TYR:CE2	2.57	0.76
2:V:224:TYR:CG	6:V:502:GTP:C6	2.73	0.76
1:c:331:LEU:CD1	2:P:176:GLN:HB3	2.15	0.76
1:e:294:PHE:N	1:e:295:ASP:N	2.33	0.76
2:G:89:PRO:CD	2:H:283:HIS:ND1	2.49	0.76
1:c:222:TYR:HE1	4:c:602:GDP:N2	1.83	0.76
1:o:30:ILE:HD11	1:o:47:ILE:HD11	1.68	0.76
1:f:281:TYR:HD2	2:R:89:PRO:CD	1.97	0.76
2:D:89:PRO:CD	2:E:283:HIS:CE1	2.67	0.76
1:l:30:ILE:HD11	1:l:47:ILE:HD11	1.65	0.76
2:O:224:TYR:HE2	6:O:502:GTP:C2	2.00	0.76
2:S:224:TYR:OH	6:S:502:GTP:N9	2.17	0.76
1:a:30:ILE:HD11	1:a:47:ILE:HD11	1.66	0.76
1:l:55:THR:HG1	1:m:283:ALA:HA	1.47	0.76
1:u:87:PRO:CG	1:v:281:TYR:HE2	1.99	0.76
1:c:30:ILE:HD11	1:c:47:ILE:HD11	1.66	0.76
1:h:30:ILE:HD11	1:h:47:ILE:HD11	1.66	0.76
2:R:224:TYR:CE2	6:R:502:GTP:N3	2.54	0.76
2:R:326:LYS:CG	1:r:220:PRO:HD2	2.11	0.76
1:b:220:PRO:HD2	2:B:326:LYS:CG	2.11	0.76
3:g:601:TA1:H261	3:g:601:TA1:H463	1.66	0.76
1:d:12:CYS:SG	4:d:602:GDP:C4	2.78	0.75
3:h:601:TA1:H261	3:h:601:TA1:H463	1.67	0.75
1:i:179:VAL:H	2:I:258:ASN:HD22	1.35	0.75
2:N:224:TYR:HE2	6:N:502:GTP:N3	1.74	0.75
2:S:224:TYR:CE2	6:S:502:GTP:C5	2.73	0.75
2:S:326:LYS:CE	1:s:218:THR:O	2.33	0.75
2:N:224:TYR:CD2	6:N:502:GTP:C6	2.74	0.75
2:Q:171:ILE:CD1	6:Q:502:GTP:N3	2.49	0.75
1:p:30:ILE:HD11	1:p:47:ILE:HD11	1.68	0.75
1:i:30:ILE:HD11	1:i:47:ILE:HD11	1.65	0.75
1:k:55:THR:HG1	1:l:283:ALA:HA	1.46	0.75
2:K:88:HIS:CD2	2:L:283:HIS:CG	2.73	0.75
1:r:30:ILE:HD11	1:r:47:ILE:HD11	1.67	0.75
1:e:30:ILE:HD11	1:e:47:ILE:HD11	1.68	0.75
2:R:258:ASN:ND2	1:r:179:VAL:H	1.84	0.75
1:b:11:GLN:N	4:b:602:GDP:H4'	2.00	0.75
1:e:12:CYS:HB2	4:e:602:GDP:C4	2.21	0.75
1:g:30:ILE:HD11	1:g:47:ILE:HD11	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:219:THR:HA	2:B:326:LYS:HE2	1.69	0.75
1:f:12:CYS:SG	4:f:602:GDP:N3	2.57	0.75
2:F:89:PRO:CD	2:G:283:HIS:CE1	2.68	0.75
1:q:354:CYS:SG	1:q:355:ASP:N	2.60	0.75
1:z:30:ILE:HD11	1:z:47:ILE:HD11	1.69	0.75
1:h:179:VAL:H	2:H:258:ASN:HD22	1.34	0.75
1:k:354:CYS:SG	1:k:355:ASP:N	2.60	0.75
2:Y:258:ASN:HD22	1:y:179:VAL:H	1.35	0.75
1:r:354:CYS:SG	1:r:355:ASP:N	2.60	0.75
1:c:87:PRO:HD3	1:d:281:TYR:HD2	1.50	0.75
1:e:222:TYR:CE1	4:e:602:GDP:C5	2.74	0.75
1:f:179:VAL:H	2:F:258:ASN:HD22	1.34	0.75
1:m:222:TYR:CD1	4:m:602:GDP:C2	2.75	0.75
2:V:224:TYR:CE2	6:V:502:GTP:C5	2.74	0.75
1:u:354:CYS:SG	1:u:355:ASP:N	2.60	0.75
1:x:354:CYS:SG	1:x:355:ASP:N	2.60	0.75
1:b:350:LYS:CG	2:O:179:THR:O	2.28	0.74
2:R:224:TYR:CZ	6:R:502:GTP:C5	2.74	0.74
2:U:432:TYR:HA	2:U:435:VAL:HG12	1.69	0.74
2:H:432:TYR:HA	2:H:435:VAL:HG12	1.69	0.74
1:e:354:CYS:SG	1:e:355:ASP:N	2.60	0.74
2:V:432:TYR:HA	2:V:435:VAL:HG12	1.69	0.74
1:n:30:ILE:HD11	1:n:47:ILE:HD11	1.68	0.74
1:u:30:ILE:HD11	1:u:47:ILE:HD11	1.68	0.74
1:e:234:SER:CB	3:e:601:TA1:H401	2.15	0.74
1:m:179:VAL:H	2:M:258:ASN:HD22	1.33	0.74
2:P:88:HIS:CD2	2:Q:283:HIS:HB2	2.22	0.74
2:P:432:TYR:HA	2:P:435:VAL:HG12	1.69	0.74
2:A:88:HIS:HA	2:B:283:HIS:CE1	2.21	0.74
2:T:432:TYR:HA	2:T:435:VAL:HG12	1.69	0.74
2:C:432:TYR:HA	2:C:435:VAL:HG12	1.69	0.74
2:G:432:TYR:HA	2:G:435:VAL:HG12	1.69	0.74
1:a:283:ALA:HB2	1:m:54:ALA:HA	1.69	0.74
2:I:432:TYR:HA	2:I:435:VAL:HG12	1.69	0.74
1:y:354:CYS:SG	1:y:355:ASP:N	2.60	0.74
1:e:55:THR:HB	2:F:284:GLU:CD	2.12	0.74
1:e:222:TYR:HE1	4:e:602:GDP:N3	1.67	0.74
2:S:11:GLN:HB3	6:S:502:GTP:O2A	1.88	0.74
2:Z:432:TYR:HA	2:Z:435:VAL:HG12	1.69	0.74
2:M:432:TYR:HA	2:M:435:VAL:HG12	1.69	0.74
1:y:30:ILE:HD11	1:y:47:ILE:HD11	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:179:VAL:H	2:E:258:ASN:HD22	1.35	0.74
1:h:354:CYS:SG	1:h:355:ASP:N	2.60	0.74
1:l:354:CYS:SG	1:l:355:ASP:N	2.60	0.74
1:e:222:TYR:HE1	4:e:602:GDP:N2	1.80	0.74
1:m:15:GLN:HG3	4:m:602:GDP:O6	1.86	0.74
2:W:432:TYR:HA	2:W:435:VAL:HG12	1.69	0.74
2:Z:324:VAL:HG11	1:z:219:THR:HB	1.70	0.74
1:w:30:ILE:HD11	1:w:47:ILE:HD11	1.68	0.74
2:P:169:PHE:CE1	2:P:235:VAL:HG22	2.23	0.74
2:C:169:PHE:CE1	2:C:235:VAL:HG22	2.23	0.74
2:E:169:PHE:CE1	2:E:235:VAL:HG22	2.23	0.74
1:t:30:ILE:HD11	1:t:47:ILE:HD11	1.67	0.74
1:d:55:THR:HG1	1:e:283:ALA:HA	1.52	0.74
2:N:432:TYR:HA	2:N:435:VAL:HG12	1.69	0.74
2:S:432:TYR:HA	2:S:435:VAL:HG12	1.69	0.74
2:A:432:TYR:HA	2:A:435:VAL:HG12	1.69	0.74
2:F:432:TYR:HA	2:F:435:VAL:HG12	1.69	0.74
2:J:432:TYR:HA	2:J:435:VAL:HG12	1.69	0.74
2:Q:169:PHE:CE1	2:Q:235:VAL:HG22	2.23	0.73
2:J:128:GLN:NE2	2:K:285:GLN:HG3	2.03	0.73
1:z:354:CYS:SG	1:z:355:ASP:N	2.60	0.73
2:O:432:TYR:HA	2:O:435:VAL:HG12	1.69	0.73
2:V:171:ILE:HD11	6:V:502:GTP:HN22	1.51	0.73
2:L:88:HIS:CD2	2:M:283:HIS:CG	2.75	0.73
2:W:171:ILE:CD1	6:W:502:GTP:N3	2.51	0.73
2:D:169:PHE:CE1	2:D:235:VAL:HG22	2.24	0.73
2:N:324:VAL:HG11	1:n:219:THR:HB	1.69	0.73
2:Q:432:TYR:HA	2:Q:435:VAL:HG12	1.69	0.73
2:A:169:PHE:CE1	2:A:235:VAL:HG22	2.23	0.73
1:x:30:ILE:HD11	1:x:47:ILE:HD11	1.68	0.73
1:j:222:TYR:CE2	4:j:602:GDP:C5	2.77	0.73
2:S:169:PHE:CE1	2:S:235:VAL:HG22	2.24	0.73
2:D:432:TYR:HA	2:D:435:VAL:HG12	1.69	0.73
1:c:354:CYS:SG	1:c:355:ASP:N	2.60	0.73
2:O:171:ILE:CD1	6:O:502:GTP:HN22	2.02	0.73
2:R:169:PHE:CE1	2:R:235:VAL:HG22	2.23	0.73
2:R:432:TYR:HA	2:R:435:VAL:HG12	1.69	0.73
2:Y:171:ILE:CD1	6:Y:502:GTP:C2	2.72	0.73
2:Y:324:VAL:HG11	1:y:219:THR:HB	1.70	0.73
2:Y:432:TYR:HA	2:Y:435:VAL:HG12	1.69	0.73
2:Z:169:PHE:CE1	2:Z:235:VAL:HG22	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:169:PHE:CE1	2:F:235:VAL:HG22	2.23	0.73
2:G:169:PHE:CE1	2:G:235:VAL:HG22	2.23	0.73
1:s:354:CYS:SG	1:s:355:ASP:N	2.60	0.73
1:b:138:SER:OG	4:b:602:GDP:C5	2.42	0.73
1:m:354:CYS:SG	1:m:355:ASP:N	2.60	0.73
2:Q:258:ASN:HD22	1:q:179:VAL:H	1.36	0.73
2:T:11:GLN:HB3	6:T:502:GTP:O2A	1.89	0.73
2:X:432:TYR:HA	2:X:435:VAL:HG12	1.69	0.73
2:L:432:TYR:HA	2:L:435:VAL:HG12	1.69	0.73
1:c:179:VAL:H	2:C:258:ASN:HD22	1.37	0.73
2:F:89:PRO:CD	2:G:283:HIS:ND1	2.52	0.73
2:L:169:PHE:CE1	2:L:235:VAL:HG22	2.23	0.73
2:M:169:PHE:CE1	2:M:235:VAL:HG22	2.23	0.73
2:N:169:PHE:CE1	2:N:235:VAL:HG22	2.24	0.73
2:B:432:TYR:HA	2:B:435:VAL:HG12	1.69	0.73
2:E:432:TYR:HA	2:E:435:VAL:HG12	1.69	0.73
2:K:432:TYR:HA	2:K:435:VAL:HG12	1.69	0.73
1:p:354:CYS:SG	1:p:355:ASP:N	2.60	0.73
2:T:169:PHE:CE1	2:T:235:VAL:HG22	2.24	0.73
2:V:326:LYS:CG	1:v:220:PRO:HD2	2.10	0.73
2:F:88:HIS:HA	2:G:283:HIS:CG	2.21	0.73
2:H:89:PRO:CD	2:I:283:HIS:CE1	2.70	0.73
1:v:354:CYS:SG	1:v:355:ASP:N	2.60	0.73
1:v:30:ILE:HD11	1:v:47:ILE:HD11	1.69	0.72
1:c:281:TYR:CD2	1:o:87:PRO:HD3	2.23	0.72
1:f:354:CYS:SG	1:f:355:ASP:N	2.61	0.72
1:i:354:CYS:SG	1:i:355:ASP:N	2.61	0.72
2:O:169:PHE:CE1	2:O:235:VAL:HG22	2.23	0.72
2:Q:224:TYR:CD2	6:Q:502:GTP:N1	2.57	0.72
2:S:67:PHE:HB2	2:S:92:LEU:HD23	1.71	0.72
2:U:169:PHE:CE1	2:U:235:VAL:HG22	2.24	0.72
2:Y:169:PHE:CE1	2:Y:235:VAL:HG22	2.23	0.72
2:H:169:PHE:CE1	2:H:235:VAL:HG22	2.23	0.72
2:I:169:PHE:CE1	2:I:235:VAL:HG22	2.23	0.72
1:c:281:TYR:CE2	1:o:87:PRO:HD3	2.25	0.72
2:Z:224:TYR:CD2	6:Z:502:GTP:C2	2.67	0.72
1:c:360:GLY:HA3	3:c:601:TA1:C44	2.19	0.72
1:i:256:ASN:HA	2:V:404:PHE:CE1	2.25	0.72
1:a:222:TYR:OH	4:a:602:GDP:C2	2.42	0.72
1:c:12:CYS:SG	4:c:602:GDP:C4	2.82	0.72
2:W:258:ASN:HD22	1:w:179:VAL:H	1.35	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:67:PHE:HB2	2:D:92:LEU:HD23	1.71	0.72
2:G:67:PHE:HB2	2:G:92:LEU:HD23	1.71	0.72
1:n:281:TYR:HE2	1:z:87:PRO:CD	1.89	0.72
1:n:354:CYS:SG	1:n:355:ASP:N	2.60	0.72
1:l:222:TYR:CZ	4:l:602:GDP:C4	2.76	0.72
2:T:67:PHE:HB2	2:T:92:LEU:HD23	1.71	0.72
2:V:169:PHE:CE1	2:V:235:VAL:HG22	2.24	0.72
2:J:169:PHE:CE1	2:J:235:VAL:HG22	2.23	0.72
1:j:256:ASN:HA	2:W:404:PHE:CE1	2.25	0.72
2:S:224:TYR:CE2	6:S:502:GTP:C6	2.78	0.72
2:X:67:PHE:HB2	2:X:92:LEU:HD23	1.71	0.72
2:F:67:PHE:HB2	2:F:92:LEU:HD23	1.71	0.72
2:K:67:PHE:HB2	2:K:92:LEU:HD23	1.71	0.72
2:L:67:PHE:HB2	2:L:92:LEU:HD23	1.71	0.72
1:a:141:GLY:CA	4:a:602:GDP:H2'	2.15	0.72
2:W:169:PHE:CE1	2:W:235:VAL:HG22	2.23	0.72
2:X:169:PHE:CE1	2:X:235:VAL:HG22	2.23	0.72
2:Z:67:PHE:HB2	2:Z:92:LEU:HD23	1.71	0.72
2:M:67:PHE:HB2	2:M:92:LEU:HD23	1.71	0.72
1:a:220:PRO:HD2	2:A:326:LYS:CG	2.11	0.72
1:d:360:GLY:HA3	3:d:601:TA1:H443	1.72	0.72
1:j:331:LEU:CD1	2:W:176:GLN:HB3	2.20	0.72
1:k:179:VAL:H	2:K:258:ASN:HD22	1.37	0.72
2:O:12:ALA:HB2	6:O:502:GTP:C4	2.25	0.72
2:W:326:LYS:CG	1:w:220:PRO:HD2	2.12	0.72
2:B:169:PHE:CE1	2:B:235:VAL:HG22	2.25	0.72
2:J:67:PHE:HB2	2:J:92:LEU:HD23	1.71	0.72
2:K:169:PHE:CE1	2:K:235:VAL:HG22	2.23	0.72
1:b:354:CYS:SG	1:b:355:ASP:N	2.60	0.71
1:m:331:LEU:CD1	2:Z:176:GLN:HB3	2.20	0.71
2:R:171:ILE:CD1	6:R:502:GTP:N3	2.53	0.71
2:S:224:TYR:OH	6:S:502:GTP:C4	2.43	0.71
2:Y:67:PHE:HB2	2:Y:92:LEU:HD23	1.71	0.71
2:E:67:PHE:HB2	2:E:92:LEU:HD23	1.71	0.71
2:L:88:HIS:CA	2:M:283:HIS:CD2	2.67	0.71
2:Q:326:LYS:HG2	1:q:220:PRO:CD	2.08	0.71
1:a:54:ALA:HA	1:b:283:ALA:HB2	1.71	0.71
1:e:11:GLN:HB3	4:e:602:GDP:O1A	1.89	0.71
2:N:224:TYR:CD2	6:N:502:GTP:C2	2.78	0.71
2:R:67:PHE:HB2	2:R:92:LEU:HD23	1.71	0.71
2:U:67:PHE:HB2	2:U:92:LEU:HD23	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:258:ASN:HD22	1:v:179:VAL:H	1.37	0.71
2:W:67:PHE:HB2	2:W:92:LEU:HD23	1.71	0.71
2:X:258:ASN:HD22	1:x:179:VAL:H	1.37	0.71
2:Y:224:TYR:OH	6:Y:502:GTP:C4	2.43	0.71
2:B:67:PHE:HB2	2:B:92:LEU:HD23	1.71	0.71
2:G:88:HIS:HA	2:H:283:HIS:CG	2.22	0.71
3:f:601:TA1:H463	3:f:601:TA1:H261	1.73	0.71
1:l:12:CYS:SG	4:l:602:GDP:N3	2.62	0.71
2:I:67:PHE:HB2	2:I:92:LEU:HD23	1.71	0.71
1:l:222:TYR:CE1	4:l:602:GDP:N3	2.57	0.71
2:Y:317:LEU:HB3	2:Y:319:TYR:HE1	1.55	0.71
2:C:67:PHE:HB2	2:C:92:LEU:HD23	1.71	0.71
2:D:88:HIS:CA	2:E:283:HIS:CD2	2.65	0.71
1:o:354:CYS:SG	1:o:355:ASP:N	2.60	0.71
2:A:67:PHE:HB2	2:A:92:LEU:HD23	1.71	0.71
1:x:87:PRO:CD	1:y:281:TYR:HE2	1.93	0.71
2:R:171:ILE:HD13	6:R:502:GTP:N3	2.05	0.71
2:V:67:PHE:HB2	2:V:92:LEU:HD23	1.71	0.71
2:H:67:PHE:HB2	2:H:92:LEU:HD23	1.71	0.71
2:Q:67:PHE:HB2	2:Q:92:LEU:HD23	1.72	0.71
1:b:12:CYS:N	4:b:602:GDP:O4'	2.24	0.71
1:e:222:TYR:CZ	4:e:602:GDP:N3	2.53	0.71
1:g:256:ASN:HA	2:T:404:PHE:CE1	2.26	0.71
1:k:227:HIS:HB3	3:k:601:TA1:HC71	1.72	0.71
1:c:23:VAL:CG1	3:c:601:TA1:C41	2.69	0.70
1:j:354:CYS:SG	1:j:355:ASP:N	2.60	0.70
2:O:67:PHE:HB2	2:O:92:LEU:HD23	1.71	0.70
2:P:67:PHE:HB2	2:P:92:LEU:HD23	1.71	0.70
2:W:171:ILE:HD13	6:W:502:GTP:N3	2.06	0.70
2:D:88:HIS:HA	2:E:283:HIS:CG	2.26	0.70
1:t:354:CYS:SG	1:t:355:ASP:N	2.60	0.70
1:g:179:VAL:H	2:G:258:ASN:HD22	1.40	0.70
2:P:143:GLY:HA3	6:P:502:GTP:O2B	1.91	0.70
1:g:331:LEU:CD1	2:T:176:GLN:HB3	2.21	0.70
3:i:601:TA1:H463	3:i:601:TA1:H261	1.72	0.70
2:N:67:PHE:HB2	2:N:92:LEU:HD23	1.72	0.70
2:W:100:ALA:N	6:W:502:GTP:O2G	2.22	0.70
1:j:179:VAL:H	2:J:258:ASN:HD22	1.39	0.70
1:m:12:CYS:CB	4:m:602:GDP:C4	2.73	0.70
1:g:54:ALA:HA	1:h:283:ALA:HB2	1.73	0.70
1:h:222:TYR:CE2	4:h:602:GDP:N7	2.59	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:354:CYS:SG	1:g:355:ASP:N	2.61	0.70
1:j:350:LYS:CG	2:W:179:THR:O	2.36	0.70
2:Q:11:GLN:HB3	6:Q:502:GTP:O2A	1.92	0.70
2:K:88:HIS:CA	2:L:283:HIS:CD2	2.70	0.70
2:N:12:ALA:HB2	6:N:502:GTP:C4	2.27	0.70
2:Z:171:ILE:CD1	6:Z:502:GTP:N3	2.55	0.70
2:Z:317:LEU:HB3	2:Z:319:TYR:HE1	1.57	0.70
1:w:354:CYS:SG	1:w:355:ASP:N	2.60	0.70
1:c:222:TYR:CZ	4:c:602:GDP:N3	2.59	0.70
1:d:179:VAL:H	2:D:258:ASN:HD22	1.38	0.70
2:A:283:HIS:NE2	2:M:88:HIS:HA	2.06	0.70
1:s:86:ARG:HG3	1:t:281:TYR:HB3	1.73	0.70
2:N:224:TYR:CE2	6:N:502:GTP:C5	2.80	0.70
1:a:354:CYS:SG	1:a:355:ASP:N	2.60	0.69
1:d:354:CYS:SG	1:d:355:ASP:N	2.60	0.69
1:c:222:TYR:CE2	4:c:602:GDP:C5	2.81	0.69
1:g:222:TYR:CZ	4:g:602:GDP:C4	2.59	0.69
2:T:326:LYS:HE2	1:t:218:THR:O	1.92	0.69
2:F:89:PRO:HD3	2:G:283:HIS:CG	2.26	0.69
1:k:350:LYS:CG	2:X:179:THR:O	2.34	0.69
2:O:324:VAL:HG11	1:o:219:THR:HB	1.74	0.69
1:d:220:PRO:HD2	2:D:326:LYS:CG	2.15	0.69
1:e:360:GLY:HA3	3:e:601:TA1:C44	2.21	0.69
2:T:224:TYR:OH	6:T:502:GTP:C4	2.46	0.69
1:b:12:CYS:CB	4:b:602:GDP:N9	2.18	0.69
1:c:141:GLY:N	4:c:602:GDP:H4'	2.07	0.69
2:X:171:ILE:CD1	6:X:502:GTP:N2	2.55	0.69
1:a:359:ARG:N	3:a:601:TA1:O13	2.25	0.69
1:f:12:CYS:SG	4:f:602:GDP:C4	2.85	0.69
1:j:358:PRO:HB2	3:j:601:TA1:H281	1.74	0.69
2:T:317:LEU:HB3	2:T:319:TYR:HE1	1.58	0.69
2:F:88:HIS:CA	2:G:283:HIS:CD2	2.66	0.69
1:b:358:PRO:HB2	3:b:601:TA1:H281	1.73	0.69
1:c:17:GLY:HA2	1:c:20:PHE:HB3	1.75	0.69
1:i:358:PRO:HB2	3:i:601:TA1:H281	1.73	0.69
2:N:171:ILE:CD1	6:N:502:GTP:N3	2.56	0.69
2:K:317:LEU:HB3	2:K:319:TYR:HE1	1.58	0.69
2:L:88:HIS:HA	2:M:283:HIS:CG	2.28	0.69
1:a:144:GLY:H	4:a:602:GDP:H3'	1.58	0.69
3:b:601:TA1:H261	3:b:601:TA1:H463	1.75	0.69
1:d:17:GLY:HA2	1:d:20:PHE:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:88:HIS:HA	2:K:283:HIS:CG	2.28	0.68
2:R:224:TYR:CZ	6:R:502:GTP:C4	2.81	0.68
2:S:317:LEU:HB3	2:S:319:TYR:HE1	1.58	0.68
2:L:317:LEU:HB3	2:L:319:TYR:HE1	1.59	0.68
2:M:317:LEU:HB3	2:M:319:TYR:HE1	1.59	0.68
1:n:17:GLY:HA2	1:n:20:PHE:HB3	1.76	0.68
1:e:17:GLY:HA2	1:e:20:PHE:HB3	1.76	0.68
2:N:88:HIS:CD2	2:O:283:HIS:HB2	2.27	0.68
2:W:317:LEU:HB3	2:W:319:TYR:HE1	1.58	0.68
2:F:317:LEU:HB3	2:F:319:TYR:HE1	1.58	0.68
2:J:317:LEU:HB3	2:J:319:TYR:HE1	1.58	0.68
2:L:89:PRO:CD	2:M:283:HIS:CE1	2.69	0.68
1:a:17:GLY:HA2	1:a:20:PHE:HB3	1.76	0.68
1:c:23:VAL:HG13	3:c:601:TA1:H411	1.75	0.68
1:f:280:GLN:O	2:R:56:THR:HG21	1.94	0.68
3:k:601:TA1:H261	3:k:601:TA1:H463	1.76	0.68
1:l:11:GLN:HB3	4:l:602:GDP:O1A	1.93	0.68
1:c:87:PRO:CD	1:d:281:TYR:HD2	2.05	0.68
3:l:601:TA1:H261	3:l:601:TA1:H463	1.75	0.68
2:X:317:LEU:HB3	2:X:319:TYR:HE1	1.59	0.68
2:A:317:LEU:HB3	2:A:319:TYR:HE1	1.59	0.68
1:o:17:GLY:HA2	1:o:20:PHE:HB3	1.75	0.68
1:p:17:GLY:HA2	1:p:20:PHE:HB3	1.76	0.68
1:b:17:GLY:HA2	1:b:20:PHE:HB3	1.76	0.68
1:l:17:GLY:HA2	1:l:20:PHE:HB3	1.76	0.68
2:N:317:LEU:HB3	2:N:319:TYR:HE1	1.59	0.68
2:O:224:TYR:CZ	6:O:502:GTP:C5	2.81	0.68
1:u:17:GLY:HA2	1:u:20:PHE:HB3	1.75	0.68
1:y:87:PRO:CG	1:z:281:TYR:HE2	2.06	0.68
1:z:17:GLY:HA2	1:z:20:PHE:HB3	1.76	0.68
1:r:17:GLY:HA2	1:r:20:PHE:HB3	1.76	0.68
1:c:231:ALA:HB1	3:c:601:TA1:C39	2.23	0.68
1:d:11:GLN:HB3	4:d:602:GDP:O1A	1.92	0.68
2:N:326:LYS:CG	1:n:220:PRO:HD2	2.15	0.68
2:O:224:TYR:CE2	6:O:502:GTP:N1	2.59	0.68
2:X:324:VAL:HG11	1:x:219:THR:HB	1.76	0.68
1:y:17:GLY:HA2	1:y:20:PHE:HB3	1.76	0.68
1:k:17:GLY:HA2	1:k:20:PHE:HB3	1.76	0.68
1:l:54:ALA:HA	1:m:283:ALA:HB2	1.76	0.68
1:m:17:GLY:HA2	1:m:20:PHE:HB3	1.76	0.68
2:V:317:LEU:HB3	2:V:319:TYR:HE1	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:17:GLY:HA2	1:q:20:PHE:HB3	1.76	0.68
1:d:219:THR:HB	2:D:324:VAL:HG11	1.74	0.68
1:d:234:SER:HB3	3:d:601:TA1:H401	1.75	0.68
1:e:331:LEU:CD1	2:R:176:GLN:HB3	2.24	0.68
2:O:317:LEU:HB3	2:O:319:TYR:HE1	1.59	0.68
2:W:224:TYR:CG	6:W:502:GTP:C6	2.82	0.68
2:D:89:PRO:CD	2:E:283:HIS:ND1	2.57	0.68
2:G:317:LEU:HB3	2:G:319:TYR:HE1	1.59	0.68
1:o:277:GLY:N	1:o:279:GLN:OE1	2.27	0.68
1:t:17:GLY:HA2	1:t:20:PHE:HB3	1.76	0.68
1:b:277:GLY:N	1:b:279:GLN:OE1	2.28	0.67
1:c:277:GLY:N	1:c:279:GLN:OE1	2.28	0.67
1:f:17:GLY:HA2	1:f:20:PHE:HB3	1.76	0.67
1:h:222:TYR:CZ	4:h:602:GDP:C6	2.77	0.67
1:l:277:GLY:N	1:l:279:GLN:OE1	2.27	0.67
1:m:277:GLY:N	1:m:279:GLN:OE1	2.28	0.67
2:N:224:TYR:CE2	6:N:502:GTP:C6	2.81	0.67
2:P:317:LEU:HB3	2:P:319:TYR:HE1	1.59	0.67
2:B:317:LEU:HB3	2:B:319:TYR:HE1	1.59	0.67
1:n:277:GLY:N	1:n:279:GLN:OE1	2.28	0.67
1:y:277:GLY:N	1:y:279:GLN:OE1	2.28	0.67
1:a:277:GLY:N	1:a:279:GLN:OE1	2.27	0.67
1:d:277:GLY:N	1:d:279:GLN:OE1	2.28	0.67
1:g:17:GLY:HA2	1:g:20:PHE:HB3	1.76	0.67
1:h:17:GLY:HA2	1:h:20:PHE:HB3	1.76	0.67
1:j:17:GLY:HA2	1:j:20:PHE:HB3	1.76	0.67
1:j:222:TYR:CZ	4:j:602:GDP:C4	2.82	0.67
1:k:277:GLY:N	1:k:279:GLN:OE1	2.28	0.67
1:l:12:CYS:SG	4:l:602:GDP:C2	2.87	0.67
2:U:317:LEU:HB3	2:U:319:TYR:HE1	1.58	0.67
2:C:128:GLN:NE2	2:D:285:GLN:HG3	2.09	0.67
1:q:277:GLY:N	1:q:279:GLN:OE1	2.28	0.67
1:s:17:GLY:HA2	1:s:20:PHE:HB3	1.76	0.67
1:x:277:GLY:N	1:x:279:GLN:OE1	2.28	0.67
1:z:277:GLY:N	1:z:279:GLN:OE1	2.28	0.67
1:e:378:PHE:CE2	1:e:418:LEU:HD11	2.30	0.67
2:U:224:TYR:CZ	6:U:502:GTP:N9	2.62	0.67
2:Y:171:ILE:HD13	6:Y:502:GTP:N2	1.95	0.67
2:Y:326:LYS:CG	1:y:220:PRO:HD2	2.16	0.67
2:C:317:LEU:HB3	2:C:319:TYR:HE1	1.59	0.67
2:E:317:LEU:HB3	2:E:319:TYR:HE1	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:317:LEU:HB3	2:I:319:TYR:HE1	1.59	0.67
1:p:277:GLY:N	1:p:279:GLN:OE1	2.28	0.67
1:v:17:GLY:HA2	1:v:20:PHE:HB3	1.75	0.67
1:x:17:GLY:HA2	1:x:20:PHE:HB3	1.76	0.67
1:z:378:PHE:CE2	1:z:418:LEU:HD11	2.30	0.67
1:a:234:SER:HB3	3:a:601:TA1:H401	1.77	0.67
1:h:222:TYR:CE2	4:h:602:GDP:C6	2.82	0.67
1:k:54:ALA:HA	1:l:283:ALA:HB2	1.77	0.67
2:V:224:TYR:CE1	6:V:502:GTP:C5	2.83	0.67
1:n:378:PHE:CE2	1:n:418:LEU:HD11	2.30	0.67
1:r:277:GLY:N	1:r:279:GLN:OE1	2.28	0.67
1:a:256:ASN:HA	2:N:404:PHE:CE1	2.30	0.67
1:a:378:PHE:CE2	1:a:418:LEU:HD11	2.30	0.67
1:c:234:SER:HB3	3:c:601:TA1:H401	1.75	0.67
1:f:331:LEU:CD1	2:S:176:GLN:HB3	2.25	0.67
1:l:350:LYS:CG	2:Y:179:THR:O	2.35	0.67
1:d:378:PHE:CE2	1:d:418:LEU:HD11	2.30	0.67
1:h:331:LEU:CD1	2:U:176:GLN:HB3	2.24	0.67
1:m:378:PHE:CE2	1:m:418:LEU:HD11	2.30	0.67
2:S:326:LYS:CE	1:s:219:THR:HA	2.18	0.67
2:T:100:ALA:N	6:T:502:GTP:O2G	2.25	0.67
2:V:171:ILE:CD1	6:V:502:GTP:HN22	2.06	0.67
1:r:378:PHE:CE2	1:r:418:LEU:HD11	2.30	0.67
1:s:378:PHE:CE2	1:s:418:LEU:HD11	2.30	0.67
1:w:277:GLY:N	1:w:279:GLN:OE1	2.28	0.67
1:e:219:THR:HB	2:E:324:VAL:HG11	1.74	0.67
1:f:378:PHE:CE2	1:f:418:LEU:HD11	2.30	0.67
1:m:222:TYR:OH	4:m:602:GDP:N3	2.28	0.67
2:T:326:LYS:NZ	1:t:218:THR:O	2.28	0.67
2:H:317:LEU:HB3	2:H:319:TYR:HE1	1.59	0.67
1:q:378:PHE:CE2	1:q:418:LEU:HD11	2.30	0.67
1:y:378:PHE:CE2	1:y:418:LEU:HD11	2.30	0.67
1:d:151:LEU:O	1:d:155:ILE:HG13	1.95	0.67
1:e:277:GLY:N	1:e:279:GLN:OE1	2.28	0.67
1:h:358:PRO:HB2	3:h:601:TA1:H281	1.74	0.67
1:i:331:LEU:CD1	2:V:176:GLN:HB3	2.25	0.67
1:j:277:GLY:N	1:j:279:GLN:OE1	2.28	0.67
2:O:224:TYR:OH	6:O:502:GTP:C4	2.48	0.67
2:Q:317:LEU:HB3	2:Q:319:TYR:HE1	1.59	0.67
2:Y:11:GLN:CB	6:Y:502:GTP:O2A	2.28	0.67
2:D:317:LEU:HB3	2:D:319:TYR:HE1	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:179:VAL:N	2:B:258:ASN:HD22	1.92	0.67
1:i:17:GLY:HA2	1:i:20:PHE:HB3	1.76	0.67
1:k:331:LEU:CD1	2:X:176:GLN:HB3	2.25	0.67
1:l:151:LEU:O	1:l:155:ILE:HG13	1.95	0.67
2:Q:224:TYR:CE2	6:Q:502:GTP:C5	2.83	0.67
2:R:258:ASN:HD22	1:r:179:VAL:H	1.43	0.67
1:u:151:LEU:O	1:u:155:ILE:HG13	1.95	0.67
1:w:17:GLY:HA2	1:w:20:PHE:HB3	1.76	0.67
1:a:283:ALA:HA	1:m:55:THR:HG1	1.57	0.67
1:g:378:PHE:CE2	1:g:418:LEU:HD11	2.30	0.67
1:h:361:LEU:HD23	3:h:601:TA1:H442	1.76	0.67
2:O:88:HIS:CD2	2:C:283:HIS:HB3	2.26	0.67
2:K:88:HIS:HA	2:L:283:HIS:CG	2.30	0.67
2:K:89:PRO:CD	2:L:283:HIS:CE1	2.73	0.67
1:o:378:PHE:CE2	1:o:418:LEU:HD11	2.30	0.67
1:s:277:GLY:N	1:s:279:GLN:OE1	2.28	0.67
1:x:378:PHE:CE2	1:x:418:LEU:HD11	2.30	0.67
1:c:23:VAL:HG11	3:c:601:TA1:H411	1.77	0.66
1:l:378:PHE:CE2	1:l:418:LEU:HD11	2.30	0.66
2:R:224:TYR:CG	6:R:502:GTP:C6	2.83	0.66
1:e:139:LEU:HD13	1:e:168:SER:HB2	1.77	0.66
1:f:54:ALA:HA	1:g:283:ALA:HB2	1.76	0.66
1:f:350:LYS:CG	2:S:179:THR:O	2.39	0.66
1:h:151:LEU:O	1:h:155:ILE:HG13	1.95	0.66
1:i:277:GLY:N	1:i:279:GLN:OE1	2.28	0.66
1:k:151:LEU:O	1:k:155:ILE:HG13	1.95	0.66
1:k:378:PHE:CE2	1:k:418:LEU:HD11	2.30	0.66
1:m:222:TYR:CE1	4:m:602:GDP:N3	2.54	0.66
2:F:40:LYS:HD2	2:F:42:ILE:HD11	1.76	0.66
1:y:139:LEU:HD13	1:y:168:SER:HB2	1.78	0.66
1:b:378:PHE:CE2	1:b:418:LEU:HD11	2.30	0.66
1:c:151:LEU:O	1:c:155:ILE:HG13	1.95	0.66
1:g:151:LEU:O	1:g:155:ILE:HG13	1.95	0.66
1:i:222:TYR:CE2	4:i:602:GDP:C5	2.84	0.66
1:m:151:LEU:O	1:m:155:ILE:HG13	1.95	0.66
2:Q:224:TYR:CD2	6:Q:502:GTP:C6	2.82	0.66
1:n:151:LEU:O	1:n:155:ILE:HG13	1.95	0.66
1:t:378:PHE:CE2	1:t:418:LEU:HD11	2.30	0.66
1:w:87:PRO:CD	1:x:281:TYR:HD2	1.79	0.66
1:y:151:LEU:O	1:y:155:ILE:HG13	1.95	0.66
1:z:151:LEU:O	1:z:155:ILE:HG13	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:151:LEU:O	1:a:155:ILE:HG13	1.95	0.66
1:e:151:LEU:O	1:e:155:ILE:HG13	1.95	0.66
1:f:277:GLY:N	1:f:279:GLN:OE1	2.27	0.66
1:h:378:PHE:CE2	1:h:418:LEU:HD11	2.30	0.66
2:R:317:LEU:HB3	2:R:319:TYR:HE1	1.59	0.66
2:U:171:ILE:CD1	6:U:502:GTP:N2	2.57	0.66
2:G:88:HIS:CA	2:H:283:HIS:CD2	2.65	0.66
1:o:139:LEU:HD13	1:o:168:SER:HB2	1.78	0.66
1:t:151:LEU:O	1:t:155:ILE:HG13	1.96	0.66
1:u:139:LEU:HD13	1:u:168:SER:HB2	1.78	0.66
1:v:277:GLY:N	1:v:279:GLN:OE1	2.28	0.66
1:x:151:LEU:O	1:x:155:ILE:HG13	1.95	0.66
1:h:277:GLY:N	1:h:279:GLN:OE1	2.27	0.66
1:q:151:LEU:O	1:q:155:ILE:HG13	1.96	0.66
1:z:139:LEU:HD13	1:z:168:SER:HB2	1.78	0.66
1:b:331:LEU:CD1	2:O:176:GLN:HB3	2.26	0.66
1:j:151:LEU:O	1:j:155:ILE:HG13	1.95	0.66
2:O:224:TYR:OH	6:O:502:GTP:N9	2.29	0.66
2:U:326:LYS:HG2	1:u:220:PRO:CD	2.11	0.66
1:u:378:PHE:CE2	1:u:418:LEU:HD11	2.30	0.66
1:w:378:PHE:CE2	1:w:418:LEU:HD11	2.30	0.66
1:c:219:THR:HB	2:C:324:VAL:HG11	1.76	0.66
1:c:378:PHE:CE2	1:c:418:LEU:HD11	2.30	0.66
1:f:151:LEU:O	1:f:155:ILE:HG13	1.95	0.66
1:g:12:CYS:SG	4:g:602:GDP:C5	2.89	0.66
1:h:215:LEU:CD2	3:h:601:TA1:C14	2.73	0.66
1:k:139:LEU:HD13	1:k:168:SER:HB2	1.78	0.66
1:b:137:HIS:HA	4:b:602:GDP:O3'	1.95	0.66
1:v:139:LEU:HD13	1:v:168:SER:HB2	1.78	0.66
1:c:99:ASN:OD1	4:c:602:GDP:H5'	1.96	0.66
1:l:331:LEU:CD1	2:Y:176:GLN:HB3	2.25	0.66
2:Q:224:TYR:CZ	6:Q:502:GTP:C5	2.84	0.66
2:Z:171:ILE:HD11	6:Z:502:GTP:N2	2.11	0.66
1:r:139:LEU:HD13	1:r:168:SER:HB2	1.78	0.66
1:w:151:LEU:O	1:w:155:ILE:HG13	1.95	0.66
1:b:12:CYS:CA	4:b:602:GDP:H1'	2.23	0.66
1:c:139:LEU:HD13	1:c:168:SER:HB2	1.77	0.66
2:S:439:SER:O	1:s:390:ARG:NH2	2.29	0.66
2:Z:171:ILE:CD1	6:Z:502:GTP:C2	2.79	0.66
2:Z:224:TYR:HD2	6:Z:502:GTP:N1	1.84	0.66
1:a:331:LEU:CD1	2:N:176:GLN:HB3	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:138:SER:CB	4:b:602:GDP:C1'	2.74	0.65
1:b:138:SER:OG	4:b:602:GDP:C4	2.49	0.65
1:h:139:LEU:HD13	1:h:168:SER:HB2	1.79	0.65
1:j:378:PHE:CE2	1:j:418:LEU:HD11	2.30	0.65
1:l:139:LEU:HD13	1:l:168:SER:HB2	1.79	0.65
2:P:326:LYS:CE	1:p:218:THR:O	2.45	0.65
1:p:151:LEU:O	1:p:155:ILE:HG13	1.96	0.65
1:r:151:LEU:O	1:r:155:ILE:HG13	1.96	0.65
1:s:139:LEU:HD13	1:s:168:SER:HB2	1.78	0.65
1:x:139:LEU:HD13	1:x:168:SER:HB2	1.78	0.65
1:a:227:HIS:HB3	3:a:601:TA1:HC71	1.77	0.65
1:i:378:PHE:CE2	1:i:418:LEU:HD11	2.30	0.65
2:N:258:ASN:HD22	1:n:179:VAL:H	1.42	0.65
2:R:224:TYR:HE2	6:R:502:GTP:N3	1.92	0.65
2:T:228:ASN:HD21	6:T:502:GTP:HN1	1.42	0.65
1:g:23:VAL:CG1	3:g:601:TA1:H421	2.24	0.65
1:t:277:GLY:N	1:t:279:GLN:OE1	2.28	0.65
1:d:139:LEU:HD13	1:d:168:SER:HB2	1.77	0.65
1:h:222:TYR:CE1	4:h:602:GDP:C6	2.84	0.65
1:i:151:LEU:O	1:i:155:ILE:HG13	1.95	0.65
1:m:360:GLY:HA3	3:m:601:TA1:C44	2.24	0.65
2:S:224:TYR:CE1	6:S:502:GTP:C5	2.85	0.65
2:W:224:TYR:HD2	6:W:502:GTP:N1	1.89	0.65
1:p:139:LEU:HD13	1:p:168:SER:HB2	1.78	0.65
1:u:277:GLY:N	1:u:279:GLN:OE1	2.28	0.65
1:v:151:LEU:O	1:v:155:ILE:HG13	1.95	0.65
1:v:378:PHE:CE2	1:v:418:LEU:HD11	2.30	0.65
2:O:284:GLU:HB2	2:O:286:LEU:HG	1.79	0.65
1:p:378:PHE:CE2	1:p:418:LEU:HD11	2.32	0.65
1:t:139:LEU:HD13	1:t:168:SER:HB2	1.78	0.65
1:a:219:THR:HB	2:A:324:VAL:HG11	1.77	0.65
1:g:12:CYS:SG	4:g:602:GDP:C6	2.89	0.65
1:g:277:GLY:N	1:g:279:GLN:OE1	2.27	0.65
1:k:23:VAL:HG13	3:k:601:TA1:H411	1.79	0.65
2:Q:171:ILE:HD11	6:Q:502:GTP:N2	2.11	0.65
1:o:151:LEU:O	1:o:155:ILE:HG13	1.95	0.65
1:b:151:LEU:O	1:b:155:ILE:HG13	1.95	0.65
1:c:23:VAL:HG13	3:c:601:TA1:C41	2.27	0.65
1:i:139:LEU:HD13	1:i:168:SER:HB2	1.79	0.65
1:w:139:LEU:HD13	1:w:168:SER:HB2	1.77	0.65
1:b:144:GLY:CA	4:b:602:GDP:H3'	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:326:LYS:HG2	1:r:220:PRO:CD	2.14	0.65
2:A:285:GLN:HG3	2:M:128:GLN:CD	2.22	0.65
2:D:264:ARG:HA	2:D:266:HIS:CE1	2.32	0.65
2:E:284:GLU:HB2	2:E:286:LEU:HG	1.79	0.65
2:H:88:HIS:CD2	2:I:283:HIS:CG	2.81	0.65
1:n:139:LEU:HD13	1:n:168:SER:HB2	1.78	0.65
1:b:139:LEU:HD13	1:b:168:SER:HB2	1.79	0.65
1:g:139:LEU:HD13	1:g:168:SER:HB2	1.79	0.65
1:k:222:TYR:CG	4:k:602:GDP:C6	2.85	0.65
1:m:139:LEU:HD13	1:m:168:SER:HB2	1.79	0.65
2:S:224:TYR:HE2	6:S:502:GTP:N3	1.83	0.65
2:E:264:ARG:HA	2:E:266:HIS:CE1	2.32	0.65
1:f:139:LEU:HD13	1:f:168:SER:HB2	1.78	0.65
2:N:284:GLU:HB2	2:N:286:LEU:HG	1.79	0.65
2:F:264:ARG:HA	2:F:266:HIS:CE1	2.32	0.65
2:M:284:GLU:HB2	2:M:286:LEU:HG	1.79	0.65
1:c:140:GLY:C	4:c:602:GDP:H4'	2.22	0.64
1:j:222:TYR:CG	4:j:602:GDP:C6	2.86	0.64
1:m:360:GLY:CA	3:m:601:TA1:H443	2.26	0.64
2:N:171:ILE:CD1	6:N:502:GTP:HN22	2.05	0.64
2:R:264:ARG:HA	2:R:266:HIS:CE1	2.32	0.64
2:S:264:ARG:HA	2:S:266:HIS:CE1	2.32	0.64
2:C:264:ARG:HA	2:C:266:HIS:CE1	2.32	0.64
1:s:151:LEU:O	1:s:155:ILE:HG13	1.96	0.64
1:a:144:GLY:H	4:a:602:GDP:C3'	2.10	0.64
1:g:12:CYS:SG	4:g:602:GDP:C4	2.90	0.64
3:j:601:TA1:H261	3:j:601:TA1:H463	1.78	0.64
1:k:222:TYR:CZ	4:k:602:GDP:C4	2.86	0.64
2:N:262:TYR:HE2	2:N:435:VAL:HG23	1.62	0.64
2:U:224:TYR:HD2	6:U:502:GTP:N1	1.92	0.64
2:X:100:ALA:N	6:X:502:GTP:O2G	2.30	0.64
2:Z:171:ILE:CD1	6:Z:502:GTP:N2	2.60	0.64
2:G:264:ARG:HA	2:G:266:HIS:CE1	2.32	0.64
1:q:139:LEU:HD13	1:q:168:SER:HB2	1.78	0.64
1:b:138:SER:HB3	4:b:602:GDP:C1'	2.26	0.64
1:c:88:ASP:OD2	1:d:282:ARG:NH2	2.31	0.64
1:h:256:ASN:HA	2:U:404:PHE:CE1	2.32	0.64
2:O:264:ARG:HA	2:O:266:HIS:CE1	2.32	0.64
2:Z:284:GLU:HB2	2:Z:286:LEU:HG	1.79	0.64
2:Z:326:LYS:CG	1:z:220:PRO:HD2	2.19	0.64
2:A:284:GLU:HB2	2:A:286:LEU:HG	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:284:GLU:HB2	2:G:286:LEU:HG	1.79	0.64
2:H:89:PRO:CD	2:I:283:HIS:ND1	2.61	0.64
2:H:262:TYR:HE2	2:H:435:VAL:HG23	1.63	0.64
1:f:281:TYR:CD2	2:R:89:PRO:CD	2.69	0.64
2:P:264:ARG:HA	2:P:266:HIS:CE1	2.32	0.64
2:Q:264:ARG:HA	2:Q:266:HIS:CE1	2.33	0.64
2:S:171:ILE:HD11	6:S:502:GTP:HN22	1.61	0.64
2:T:264:ARG:HA	2:T:266:HIS:CE1	2.32	0.64
1:a:11:GLN:H	4:a:602:GDP:C4'	2.11	0.64
2:O:262:TYR:HE2	2:O:435:VAL:HG23	1.62	0.64
2:P:277:SER:OG	2:P:280:LYS:HG3	1.97	0.64
2:W:224:TYR:OH	6:W:502:GTP:C4	2.51	0.64
2:I:89:PRO:CD	2:J:283:HIS:CE1	2.73	0.64
2:O:258:ASN:HD22	1:o:179:VAL:H	1.45	0.64
2:R:98:ASP:HB2	6:R:502:GTP:O2G	1.98	0.64
2:S:284:GLU:HB2	2:S:286:LEU:HG	1.80	0.64
2:U:224:TYR:OH	6:U:502:GTP:C1'	2.46	0.64
3:e:601:TA1:H261	3:e:601:TA1:H463	1.80	0.64
1:j:139:LEU:HD13	1:j:168:SER:HB2	1.78	0.64
2:P:88:HIS:CD2	2:Q:283:HIS:CB	2.80	0.64
2:Y:264:ARG:HA	2:Y:266:HIS:CE1	2.32	0.64
2:B:264:ARG:HA	2:B:266:HIS:CE1	2.33	0.64
2:F:284:GLU:HB2	2:F:286:LEU:HG	1.80	0.64
2:L:284:GLU:HB2	2:L:286:LEU:HG	1.79	0.64
1:a:139:LEU:HD13	1:a:168:SER:HB2	1.79	0.64
1:d:231:ALA:CB	3:d:601:TA1:C39	2.76	0.64
1:e:222:TYR:CD1	4:e:602:GDP:C2	2.69	0.64
1:h:350:LYS:CG	2:U:179:THR:O	2.38	0.64
2:N:264:ARG:HA	2:N:266:HIS:CE1	2.32	0.64
2:P:284:GLU:HB2	2:P:286:LEU:HG	1.79	0.64
2:X:224:TYR:CE1	6:X:502:GTP:C5	2.86	0.64
2:A:89:PRO:CD	2:B:283:HIS:ND1	2.52	0.64
2:L:264:ARG:HA	2:L:266:HIS:CE1	2.32	0.64
1:i:234:SER:HB3	3:i:601:TA1:H401	1.80	0.64
2:T:284:GLU:HB2	2:T:286:LEU:HG	1.80	0.64
2:U:171:ILE:HD12	6:U:502:GTP:HN22	1.62	0.64
2:Z:264:ARG:HA	2:Z:266:HIS:CE1	2.32	0.64
2:H:264:ARG:HA	2:H:266:HIS:CE1	2.32	0.64
2:J:71:GLU:HB2	2:J:98:ASP:HB3	1.80	0.64
2:X:264:ARG:HA	2:X:266:HIS:CE1	2.32	0.64
2:A:264:ARG:HA	2:A:266:HIS:CE1	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:284:GLU:HB2	2:H:286:LEU:HG	1.80	0.64
2:I:262:TYR:HE2	2:I:435:VAL:HG23	1.63	0.64
2:K:264:ARG:HA	2:K:266:HIS:CE1	2.32	0.64
1:i:350:LYS:CG	2:V:179:THR:O	2.36	0.63
2:R:284:GLU:HB2	2:R:286:LEU:HG	1.80	0.63
2:U:264:ARG:HA	2:U:266:HIS:CE1	2.32	0.63
2:I:284:GLU:HB2	2:I:286:LEU:HG	1.79	0.63
2:M:264:ARG:HA	2:M:266:HIS:CE1	2.32	0.63
1:c:227:HIS:HB3	3:c:601:TA1:HC71	1.79	0.63
2:Q:284:GLU:HB2	2:Q:286:LEU:HG	1.79	0.63
2:V:262:TYR:HE2	2:V:435:VAL:HG23	1.63	0.63
2:C:262:TYR:HE2	2:C:435:VAL:HG23	1.63	0.63
2:C:284:GLU:HB2	2:C:286:LEU:HG	1.80	0.63
1:d:231:ALA:HA	3:d:601:TA1:C40	2.29	0.63
1:k:222:TYR:CE2	4:k:602:GDP:C5	2.87	0.63
2:R:262:TYR:CB	2:R:263:PRO:HD2	2.25	0.63
2:Y:224:TYR:CG	6:Y:502:GTP:C6	2.86	0.63
2:G:262:TYR:HE2	2:G:435:VAL:HG23	1.63	0.63
1:p:86:ARG:HG3	1:q:281:TYR:CG	2.33	0.63
1:f:222:TYR:CZ	4:f:602:GDP:N3	2.57	0.63
1:h:169:VAL:HG21	4:h:602:GDP:N2	2.14	0.63
1:h:169:VAL:HG21	4:h:602:GDP:HN22	1.62	0.63
2:U:284:GLU:HB2	2:U:286:LEU:HG	1.80	0.63
2:Y:262:TYR:HE2	2:Y:435:VAL:HG23	1.63	0.63
2:Y:284:GLU:HB2	2:Y:286:LEU:HG	1.79	0.63
2:D:284:GLU:HB2	2:D:286:LEU:HG	1.79	0.63
1:b:11:GLN:N	4:b:602:GDP:C4'	2.60	0.63
2:Z:224:TYR:OH	6:Z:502:GTP:C4	2.51	0.63
2:E:262:TYR:CB	2:E:263:PRO:HD2	2.25	0.63
2:K:71:GLU:HB2	2:K:98:ASP:HB3	1.80	0.63
2:V:224:TYR:HE2	6:V:502:GTP:N3	1.86	0.63
2:V:264:ARG:HA	2:V:266:HIS:CE1	2.32	0.63
2:W:71:GLU:HB2	2:W:98:ASP:HB3	1.81	0.63
2:W:264:ARG:HA	2:W:266:HIS:CE1	2.32	0.63
2:X:284:GLU:HB2	2:X:286:LEU:HG	1.79	0.63
2:A:262:TYR:HE2	2:A:435:VAL:HG23	1.63	0.63
2:K:284:GLU:HB2	2:K:286:LEU:HG	1.79	0.63
1:b:11:GLN:HB3	4:b:602:GDP:O1A	1.99	0.63
2:T:224:TYR:CE1	6:T:502:GTP:C5	2.87	0.63
2:V:71:GLU:HB2	2:V:98:ASP:HB3	1.81	0.63
2:I:71:GLU:HB2	2:I:98:ASP:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:264:ARG:HA	2:J:266:HIS:CE1	2.32	0.63
2:L:262:TYR:HE2	2:L:435:VAL:HG23	1.64	0.63
1:e:11:GLN:HB2	4:e:602:GDP:O2B	1.99	0.63
1:m:12:CYS:CB	4:m:602:GDP:N3	2.62	0.63
2:O:326:LYS:CG	1:o:220:PRO:HD2	2.20	0.63
2:Q:262:TYR:HE2	2:Q:435:VAL:HG23	1.64	0.63
2:S:326:LYS:HD3	1:s:212:PHE:CE1	2.34	0.63
2:X:262:TYR:HE2	2:X:435:VAL:HG23	1.64	0.63
2:I:264:ARG:HA	2:I:266:HIS:CE1	2.32	0.63
1:v:87:PRO:HD3	1:w:281:TYR:HE2	1.55	0.63
1:b:212:PHE:CZ	2:B:326:LYS:HD3	2.34	0.63
1:c:12:CYS:HB2	4:c:602:GDP:C4	2.34	0.63
1:m:23:VAL:HG13	3:m:601:TA1:C42	2.29	0.63
2:S:262:TYR:HE2	2:S:435:VAL:HG23	1.64	0.63
2:U:71:GLU:HB2	2:U:98:ASP:HB3	1.80	0.63
1:p:86:ARG:HD3	1:q:281:TYR:HB3	1.80	0.63
1:f:219:THR:HB	2:F:324:VAL:HG11	1.81	0.62
1:k:222:TYR:CE1	4:k:602:GDP:C2	2.87	0.62
2:V:284:GLU:HB2	2:V:286:LEU:HG	1.80	0.62
2:W:284:GLU:HB2	2:W:286:LEU:HG	1.80	0.62
2:I:89:PRO:CD	2:J:283:HIS:ND1	2.62	0.62
2:L:71:GLU:HB2	2:L:98:ASP:HB3	1.80	0.62
1:a:11:GLN:N	4:a:602:GDP:H4'	2.13	0.62
3:a:601:TA1:H463	3:a:601:TA1:H261	1.80	0.62
1:b:256:ASN:HA	2:O:404:PHE:CE1	2.34	0.62
1:m:222:TYR:CE2	4:m:602:GDP:C4	2.86	0.62
2:U:224:TYR:CE2	6:U:502:GTP:N1	2.56	0.62
2:Z:262:TYR:HE2	2:Z:435:VAL:HG23	1.63	0.62
2:B:284:GLU:HB2	2:B:286:LEU:HG	1.80	0.62
2:F:71:GLU:HB2	2:F:98:ASP:HB3	1.79	0.62
2:H:71:GLU:HB2	2:H:98:ASP:HB3	1.80	0.62
1:b:390:ARG:NH2	2:B:439:SER:O	2.32	0.62
3:h:601:TA1:H463	3:h:601:TA1:C26	2.29	0.62
1:i:54:ALA:HA	1:j:283:ALA:HB2	1.81	0.62
2:T:262:TYR:HE2	2:T:435:VAL:HG23	1.64	0.62
2:U:262:TYR:HE2	2:U:435:VAL:HG23	1.64	0.62
2:J:284:GLU:HB2	2:J:286:LEU:HG	1.80	0.62
2:X:326:LYS:CG	1:x:220:PRO:HD2	2.21	0.62
2:D:262:TYR:HE2	2:D:435:VAL:HG23	1.64	0.62
1:m:222:TYR:OH	4:m:602:GDP:C4	2.51	0.62
2:P:262:TYR:HE2	2:P:435:VAL:HG23	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:71:GLU:HB2	2:R:98:ASP:HB3	1.80	0.62
2:A:71:GLU:HB2	2:A:98:ASP:HB3	1.80	0.62
1:c:231:ALA:HA	3:c:601:TA1:C40	2.29	0.62
1:f:141:GLY:HA3	4:f:602:GDP:O5'	2.00	0.62
2:Q:71:GLU:HB2	2:Q:98:ASP:HB3	1.81	0.62
2:R:224:TYR:CE2	6:R:502:GTP:C6	2.88	0.62
2:W:262:TYR:CB	2:W:263:PRO:HD2	2.25	0.62
2:X:71:GLU:HB2	2:X:98:ASP:HB3	1.81	0.62
2:Y:224:TYR:OH	6:Y:502:GTP:N9	2.32	0.62
2:D:71:GLU:HB2	2:D:98:ASP:HB3	1.80	0.62
2:K:262:TYR:HE2	2:K:435:VAL:HG23	1.64	0.62
1:v:87:PRO:CG	1:w:281:TYR:HE2	2.12	0.62
1:a:138:SER:OG	4:a:602:GDP:C2	2.52	0.62
2:Q:224:TYR:CE2	6:Q:502:GTP:C2	2.88	0.62
2:S:71:GLU:HB2	2:S:98:ASP:HB3	1.80	0.62
2:F:262:TYR:HE2	2:F:435:VAL:HG23	1.64	0.62
1:i:222:TYR:CZ	4:i:602:GDP:C5	2.87	0.62
2:R:262:TYR:HE2	2:R:435:VAL:HG23	1.63	0.62
2:E:71:GLU:HB2	2:E:98:ASP:HB3	1.81	0.62
1:i:227:HIS:HB3	3:i:601:TA1:C07	2.28	0.62
2:V:250:VAL:HG13	2:V:254:GLU:HB2	1.82	0.62
2:Z:258:ASN:HD22	1:z:179:VAL:H	1.47	0.62
2:B:71:GLU:HB2	2:B:98:ASP:HB3	1.80	0.62
2:E:262:TYR:HE2	2:E:435:VAL:HG23	1.64	0.62
2:M:71:GLU:HB2	2:M:98:ASP:HB3	1.80	0.62
2:T:71:GLU:HB2	2:T:98:ASP:HB3	1.80	0.62
2:T:250:VAL:HG13	2:T:254:GLU:HB2	1.82	0.62
2:T:326:LYS:CE	1:t:218:THR:O	2.48	0.62
2:W:250:VAL:HG13	2:W:254:GLU:HB2	1.82	0.62
2:B:262:TYR:HE2	2:B:435:VAL:HG23	1.65	0.62
2:G:71:GLU:HB2	2:G:98:ASP:HB3	1.80	0.62
1:p:86:ARG:HG3	1:q:281:TYR:CB	2.30	0.62
1:f:358:PRO:HB2	3:f:601:TA1:H281	1.82	0.61
1:l:222:TYR:CE1	4:l:602:GDP:C4	2.88	0.61
1:l:222:TYR:CG	4:l:602:GDP:C6	2.88	0.61
2:P:12:ALA:CA	6:P:502:GTP:N7	2.60	0.61
2:W:262:TYR:HE2	2:W:435:VAL:HG23	1.63	0.61
2:Y:71:GLU:HB2	2:Y:98:ASP:HB3	1.81	0.61
2:I:250:VAL:HG13	2:I:254:GLU:HB2	1.82	0.61
2:J:250:VAL:HG13	2:J:254:GLU:HB2	1.82	0.61
1:b:361:LEU:HD23	3:b:601:TA1:H442	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:12:CYS:CB	4:d:602:GDP:C4	2.83	0.61
1:g:55:THR:HG1	1:h:283:ALA:HA	1.61	0.61
2:C:71:GLU:HB2	2:C:98:ASP:HB3	1.81	0.61
2:G:250:VAL:HG13	2:G:254:GLU:HB2	1.82	0.61
1:j:222:TYR:CZ	4:j:602:GDP:C5	2.88	0.61
1:l:219:THR:HB	2:L:324:VAL:HG11	1.81	0.61
1:c:12:CYS:HB2	4:c:602:GDP:C5	2.35	0.61
1:c:256:ASN:HA	2:P:404:PHE:CE1	2.35	0.61
1:e:234:SER:HB3	3:e:601:TA1:C40	2.22	0.61
1:g:222:TYR:OH	4:g:602:GDP:N9	2.34	0.61
1:l:222:TYR:CD1	4:l:602:GDP:C6	2.87	0.61
2:U:250:VAL:HG13	2:U:254:GLU:HB2	1.82	0.61
2:H:250:VAL:HG13	2:H:254:GLU:HB2	1.82	0.61
1:b:138:SER:HB3	4:b:602:GDP:C8	2.35	0.61
1:d:222:TYR:CE2	4:d:602:GDP:C5	2.88	0.61
2:P:71:GLU:HB2	2:P:98:ASP:HB3	1.81	0.61
2:P:250:VAL:HG13	2:P:254:GLU:HB2	1.81	0.61
2:K:250:VAL:HG13	2:K:254:GLU:HB2	1.82	0.61
1:f:234:SER:HB3	3:f:601:TA1:H401	1.83	0.61
2:X:250:VAL:HG13	2:X:254:GLU:HB2	1.82	0.61
2:Z:71:GLU:HB2	2:Z:98:ASP:HB3	1.81	0.61
2:M:262:TYR:HE2	2:M:435:VAL:HG23	1.64	0.61
3:d:601:TA1:H261	3:d:601:TA1:H463	1.83	0.61
2:N:71:GLU:HB2	2:N:98:ASP:HB3	1.82	0.61
2:O:250:VAL:HG13	2:O:254:GLU:HB2	1.82	0.61
2:Q:326:LYS:NZ	1:q:218:THR:O	2.31	0.61
2:W:326:LYS:HG2	1:w:220:PRO:CD	2.16	0.61
2:Y:250:VAL:HG13	2:Y:254:GLU:HB2	1.81	0.61
1:f:281:TYR:HB3	2:R:88:HIS:HD2	1.64	0.61
2:O:71:GLU:HB2	2:O:98:ASP:HB3	1.81	0.61
2:R:250:VAL:HG13	2:R:254:GLU:HB2	1.82	0.61
2:F:250:VAL:HG13	2:F:254:GLU:HB2	1.82	0.61
1:v:87:PRO:CD	1:w:281:TYR:HE2	2.06	0.61
1:b:144:GLY:H	4:b:602:GDP:C5'	2.14	0.61
1:c:281:TYR:CD2	1:o:87:PRO:CD	2.83	0.61
3:g:601:TA1:H463	3:g:601:TA1:C26	2.30	0.61
1:k:219:THR:HB	2:K:324:VAL:HG11	1.82	0.61
2:N:250:VAL:HG13	2:N:254:GLU:HB2	1.82	0.61
2:H:89:PRO:HD3	2:I:283:HIS:NE2	2.13	0.61
1:b:208:TYR:CE1	2:B:326:LYS:HB3	2.35	0.61
1:d:54:ALA:HA	1:e:283:ALA:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:12:CYS:CB	4:e:602:GDP:C4	2.84	0.61
2:E:250:VAL:HG13	2:E:254:GLU:HB2	1.82	0.61
1:m:256:ASN:HA	2:Z:404:PHE:CE1	2.36	0.60
2:S:250:VAL:HG13	2:S:254:GLU:HB2	1.82	0.60
2:L:250:VAL:HG13	2:L:254:GLU:HB2	1.82	0.60
1:l:361:LEU:HD23	3:l:601:TA1:H442	1.82	0.60
1:f:361:LEU:HD23	3:f:601:TA1:H442	1.83	0.60
1:h:54:ALA:HA	1:i:283:ALA:HB2	1.82	0.60
1:h:219:THR:HB	2:H:324:VAL:HG11	1.81	0.60
2:V:326:LYS:HG2	1:v:220:PRO:CD	2.15	0.60
2:W:224:TYR:CE2	6:W:502:GTP:N1	2.53	0.60
2:A:250:VAL:HG13	2:A:254:GLU:HB2	1.82	0.60
2:C:250:VAL:HG13	2:C:254:GLU:HB2	1.82	0.60
1:w:87:PRO:CG	1:x:281:TYR:HE2	2.13	0.60
1:g:347:ASN:O	2:T:181:VAL:HG21	1.92	0.60
2:U:171:ILE:HD11	6:U:502:GTP:N2	2.14	0.60
2:U:326:LYS:NZ	1:u:218:THR:O	2.32	0.60
2:B:250:VAL:HG13	2:B:254:GLU:HB2	1.82	0.60
1:a:141:GLY:HA3	4:a:602:GDP:O2'	2.01	0.60
1:e:220:PRO:HD2	2:E:326:LYS:CG	2.17	0.60
1:l:358:PRO:HB2	3:l:601:TA1:H281	1.82	0.60
2:Z:250:VAL:HG13	2:Z:254:GLU:HB2	1.81	0.60
1:x:87:PRO:CG	1:y:281:TYR:HE2	2.15	0.60
2:S:326:LYS:CD	1:s:220:PRO:HD2	2.30	0.60
2:J:262:TYR:HE2	2:J:435:VAL:HG23	1.64	0.60
1:b:222:TYR:OH	4:b:602:GDP:C5	2.55	0.60
1:d:12:CYS:HB2	4:d:602:GDP:C5	2.37	0.60
1:i:222:TYR:CG	4:i:602:GDP:C6	2.89	0.60
1:d:169:VAL:HG21	4:d:602:GDP:N2	2.16	0.60
1:a:55:THR:HG1	1:b:283:ALA:HA	1.64	0.60
1:d:218:THR:O	2:D:326:LYS:NZ	2.32	0.60
1:i:215:LEU:HD21	3:i:601:TA1:O06	2.02	0.60
2:Q:250:VAL:HG13	2:Q:254:GLU:HB2	1.82	0.60
2:U:224:TYR:OH	6:U:502:GTP:C8	2.54	0.60
2:J:262:TYR:CB	2:J:263:PRO:HD2	2.26	0.60
1:e:256:ASN:HA	2:R:404:PHE:CE1	2.37	0.60
2:U:140:SER:OG	6:U:502:GTP:H4'	2.02	0.60
1:d:169:VAL:HG21	4:d:602:GDP:HN22	1.67	0.59
2:H:89:PRO:HD3	2:I:283:HIS:CG	2.37	0.59
2:M:250:VAL:HG13	2:M:254:GLU:HB2	1.82	0.59
1:e:222:TYR:OH	4:e:602:GDP:N9	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:361:LEU:HD23	3:i:601:TA1:H442	1.82	0.59
1:b:144:GLY:HA2	4:b:602:GDP:H3'	1.85	0.59
1:d:99:ASN:OD1	4:d:602:GDP:H5'	2.01	0.59
2:D:250:VAL:HG13	2:D:254:GLU:HB2	1.82	0.59
1:h:67:ASP:HB2	1:h:73:MET:HE2	1.84	0.59
1:k:222:TYR:CD1	4:k:602:GDP:N1	2.71	0.59
1:e:222:TYR:CE2	4:e:602:GDP:C5	2.90	0.59
1:f:55:THR:HG1	1:g:283:ALA:HA	1.67	0.59
1:i:219:THR:HB	2:I:324:VAL:HG11	1.84	0.59
1:a:143:THR:H	4:a:602:GDP:H3'	1.67	0.59
1:b:13:GLY:HA3	4:b:602:GDP:O3'	2.02	0.59
1:d:23:VAL:HG13	3:d:601:TA1:C42	2.32	0.59
1:j:231:ALA:HB1	3:j:601:TA1:C39	2.32	0.59
2:T:224:TYR:CG	6:T:502:GTP:O6	2.56	0.59
2:N:12:ALA:CB	6:N:502:GTP:C4	2.86	0.59
1:x:261:PRO:O	1:x:262:ARG:HB3	2.03	0.59
1:c:23:VAL:HG22	3:c:601:TA1:H321	1.85	0.59
1:h:210:ILE:HG23	1:h:273:LEU:HD13	1.84	0.59
2:N:71:GLU:HG2	2:N:73:THR:H	1.68	0.59
2:N:88:HIS:CD2	2:O:283:HIS:CB	2.86	0.59
2:L:89:PRO:CD	2:M:283:HIS:ND1	2.64	0.59
1:s:87:PRO:HG2	1:t:281:TYR:HE2	1.65	0.59
1:y:210:ILE:HG23	1:y:273:LEU:HD13	1.85	0.58
1:c:12:CYS:SG	4:c:602:GDP:N2	2.70	0.58
1:l:210:ILE:HG23	1:l:273:LEU:HD13	1.85	0.58
2:U:71:GLU:HG2	2:U:73:THR:H	1.69	0.58
2:A:71:GLU:HG2	2:A:73:THR:H	1.69	0.58
2:H:89:PRO:HD3	2:I:283:HIS:CD2	2.38	0.58
2:K:89:PRO:CD	2:L:283:HIS:ND1	2.65	0.58
1:r:261:PRO:O	1:r:262:ARG:HB3	2.03	0.58
1:a:361:LEU:CD2	3:a:601:TA1:H171	2.33	0.58
1:j:54:ALA:CA	1:k:283:ALA:HB2	2.30	0.58
1:m:222:TYR:CE2	4:m:602:GDP:C5	2.91	0.58
3:m:601:TA1:H261	3:m:601:TA1:H463	1.85	0.58
2:O:71:GLU:HG2	2:O:73:THR:H	1.69	0.58
2:B:71:GLU:HG2	2:B:73:THR:H	1.69	0.58
1:i:256:ASN:HA	2:V:404:PHE:HE1	1.67	0.58
2:X:224:TYR:OH	6:X:502:GTP:N9	2.36	0.58
2:Z:71:GLU:HG2	2:Z:73:THR:H	1.68	0.58
1:s:87:PRO:HG2	1:t:281:TYR:CE2	2.36	0.58
1:v:261:PRO:O	1:v:262:ARG:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:z:261:PRO:O	1:z:262:ARG:HB3	2.04	0.58
1:i:261:PRO:O	1:i:262:ARG:HB3	2.04	0.58
1:m:261:PRO:O	1:m:262:ARG:HB3	2.04	0.58
2:O:224:TYR:CD2	6:O:502:GTP:C6	2.91	0.58
2:Q:224:TYR:CG	6:Q:502:GTP:C6	2.91	0.58
2:S:140:SER:OG	6:S:502:GTP:H4'	2.04	0.58
2:S:284:GLU:CD	1:r:55:THR:HB	2.26	0.58
2:A:80:THR:HB	2:A:84:ARG:HD2	1.86	0.58
2:H:80:THR:HB	2:H:84:ARG:HD2	1.86	0.58
1:q:210:ILE:HG23	1:q:273:LEU:HD13	1.85	0.58
1:d:210:ILE:HG23	1:d:273:LEU:HD13	1.85	0.58
1:h:222:TYR:CZ	4:h:602:GDP:C2	2.91	0.58
2:O:200:CYS:HG	2:O:202:PHE:HE1	1.51	0.58
2:P:326:LYS:NZ	1:p:218:THR:O	2.36	0.58
2:U:80:THR:HB	2:U:84:ARG:HD2	1.86	0.58
2:V:71:GLU:HG2	2:V:73:THR:H	1.69	0.58
2:W:80:THR:HB	2:W:84:ARG:HD2	1.86	0.58
2:H:71:GLU:HG2	2:H:73:THR:H	1.69	0.58
2:J:80:THR:HB	2:J:84:ARG:HD2	1.86	0.58
1:w:210:ILE:HG23	1:w:273:LEU:HD13	1.85	0.58
1:a:210:ILE:HG23	1:a:273:LEU:HD13	1.85	0.58
1:b:175:VAL:HG13	2:B:329:ASN:CG	2.28	0.58
1:e:222:TYR:CG	4:e:602:GDP:C6	2.92	0.58
2:N:80:THR:HB	2:N:84:ARG:HD2	1.86	0.58
2:O:80:THR:HB	2:O:84:ARG:HD2	1.86	0.58
2:P:11:GLN:HB3	6:P:502:GTP:O2A	2.04	0.58
2:G:71:GLU:HG2	2:G:73:THR:H	1.69	0.58
2:K:80:THR:HB	2:K:84:ARG:HD2	1.86	0.58
1:k:261:PRO:O	1:k:262:ARG:HB3	2.04	0.58
2:S:80:THR:HB	2:S:84:ARG:HD2	1.86	0.58
2:S:326:LYS:HB3	1:s:208:TYR:CE1	2.38	0.58
2:T:71:GLU:HG2	2:T:73:THR:H	1.69	0.58
2:T:80:THR:HB	2:T:84:ARG:HD2	1.86	0.58
2:X:80:THR:HB	2:X:84:ARG:HD2	1.86	0.58
2:A:88:HIS:CA	2:B:283:HIS:NE2	2.57	0.58
2:C:71:GLU:HG2	2:C:73:THR:H	1.68	0.58
2:C:89:PRO:HD3	2:D:283:HIS:ND1	2.18	0.58
2:F:80:THR:HB	2:F:84:ARG:HD2	1.86	0.58
2:I:71:GLU:HG2	2:I:73:THR:H	1.69	0.58
2:L:80:THR:HB	2:L:84:ARG:HD2	1.86	0.58
1:t:261:PRO:O	1:t:262:ARG:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:210:ILE:HG23	1:u:273:LEU:HD13	1.85	0.58
1:m:219:THR:HB	2:M:324:VAL:HG11	1.85	0.58
2:P:88:HIS:HD2	2:Q:283:HIS:CB	2.17	0.58
2:Q:80:THR:HB	2:Q:84:ARG:HD2	1.86	0.58
2:W:171:ILE:HD11	6:W:502:GTP:N2	2.19	0.58
2:Y:80:THR:HB	2:Y:84:ARG:HD2	1.86	0.58
1:p:210:ILE:HG23	1:p:273:LEU:HD13	1.85	0.58
1:a:179:VAL:N	2:A:258:ASN:ND2	2.47	0.58
1:c:210:ILE:HG23	1:c:273:LEU:HD13	1.85	0.58
1:e:261:PRO:O	1:e:262:ARG:HB3	2.03	0.58
1:i:215:LEU:CD2	3:i:601:TA1:C14	2.81	0.58
2:P:80:THR:HB	2:P:84:ARG:HD2	1.86	0.58
2:G:80:THR:HB	2:G:84:ARG:HD2	1.86	0.58
2:I:80:THR:HB	2:I:84:ARG:HD2	1.86	0.58
2:M:71:GLU:HG2	2:M:73:THR:H	1.69	0.58
1:b:210:ILE:HG23	1:b:273:LEU:HD13	1.85	0.57
1:d:286:VAL:HG23	1:d:363:MET:HE3	1.86	0.57
1:j:210:ILE:HG23	1:j:273:LEU:HD13	1.86	0.57
2:S:224:TYR:OH	6:S:502:GTP:C8	2.56	0.57
2:V:80:THR:HB	2:V:84:ARG:HD2	1.86	0.57
2:W:71:GLU:HG2	2:W:73:THR:H	1.68	0.57
2:Z:80:THR:HB	2:Z:84:ARG:HD2	1.86	0.57
2:C:80:THR:HB	2:C:84:ARG:HD2	1.86	0.57
2:M:80:THR:HB	2:M:84:ARG:HD2	1.86	0.57
1:a:273:LEU:HA	3:a:601:TA1:O06	2.04	0.57
1:d:23:VAL:CG1	3:d:601:TA1:C41	2.82	0.57
1:e:358:PRO:HB2	3:e:601:TA1:H281	1.87	0.57
1:j:358:PRO:CB	3:j:601:TA1:O13	2.53	0.57
2:Y:71:GLU:HG2	2:Y:73:THR:H	1.68	0.57
2:Y:353:VAL:HG12	2:Y:354:GLY:N	2.18	0.57
2:B:80:THR:HB	2:B:84:ARG:HD2	1.86	0.57
2:D:80:THR:HB	2:D:84:ARG:HD2	1.86	0.57
1:q:261:PRO:O	1:q:262:ARG:HB3	2.03	0.57
1:b:138:SER:HB2	4:b:602:GDP:C1'	2.34	0.57
1:d:11:GLN:CB	4:d:602:GDP:O2B	2.52	0.57
1:g:23:VAL:HG13	3:g:601:TA1:C42	2.25	0.57
2:P:71:GLU:HG2	2:P:73:THR:H	1.69	0.57
2:P:206:ASN:CG	6:P:502:GTP:HN22	2.12	0.57
2:R:80:THR:HB	2:R:84:ARG:HD2	1.86	0.57
2:J:71:GLU:HG2	2:J:73:THR:H	1.69	0.57
1:n:210:ILE:HG23	1:n:273:LEU:HD13	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:261:PRO:O	1:b:262:ARG:HB3	2.04	0.57
1:f:256:ASN:HA	2:S:404:PHE:CE1	2.39	0.57
1:g:215:LEU:CD2	3:g:601:TA1:C14	2.82	0.57
2:Q:171:ILE:CD1	6:Q:502:GTP:C2	2.87	0.57
1:b:138:SER:CB	4:b:602:GDP:C8	2.87	0.57
1:f:210:ILE:HG23	1:f:273:LEU:HD13	1.85	0.57
1:g:210:ILE:HG23	1:g:273:LEU:HD13	1.85	0.57
1:i:287:PRO:O	1:i:291:GLN:HG3	2.05	0.57
1:m:287:PRO:O	1:m:291:GLN:HG3	2.05	0.57
2:S:71:GLU:HG2	2:S:73:THR:H	1.69	0.57
2:U:100:ALA:N	6:U:502:GTP:O2G	2.37	0.57
1:w:261:PRO:O	1:w:262:ARG:HB3	2.04	0.57
1:z:287:PRO:O	1:z:291:GLN:HG3	2.05	0.57
1:b:384:GLN:HA	2:B:348:PRO:HG3	1.87	0.57
1:f:222:TYR:CE2	4:f:602:GDP:C5	2.92	0.57
1:h:12:CYS:SG	4:h:602:GDP:N1	2.77	0.57
1:j:12:CYS:SG	4:j:602:GDP:N3	2.78	0.57
1:j:261:PRO:O	1:j:262:ARG:HB3	2.04	0.57
1:k:287:PRO:O	1:k:291:GLN:HG3	2.05	0.57
2:Z:317:LEU:HB3	2:Z:319:TYR:CE1	2.40	0.57
2:E:80:THR:HB	2:E:84:ARG:HD2	1.86	0.57
2:I:317:LEU:HB3	2:I:319:TYR:CE1	2.40	0.57
1:o:261:PRO:O	1:o:262:ARG:HB3	2.04	0.57
1:g:261:PRO:O	1:g:262:ARG:HB3	2.05	0.57
2:F:71:GLU:HG2	2:F:73:THR:H	1.69	0.57
2:G:89:PRO:HD3	2:H:283:HIS:CG	2.39	0.57
2:L:71:GLU:HG2	2:L:73:THR:H	1.69	0.57
1:n:281:TYR:HE2	1:z:87:PRO:CG	2.17	0.57
1:o:210:ILE:HG23	1:o:273:LEU:HD13	1.84	0.57
1:v:287:PRO:O	1:v:291:GLN:HG3	2.05	0.57
1:x:287:PRO:O	1:x:291:GLN:HG3	2.05	0.57
1:g:12:CYS:SG	4:g:602:GDP:C2	2.98	0.57
2:N:200:CYS:HG	2:N:202:PHE:HE1	1.52	0.57
2:V:317:LEU:HB3	2:V:319:TYR:CE1	2.40	0.57
2:W:317:LEU:HB3	2:W:319:TYR:CE1	2.40	0.57
2:J:317:LEU:HB3	2:J:319:TYR:CE1	2.40	0.57
1:m:23:VAL:HG13	3:m:601:TA1:H421	1.86	0.57
1:m:210:ILE:HG23	1:m:273:LEU:HD13	1.85	0.57
2:N:98:ASP:HB2	6:N:502:GTP:O2G	2.05	0.57
2:B:200:CYS:HG	2:B:202:PHE:HE1	1.52	0.57
2:H:317:LEU:HB3	2:H:319:TYR:CE1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:210:ILE:HG23	1:r:273:LEU:HD13	1.85	0.57
1:z:210:ILE:HG23	1:z:273:LEU:HD13	1.85	0.57
1:a:287:PRO:O	1:a:291:GLN:HG3	2.05	0.57
1:d:261:PRO:O	1:d:262:ARG:HB3	2.04	0.57
1:f:99:ASN:ND2	2:F:254:GLU:OE2	2.38	0.57
1:j:219:THR:HB	2:J:324:VAL:HG11	1.86	0.57
1:j:256:ASN:HA	2:W:404:PHE:HE1	1.69	0.57
1:l:231:ALA:HB1	3:l:601:TA1:C39	2.35	0.57
2:X:71:GLU:HG2	2:X:73:THR:H	1.68	0.57
2:E:317:LEU:HB3	2:E:319:TYR:CE1	2.40	0.57
2:I:88:HIS:CD2	2:J:283:HIS:CG	2.84	0.57
2:K:71:GLU:HG2	2:K:73:THR:H	1.69	0.57
1:p:261:PRO:O	1:p:262:ARG:HB3	2.03	0.57
1:y:261:PRO:O	1:y:262:ARG:HB3	2.03	0.57
1:y:287:PRO:O	1:y:291:GLN:HG3	2.05	0.57
1:c:222:TYR:OH	4:c:602:GDP:N9	2.33	0.56
1:e:359:ARG:N	3:e:601:TA1:O13	2.38	0.56
1:f:12:CYS:HB2	4:f:602:GDP:C4	2.40	0.56
1:j:287:PRO:O	1:j:291:GLN:HG3	2.05	0.56
1:l:287:PRO:O	1:l:291:GLN:HG3	2.05	0.56
2:T:224:TYR:HE2	6:T:502:GTP:C2	2.08	0.56
2:D:71:GLU:HG2	2:D:73:THR:H	1.69	0.56
2:H:236:SER:O	2:H:240:ALA:HB2	2.05	0.56
2:M:317:LEU:HB3	2:M:319:TYR:CE1	2.40	0.56
1:s:261:PRO:O	1:s:262:ARG:HB3	2.04	0.56
1:t:210:ILE:HG23	1:t:273:LEU:HD13	1.85	0.56
1:u:261:PRO:O	1:u:262:ARG:HB3	2.04	0.56
1:c:261:PRO:O	1:c:262:ARG:HB3	2.04	0.56
1:d:222:TYR:CE1	4:d:602:GDP:N3	2.73	0.56
1:h:287:PRO:O	1:h:291:GLN:HG3	2.05	0.56
1:l:261:PRO:O	1:l:262:ARG:HB3	2.03	0.56
2:N:88:HIS:HD2	2:O:283:HIS:CB	2.18	0.56
2:N:326:LYS:NZ	1:n:218:THR:O	2.36	0.56
2:Q:71:GLU:HG2	2:Q:73:THR:H	1.69	0.56
2:V:200:CYS:HG	2:V:202:PHE:HE1	1.53	0.56
2:I:236:SER:O	2:I:240:ALA:HB2	2.06	0.56
1:c:23:VAL:HG13	3:c:601:TA1:C42	2.34	0.56
1:c:99:ASN:OD1	4:c:602:GDP:C5'	2.54	0.56
1:c:287:PRO:O	1:c:291:GLN:HG3	2.05	0.56
1:d:12:CYS:HB2	4:d:602:GDP:N9	2.19	0.56
1:h:141:GLY:CA	4:h:602:GDP:O5'	2.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:215:LEU:HD21	3:h:601:TA1:C14	2.35	0.56
1:k:361:LEU:HD23	3:k:601:TA1:H442	1.87	0.56
2:T:236:SER:O	2:T:240:ALA:HB2	2.06	0.56
2:U:236:SER:O	2:U:240:ALA:HB2	2.06	0.56
2:W:88:HIS:CD2	2:X:283:HIS:HB2	2.40	0.56
2:L:317:LEU:HB3	2:L:319:TYR:CE1	2.40	0.56
1:n:287:PRO:O	1:n:291:GLN:HG3	2.05	0.56
1:o:256:ASN:HD21	1:o:350:LYS:HD2	1.69	0.56
1:s:210:ILE:HG23	1:s:273:LEU:HD13	1.86	0.56
1:w:287:PRO:O	1:w:291:GLN:HG3	2.05	0.56
1:x:210:ILE:HG23	1:x:273:LEU:HD13	1.86	0.56
1:b:219:THR:HB	2:B:324:VAL:HG11	1.86	0.56
1:c:141:GLY:CA	4:c:602:GDP:H4'	2.35	0.56
1:d:86:ARG:NH2	1:d:123:GLU:OE2	2.39	0.56
1:f:287:PRO:O	1:f:291:GLN:HG3	2.05	0.56
1:h:261:PRO:O	1:h:262:ARG:HB3	2.04	0.56
1:l:215:LEU:HD21	3:l:601:TA1:O06	2.04	0.56
1:m:222:TYR:HE1	4:m:602:GDP:N2	1.99	0.56
2:N:236:SER:O	2:N:240:ALA:HB2	2.05	0.56
2:O:236:SER:O	2:O:240:ALA:HB2	2.06	0.56
2:V:236:SER:O	2:V:240:ALA:HB2	2.06	0.56
2:A:236:SER:O	2:A:240:ALA:HB2	2.06	0.56
2:A:317:LEU:HB3	2:A:319:TYR:CE1	2.40	0.56
2:E:71:GLU:HG2	2:E:73:THR:H	1.69	0.56
2:G:236:SER:O	2:G:240:ALA:HB2	2.06	0.56
2:I:88:HIS:HA	2:J:283:HIS:CG	2.36	0.56
2:J:236:SER:O	2:J:240:ALA:HB2	2.06	0.56
1:p:287:PRO:O	1:p:291:GLN:HG3	2.05	0.56
1:s:86:ARG:NH2	1:s:123:GLU:OE2	2.38	0.56
1:s:287:PRO:O	1:s:291:GLN:HG3	2.05	0.56
1:a:261:PRO:O	1:a:262:ARG:HB3	2.04	0.56
1:c:23:VAL:HG11	3:c:601:TA1:C41	2.33	0.56
1:c:138:SER:OG	4:c:602:GDP:H1'	2.05	0.56
1:e:23:VAL:CG1	3:e:601:TA1:C41	2.84	0.56
1:i:220:PRO:HD2	2:I:326:LYS:CG	2.22	0.56
3:i:601:TA1:H463	3:i:601:TA1:C26	2.36	0.56
2:P:236:SER:O	2:P:240:ALA:HB2	2.06	0.56
2:Z:353:VAL:HG12	2:Z:354:GLY:N	2.21	0.56
2:A:200:CYS:HG	2:A:202:PHE:HE1	1.52	0.56
2:B:236:SER:O	2:B:240:ALA:HB2	2.06	0.56
2:C:236:SER:O	2:C:240:ALA:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:88:HIS:CG	2:G:283:HIS:HB3	2.31	0.56
1:n:261:PRO:O	1:n:262:ARG:HB3	2.03	0.56
1:o:287:PRO:O	1:o:291:GLN:HG3	2.05	0.56
1:u:287:PRO:O	1:u:291:GLN:HG3	2.05	0.56
1:b:287:PRO:O	1:b:291:GLN:HG3	2.05	0.56
1:g:86:ARG:NH2	1:g:123:GLU:OE2	2.39	0.56
1:i:67:ASP:HB2	1:i:73:MET:HE2	1.88	0.56
1:k:23:VAL:HG13	3:k:601:TA1:C41	2.36	0.56
1:l:227:HIS:HB3	3:l:601:TA1:HC71	1.87	0.56
2:S:317:LEU:HB3	2:S:319:TYR:CE1	2.40	0.56
2:L:236:SER:O	2:L:240:ALA:HB2	2.06	0.56
2:M:236:SER:O	2:M:240:ALA:HB2	2.06	0.56
1:d:23:VAL:CG1	3:d:601:TA1:H411	2.35	0.56
1:e:228:LEU:N	3:e:601:TA1:HC71	2.21	0.56
1:f:86:ARG:NH2	1:f:123:GLU:OE2	2.39	0.56
1:h:141:GLY:HA3	4:h:602:GDP:O5'	2.05	0.56
1:i:210:ILE:HG23	1:i:273:LEU:HD13	1.85	0.56
1:j:358:PRO:HB2	3:j:601:TA1:C28	2.35	0.56
2:N:317:LEU:HB3	2:N:319:TYR:CE1	2.40	0.56
2:O:100:ALA:N	6:O:502:GTP:O2G	2.34	0.56
2:R:44:GLY:HA3	2:R:49:PHE:HE1	1.69	0.56
2:R:71:GLU:HG2	2:R:73:THR:H	1.69	0.56
2:S:236:SER:O	2:S:240:ALA:HB2	2.06	0.56
2:T:171:ILE:CD1	6:T:502:GTP:HN22	2.19	0.56
2:Z:236:SER:O	2:Z:240:ALA:HB2	2.06	0.56
2:A:283:HIS:NE2	2:M:89:PRO:HD3	2.11	0.56
2:D:236:SER:O	2:D:240:ALA:HB2	2.05	0.56
2:F:236:SER:O	2:F:240:ALA:HB2	2.05	0.56
2:F:317:LEU:HB3	2:F:319:TYR:CE1	2.40	0.56
1:q:287:PRO:O	1:q:291:GLN:HG3	2.05	0.56
1:w:86:ARG:HA	1:x:281:TYR:CD2	2.40	0.56
1:x:86:ARG:NH2	1:x:123:GLU:OE2	2.38	0.56
1:d:256:ASN:HA	2:Q:404:PHE:CE1	2.41	0.56
1:e:86:ARG:NH2	1:e:123:GLU:OE2	2.39	0.56
1:f:322:SER:OG	1:f:325:GLU:HB2	2.06	0.56
1:g:322:SER:OG	1:g:325:GLU:HB2	2.06	0.56
1:k:256:ASN:HA	2:X:404:PHE:CE1	2.41	0.56
1:l:256:ASN:HA	2:Y:404:PHE:CE1	2.40	0.56
2:R:317:LEU:HB3	2:R:319:TYR:CE1	2.40	0.56
2:W:236:SER:O	2:W:240:ALA:HB2	2.06	0.56
2:X:236:SER:O	2:X:240:ALA:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:317:LEU:HB3	2:X:319:TYR:CE1	2.40	0.56
2:I:88:HIS:CA	2:J:283:HIS:CD2	2.73	0.56
2:K:236:SER:O	2:K:240:ALA:HB2	2.06	0.56
2:K:317:LEU:HB3	2:K:319:TYR:CE1	2.40	0.56
1:n:322:SER:OG	1:n:325:GLU:HB2	2.06	0.56
1:q:86:ARG:NH2	1:q:123:GLU:OE2	2.39	0.56
1:r:287:PRO:O	1:r:291:GLN:HG3	2.05	0.56
1:t:86:ARG:NH2	1:t:123:GLU:OE2	2.39	0.56
1:z:86:ARG:NH2	1:z:123:GLU:OE2	2.38	0.56
1:d:141:GLY:CA	4:d:602:GDP:H4'	2.36	0.56
1:e:287:PRO:O	1:e:291:GLN:HG3	2.05	0.56
1:f:261:PRO:O	1:f:262:ARG:HB3	2.04	0.56
1:h:72:THR:O	1:h:76:VAL:HG23	2.06	0.56
1:i:72:THR:O	1:i:76:VAL:HG23	2.06	0.56
1:k:86:ARG:NH2	1:k:123:GLU:OE2	2.39	0.56
2:Y:200:CYS:HG	2:Y:202:PHE:HE1	1.52	0.56
2:Y:236:SER:O	2:Y:240:ALA:HB2	2.06	0.56
2:D:317:LEU:HB3	2:D:319:TYR:CE1	2.40	0.56
1:o:86:ARG:NH2	1:o:123:GLU:OE2	2.38	0.56
1:d:141:GLY:N	4:d:602:GDP:H4'	2.21	0.56
1:h:322:SER:OG	1:h:325:GLU:HB2	2.06	0.56
1:j:72:THR:O	1:j:76:VAL:HG23	2.06	0.56
2:Q:224:TYR:CD2	6:Q:502:GTP:C2	2.94	0.56
2:Q:224:TYR:CZ	6:Q:502:GTP:C4	2.94	0.56
2:Q:317:LEU:HB3	2:Q:319:TYR:CE1	2.40	0.56
2:T:317:LEU:HB3	2:T:319:TYR:CE1	2.40	0.56
2:T:326:LYS:CE	1:t:219:THR:HA	2.23	0.56
1:o:72:THR:O	1:o:76:VAL:HG23	2.06	0.56
1:r:86:ARG:NH2	1:r:123:GLU:OE2	2.39	0.56
1:b:86:ARG:NH2	1:b:123:GLU:OE2	2.39	0.55
1:b:394:PHE:CD1	2:B:257:THR:O	2.59	0.55
1:d:287:PRO:O	1:d:291:GLN:HG3	2.05	0.55
1:e:210:ILE:HG23	1:e:273:LEU:HD13	1.88	0.55
1:e:222:TYR:OH	4:e:602:GDP:O2'	2.25	0.55
1:i:143:THR:HB	4:i:602:GDP:O1B	2.06	0.55
1:j:55:THR:HG1	1:k:283:ALA:CA	2.14	0.55
1:j:322:SER:OG	1:j:325:GLU:HB2	2.06	0.55
2:Q:236:SER:O	2:Q:240:ALA:HB2	2.06	0.55
1:o:322:SER:OG	1:o:325:GLU:HB2	2.06	0.55
1:t:86:ARG:HG3	1:u:281:TYR:HB3	1.88	0.55
1:t:287:PRO:O	1:t:291:GLN:HG3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:72:THR:O	1:b:76:VAL:HG23	2.06	0.55
1:g:287:PRO:O	1:g:291:GLN:HG3	2.05	0.55
1:k:72:THR:O	1:k:76:VAL:HG23	2.06	0.55
1:k:210:ILE:HG23	1:k:273:LEU:HD13	1.86	0.55
1:m:86:ARG:NH2	1:m:123:GLU:OE2	2.39	0.55
2:O:12:ALA:CB	6:O:502:GTP:C4	2.88	0.55
2:S:88:HIS:CD2	2:T:283:HIS:HB2	2.42	0.55
2:Y:317:LEU:HB3	2:Y:319:TYR:CE1	2.39	0.55
2:A:128:GLN:NE2	2:B:285:GLN:CG	2.62	0.55
2:F:88:HIS:CG	2:G:283:HIS:CB	2.77	0.55
2:G:200:CYS:HG	2:G:202:PHE:HE1	1.54	0.55
1:a:322:SER:OG	1:a:325:GLU:HB2	2.07	0.55
1:b:322:SER:OG	1:b:325:GLU:HB2	2.06	0.55
1:g:72:THR:O	1:g:76:VAL:HG23	2.06	0.55
1:i:86:ARG:NH2	1:i:123:GLU:OE2	2.38	0.55
1:i:215:LEU:HD21	3:i:601:TA1:C14	2.37	0.55
1:j:222:TYR:CE1	4:j:602:GDP:C2	2.95	0.55
2:T:200:CYS:HG	2:T:202:PHE:HE1	1.54	0.55
1:o:322:SER:O	1:o:326:VAL:HG23	2.06	0.55
1:a:358:PRO:CB	3:a:601:TA1:H281	2.33	0.55
1:c:86:ARG:NH2	1:c:123:GLU:OE2	2.38	0.55
1:e:228:LEU:HD23	3:e:601:TA1:H081	1.89	0.55
1:h:86:ARG:NH2	1:h:123:GLU:OE2	2.38	0.55
1:j:12:CYS:SG	4:j:602:GDP:C2	3.00	0.55
2:P:317:LEU:HB3	2:P:319:TYR:CE1	2.40	0.55
2:R:27:GLU:OE2	2:R:236:SER:OG	2.25	0.55
2:E:236:SER:O	2:E:240:ALA:HB2	2.05	0.55
1:u:72:THR:O	1:u:76:VAL:HG23	2.07	0.55
1:u:86:ARG:NH2	1:u:123:GLU:OE2	2.38	0.55
1:v:72:THR:O	1:v:76:VAL:HG23	2.07	0.55
1:v:86:ARG:NH2	1:v:123:GLU:OE2	2.39	0.55
1:v:210:ILE:HG23	1:v:273:LEU:HD13	1.86	0.55
1:z:322:SER:OG	1:z:325:GLU:HB2	2.07	0.55
1:c:11:GLN:HB2	4:c:602:GDP:O2B	2.07	0.55
1:f:141:GLY:CA	4:f:602:GDP:O5'	2.54	0.55
1:l:72:THR:O	1:l:76:VAL:HG23	2.06	0.55
2:O:317:LEU:HB3	2:O:319:TYR:CE1	2.40	0.55
2:B:317:LEU:HB3	2:B:319:TYR:CE1	2.40	0.55
2:C:27:GLU:OE2	2:C:236:SER:OG	2.25	0.55
2:C:317:LEU:HB3	2:C:319:TYR:CE1	2.40	0.55
1:w:72:THR:O	1:w:76:VAL:HG23	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:72:THR:O	1:x:76:VAL:HG23	2.07	0.55
1:c:72:THR:O	1:c:76:VAL:HG23	2.06	0.55
1:e:23:VAL:HG13	3:e:601:TA1:C42	2.37	0.55
1:i:231:ALA:HB1	3:i:601:TA1:C39	2.37	0.55
1:m:322:SER:OG	1:m:325:GLU:HB2	2.06	0.55
2:P:27:GLU:OE2	2:P:236:SER:OG	2.25	0.55
2:G:317:LEU:HB3	2:G:319:TYR:CE1	2.40	0.55
1:n:72:THR:O	1:n:76:VAL:HG23	2.06	0.55
1:p:72:THR:O	1:p:76:VAL:HG23	2.06	0.55
1:t:72:THR:O	1:t:76:VAL:HG23	2.07	0.55
1:y:72:THR:O	1:y:76:VAL:HG23	2.06	0.55
1:a:11:GLN:HB3	4:a:602:GDP:O4'	2.07	0.55
1:b:138:SER:HB2	4:b:602:GDP:C2'	2.36	0.55
1:c:231:ALA:HB1	3:c:601:TA1:H391	1.89	0.55
1:g:87:PRO:HD3	1:h:281:TYR:CD2	2.42	0.55
1:h:55:THR:HG1	1:i:283:ALA:HA	1.70	0.55
1:i:322:SER:OG	1:i:325:GLU:HB2	2.07	0.55
2:N:283:HIS:HB2	2:Z:88:HIS:CD2	2.41	0.55
2:R:45:GLY:HA2	2:R:48:SER:HA	1.89	0.55
2:R:236:SER:O	2:R:240:ALA:HB2	2.06	0.55
2:E:27:GLU:OE2	2:E:236:SER:OG	2.25	0.55
1:n:322:SER:O	1:n:326:VAL:HG23	2.07	0.55
1:p:86:ARG:NH2	1:p:123:GLU:OE2	2.38	0.55
1:r:72:THR:O	1:r:76:VAL:HG23	2.06	0.55
1:v:322:SER:OG	1:v:325:GLU:HB2	2.07	0.55
1:a:72:THR:O	1:a:76:VAL:HG23	2.06	0.55
1:e:72:THR:O	1:e:76:VAL:HG23	2.06	0.55
1:e:322:SER:OG	1:e:325:GLU:HB2	2.06	0.55
1:f:72:THR:O	1:f:76:VAL:HG23	2.07	0.55
1:f:322:SER:O	1:f:326:VAL:HG23	2.07	0.55
1:g:81:PHE:O	1:g:84:ILE:HG22	2.07	0.55
1:i:55:THR:OG1	1:j:283:ALA:CA	2.33	0.55
2:S:27:GLU:OE2	2:S:236:SER:OG	2.25	0.55
2:T:27:GLU:OE2	2:T:236:SER:OG	2.25	0.55
2:F:27:GLU:OE2	2:F:236:SER:OG	2.25	0.55
2:K:200:CYS:HG	2:K:202:PHE:HE1	1.54	0.55
1:z:72:THR:O	1:z:76:VAL:HG23	2.06	0.55
1:g:322:SER:O	1:g:326:VAL:HG23	2.07	0.55
2:O:27:GLU:OE2	2:O:236:SER:OG	2.25	0.55
2:F:200:CYS:HG	2:F:202:PHE:HE1	1.54	0.55
2:G:262:TYR:CB	2:G:263:PRO:HD2	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:y:322:SER:OG	1:y:325:GLU:HB2	2.06	0.55
1:f:81:PHE:O	1:f:84:ILE:HG22	2.07	0.55
1:j:12:CYS:SG	4:j:602:GDP:C4	2.99	0.55
1:m:72:THR:O	1:m:76:VAL:HG23	2.06	0.55
1:m:322:SER:O	1:m:326:VAL:HG23	2.07	0.55
2:T:224:TYR:OH	6:T:502:GTP:C8	2.60	0.55
2:U:27:GLU:OE2	2:U:236:SER:OG	2.25	0.55
2:Y:12:ALA:HB2	6:Y:502:GTP:C4	2.42	0.55
2:Z:224:TYR:OH	6:Z:502:GTP:N9	2.39	0.55
2:H:27:GLU:OE2	2:H:236:SER:OG	2.25	0.55
1:n:86:ARG:NH2	1:n:123:GLU:OE2	2.39	0.55
1:r:322:SER:OG	1:r:325:GLU:HB2	2.06	0.55
1:y:86:ARG:NH2	1:y:123:GLU:OE2	2.38	0.55
1:a:86:ARG:NH2	1:a:123:GLU:OE2	2.38	0.54
2:Q:88:HIS:CD2	2:R:283:HIS:HB2	2.42	0.54
2:X:101:ASN:ND2	6:X:502:GTP:O3G	2.40	0.54
2:B:27:GLU:OE2	2:B:236:SER:OG	2.25	0.54
2:F:89:PRO:HD3	2:G:283:HIS:CD2	2.41	0.54
2:L:44:GLY:HA3	2:L:49:PHE:HE1	1.72	0.54
1:t:81:PHE:O	1:t:84:ILE:HG22	2.08	0.54
1:t:322:SER:OG	1:t:325:GLU:HB2	2.07	0.54
1:u:322:SER:OG	1:u:325:GLU:HB2	2.07	0.54
1:h:81:PHE:O	1:h:84:ILE:HG22	2.08	0.54
1:i:81:PHE:O	1:i:84:ILE:HG22	2.07	0.54
1:i:222:TYR:CD1	4:i:602:GDP:C6	2.95	0.54
1:k:23:VAL:CG1	3:k:601:TA1:C41	2.85	0.54
2:Z:171:ILE:CD1	6:Z:502:GTP:HN22	2.20	0.54
2:E:200:CYS:HG	2:E:202:PHE:HE1	1.53	0.54
2:G:27:GLU:OE2	2:G:236:SER:OG	2.25	0.54
2:I:44:GLY:HA3	2:I:49:PHE:HE1	1.72	0.54
1:u:81:PHE:O	1:u:84:ILE:HG22	2.08	0.54
1:w:86:ARG:NH2	1:w:123:GLU:OE2	2.39	0.54
1:y:322:SER:O	1:y:326:VAL:HG23	2.07	0.54
1:a:322:SER:O	1:a:326:VAL:HG23	2.07	0.54
1:g:215:LEU:HD22	3:g:601:TA1:C14	2.37	0.54
1:l:86:ARG:NH2	1:l:123:GLU:OE2	2.39	0.54
3:l:601:TA1:H463	3:l:601:TA1:C26	2.38	0.54
1:m:358:PRO:HB2	3:m:601:TA1:H281	1.88	0.54
2:Z:27:GLU:OE2	2:Z:236:SER:OG	2.25	0.54
2:F:88:HIS:NE2	2:G:283:HIS:O	2.38	0.54
2:M:44:GLY:HA3	2:M:49:PHE:HE1	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:322:SER:OG	1:p:325:GLU:HB2	2.07	0.54
1:v:81:PHE:O	1:v:84:ILE:HG22	2.07	0.54
1:v:322:SER:O	1:v:326:VAL:HG23	2.07	0.54
1:b:322:SER:O	1:b:326:VAL:HG23	2.07	0.54
1:j:86:ARG:NH2	1:j:123:GLU:OE2	2.39	0.54
1:k:322:SER:OG	1:k:325:GLU:HB2	2.06	0.54
1:l:322:SER:O	1:l:326:VAL:HG23	2.07	0.54
2:S:200:CYS:HG	2:S:202:PHE:HE1	1.54	0.54
2:A:27:GLU:OE2	2:A:236:SER:OG	2.25	0.54
2:A:88:HIS:CB	2:B:283:HIS:CD2	2.89	0.54
2:D:44:GLY:HA3	2:D:49:PHE:HE1	1.73	0.54
2:K:44:GLY:HA3	2:K:49:PHE:HE1	1.73	0.54
1:q:72:THR:O	1:q:76:VAL:HG23	2.06	0.54
1:s:72:THR:O	1:s:76:VAL:HG23	2.07	0.54
1:w:322:SER:OG	1:w:325:GLU:HB2	2.07	0.54
1:a:87:PRO:HD3	1:b:281:TYR:CD2	2.41	0.54
1:c:322:SER:OG	1:c:325:GLU:HB2	2.07	0.54
1:d:72:THR:O	1:d:76:VAL:HG23	2.06	0.54
1:h:322:SER:O	1:h:326:VAL:HG23	2.08	0.54
1:i:322:SER:O	1:i:326:VAL:HG23	2.07	0.54
1:l:322:SER:OG	1:l:325:GLU:HB2	2.07	0.54
2:N:27:GLU:OE2	2:N:236:SER:OG	2.25	0.54
2:Q:143:GLY:HA3	6:Q:502:GTP:O2B	2.07	0.54
2:S:171:ILE:CD1	6:S:502:GTP:HN22	2.20	0.54
2:Z:224:TYR:CG	6:Z:502:GTP:C6	2.93	0.54
2:A:44:GLY:HA3	2:A:49:PHE:HE1	1.72	0.54
2:M:27:GLU:OE2	2:M:236:SER:OG	2.25	0.54
1:w:322:SER:O	1:w:326:VAL:HG23	2.07	0.54
1:a:23:VAL:HG13	3:a:601:TA1:C41	2.38	0.54
1:d:322:SER:OG	1:d:325:GLU:HB2	2.07	0.54
1:e:53:GLU:O	2:F:285:GLN:NE2	2.28	0.54
1:e:294:PHE:C	1:e:295:ASP:HA	2.30	0.54
1:i:347:ASN:O	2:V:181:VAL:HG21	2.02	0.54
1:j:81:PHE:O	1:j:84:ILE:HG22	2.07	0.54
2:S:44:GLY:HA3	2:S:49:PHE:HE1	1.73	0.54
1:s:81:PHE:O	1:s:84:ILE:HG22	2.08	0.54
1:x:322:SER:OG	1:x:325:GLU:HB2	2.06	0.54
1:m:222:TYR:CD1	4:m:602:GDP:N1	2.74	0.54
2:N:11:GLN:N	6:N:502:GTP:O1B	2.39	0.54
2:Q:44:GLY:HA3	2:Q:49:PHE:HE1	1.73	0.54
2:R:200:CYS:HG	2:R:202:PHE:HE1	1.53	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:326:LYS:NZ	1:r:218:THR:O	2.39	0.54
2:U:317:LEU:HB3	2:U:319:TYR:CE1	2.40	0.54
2:W:27:GLU:OE2	2:W:236:SER:OG	2.25	0.54
1:f:281:TYR:CE2	2:R:89:PRO:HD3	2.40	0.54
1:h:12:CYS:HB2	4:h:602:GDP:C5	2.42	0.54
1:j:347:ASN:O	2:W:181:VAL:HG21	2.01	0.54
2:H:44:GLY:HA3	2:H:49:PHE:HE1	1.72	0.54
1:s:322:SER:OG	1:s:325:GLU:HB2	2.07	0.54
1:w:81:PHE:O	1:w:84:ILE:HG22	2.07	0.54
1:x:322:SER:O	1:x:326:VAL:HG23	2.07	0.54
1:b:10:GLY:HA3	4:b:602:GDP:H5'	1.84	0.54
1:h:222:TYR:HE1	4:h:602:GDP:C2	2.21	0.54
2:Q:27:GLU:OE2	2:Q:236:SER:OG	2.25	0.54
2:V:44:GLY:HA3	2:V:49:PHE:HE1	1.73	0.54
2:C:44:GLY:HA3	2:C:49:PHE:HE1	1.73	0.54
2:J:27:GLU:OE2	2:J:236:SER:OG	2.25	0.54
1:q:322:SER:OG	1:q:325:GLU:HB2	2.07	0.54
1:r:322:SER:O	1:r:326:VAL:HG23	2.08	0.54
1:c:81:PHE:O	1:c:84:ILE:HG22	2.07	0.54
2:Q:171:ILE:CD1	6:Q:502:GTP:N2	2.71	0.54
2:S:326:LYS:HD3	1:s:212:PHE:CZ	2.42	0.54
2:U:224:TYR:OH	6:U:502:GTP:C4	2.56	0.54
2:Y:44:GLY:HA3	2:Y:49:PHE:HE1	1.73	0.54
2:G:44:GLY:HA3	2:G:49:PHE:HE1	1.72	0.54
2:K:27:GLU:OE2	2:K:236:SER:OG	2.25	0.54
1:g:350:LYS:CG	2:T:179:THR:O	2.45	0.53
1:k:81:PHE:O	1:k:84:ILE:HG22	2.07	0.53
1:k:222:TYR:CZ	4:k:602:GDP:C5	2.96	0.53
2:O:262:TYR:CB	2:O:263:PRO:HD2	2.25	0.53
2:X:27:GLU:OE2	2:X:236:SER:OG	2.25	0.53
2:X:44:GLY:HA3	2:X:49:PHE:HE1	1.73	0.53
2:Z:44:GLY:HA3	2:Z:49:PHE:HE1	1.73	0.53
2:B:44:GLY:HA3	2:B:49:PHE:HE1	1.73	0.53
2:D:27:GLU:OE2	2:D:236:SER:OG	2.25	0.53
1:b:81:PHE:O	1:b:84:ILE:HG22	2.08	0.53
1:b:231:ALA:HB1	3:b:601:TA1:C39	2.38	0.53
1:i:222:TYR:CZ	4:i:602:GDP:C4	2.97	0.53
1:j:358:PRO:HB3	3:j:601:TA1:O13	2.07	0.53
1:m:81:PHE:O	1:m:84:ILE:HG22	2.07	0.53
2:U:200:CYS:HG	2:U:202:PHE:HE1	1.56	0.53
2:F:44:GLY:HA3	2:F:49:PHE:HE1	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:81:PHE:O	1:o:84:ILE:HG22	2.07	0.53
1:p:81:PHE:O	1:p:84:ILE:HG22	2.08	0.53
1:a:81:PHE:O	1:a:84:ILE:HG22	2.07	0.53
1:a:361:LEU:HD23	3:a:601:TA1:H171	1.88	0.53
1:e:81:PHE:O	1:e:84:ILE:HG22	2.08	0.53
1:g:256:ASN:HA	2:T:404:PHE:HE1	1.71	0.53
2:S:171:ILE:HD11	6:S:502:GTP:N2	2.22	0.53
1:z:322:SER:O	1:z:326:VAL:HG23	2.08	0.53
1:d:81:PHE:O	1:d:84:ILE:HG22	2.07	0.53
1:h:274:THR:O	3:h:601:TA1:H192	2.08	0.53
2:O:224:TYR:CG	6:O:502:GTP:C6	2.96	0.53
2:P:44:GLY:HA3	2:P:49:PHE:HE1	1.73	0.53
2:U:44:GLY:HA3	2:U:49:PHE:HE1	1.73	0.53
2:W:200:CYS:HG	2:W:202:PHE:HE1	1.56	0.53
2:H:200:CYS:HG	2:H:202:PHE:HE1	1.57	0.53
2:K:89:PRO:HD3	2:L:283:HIS:CG	2.44	0.53
1:q:81:PHE:O	1:q:84:ILE:HG22	2.08	0.53
1:r:81:PHE:O	1:r:84:ILE:HG22	2.08	0.53
1:x:81:PHE:O	1:x:84:ILE:HG22	2.08	0.53
1:b:227:HIS:HB3	3:b:601:TA1:HC71	1.90	0.53
1:f:12:CYS:SG	4:f:602:GDP:N1	2.81	0.53
2:N:326:LYS:HG2	1:n:220:PRO:CD	2.20	0.53
2:V:45:GLY:HA2	2:V:48:SER:HA	1.91	0.53
2:Y:326:LYS:NZ	1:y:218:THR:O	2.39	0.53
2:E:44:GLY:HA3	2:E:49:PHE:HE1	1.73	0.53
2:G:45:GLY:HA2	2:G:48:SER:HA	1.91	0.53
2:I:45:GLY:HA2	2:I:48:SER:HA	1.91	0.53
1:n:81:PHE:O	1:n:84:ILE:HG22	2.08	0.53
1:b:234:SER:HB3	3:b:601:TA1:H401	1.91	0.53
1:g:219:THR:HB	2:G:324:VAL:HG11	1.90	0.53
3:j:601:TA1:H463	3:j:601:TA1:C26	2.38	0.53
1:l:81:PHE:O	1:l:84:ILE:HG22	2.08	0.53
2:N:44:GLY:HA3	2:N:49:PHE:HE1	1.73	0.53
2:O:45:GLY:HA2	2:O:48:SER:HA	1.91	0.53
2:T:45:GLY:HA2	2:T:48:SER:HA	1.91	0.53
2:I:27:GLU:OE2	2:I:236:SER:OG	2.25	0.53
1:y:81:PHE:O	1:y:84:ILE:HG22	2.07	0.53
1:d:222:TYR:CZ	4:d:602:GDP:C6	2.92	0.53
1:e:322:SER:O	1:e:326:VAL:HG23	2.08	0.53
1:f:12:CYS:HB2	4:f:602:GDP:C5	2.44	0.53
1:j:322:SER:O	1:j:326:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:45:GLY:HA2	2:S:48:SER:HA	1.91	0.53
2:V:27:GLU:OE2	2:V:236:SER:OG	2.25	0.53
2:X:306:ASP:C	2:X:308:ARG:H	2.17	0.53
2:Y:27:GLU:OE2	2:Y:236:SER:OG	2.25	0.53
2:Y:171:ILE:CD1	6:Y:502:GTP:N3	2.72	0.53
2:Z:306:ASP:C	2:Z:308:ARG:H	2.17	0.53
2:A:45:GLY:HA2	2:A:48:SER:HA	1.91	0.53
2:B:45:GLY:HA2	2:B:48:SER:HA	1.91	0.53
2:J:44:GLY:HA3	2:J:49:PHE:HE1	1.73	0.53
2:L:306:ASP:C	2:L:308:ARG:H	2.17	0.53
2:M:306:ASP:C	2:M:308:ARG:H	2.17	0.53
3:b:601:TA1:H463	3:b:601:TA1:C26	2.38	0.53
1:c:222:TYR:CE2	4:c:602:GDP:C6	2.95	0.53
2:O:306:ASP:C	2:O:308:ARG:H	2.17	0.53
2:Q:45:GLY:HA2	2:Q:48:SER:HA	1.91	0.53
2:Y:306:ASP:C	2:Y:308:ARG:H	2.17	0.53
2:A:306:ASP:C	2:A:308:ARG:H	2.17	0.53
2:C:45:GLY:HA2	2:C:48:SER:HA	1.91	0.53
2:D:45:GLY:HA2	2:D:48:SER:HA	1.91	0.53
2:F:45:GLY:HA2	2:F:48:SER:HA	1.91	0.53
2:M:200:CYS:HG	2:M:202:PHE:HE1	1.56	0.53
1:t:322:SER:O	1:t:326:VAL:HG23	2.09	0.53
1:z:81:PHE:O	1:z:84:ILE:HG22	2.08	0.53
1:k:322:SER:O	1:k:326:VAL:HG23	2.08	0.53
2:N:306:ASP:C	2:N:308:ARG:H	2.17	0.53
2:O:44:GLY:HA3	2:O:49:PHE:HE1	1.73	0.53
2:X:88:HIS:CD2	2:Y:283:HIS:HB2	2.44	0.53
2:X:353:VAL:HG12	2:X:354:GLY:N	2.24	0.53
2:E:45:GLY:HA2	2:E:48:SER:HA	1.91	0.53
2:F:40:LYS:CD	2:F:42:ILE:HD11	2.38	0.53
2:J:45:GLY:HA2	2:J:48:SER:HA	1.91	0.53
2:K:306:ASP:C	2:K:308:ARG:H	2.17	0.53
2:M:45:GLY:HA2	2:M:48:SER:HA	1.91	0.53
1:p:322:SER:O	1:p:326:VAL:HG23	2.09	0.53
1:b:394:PHE:CE1	2:B:257:THR:O	2.62	0.53
1:h:12:CYS:HB2	4:h:602:GDP:C4	2.43	0.53
2:P:45:GLY:HA2	2:P:48:SER:HA	1.91	0.53
2:T:44:GLY:HA3	2:T:49:PHE:HE1	1.73	0.53
2:K:45:GLY:HA2	2:K:48:SER:HA	1.91	0.53
1:b:13:GLY:CA	4:b:602:GDP:O3'	2.56	0.52
1:d:322:SER:O	1:d:326:VAL:HG23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:358:PRO:CB	3:i:601:TA1:H281	2.39	0.52
2:N:45:GLY:HA2	2:N:48:SER:HA	1.91	0.52
2:U:45:GLY:HA2	2:U:48:SER:HA	1.91	0.52
2:X:45:GLY:HA2	2:X:48:SER:HA	1.91	0.52
2:Z:45:GLY:HA2	2:Z:48:SER:HA	1.91	0.52
2:H:45:GLY:HA2	2:H:48:SER:HA	1.91	0.52
2:I:89:PRO:HD3	2:J:283:HIS:NE2	2.22	0.52
2:L:27:GLU:OE2	2:L:236:SER:OG	2.25	0.52
1:c:141:GLY:HA2	4:c:602:GDP:C5'	2.39	0.52
1:e:23:VAL:CG1	3:e:601:TA1:H411	2.39	0.52
1:m:99:ASN:OD1	4:m:602:GDP:C5'	2.53	0.52
2:P:262:TYR:CB	2:P:263:PRO:HD2	2.25	0.52
2:W:45:GLY:HA2	2:W:48:SER:HA	1.91	0.52
2:B:306:ASP:C	2:B:308:ARG:H	2.17	0.52
2:G:88:HIS:CD2	2:H:283:HIS:CG	2.87	0.52
3:c:601:TA1:H091	3:c:601:TA1:H141	1.91	0.52
1:g:361:LEU:HD23	3:g:601:TA1:H442	1.92	0.52
1:k:222:TYR:CD2	4:k:602:GDP:C6	2.98	0.52
2:V:56:THR:HA	2:W:285:GLN:NE2	2.24	0.52
2:W:44:GLY:HA3	2:W:49:PHE:HE1	1.73	0.52
2:Y:171:ILE:HD13	6:Y:502:GTP:C2	2.42	0.52
2:L:45:GLY:HA2	2:L:48:SER:HA	1.91	0.52
1:u:322:SER:O	1:u:326:VAL:HG23	2.09	0.52
1:a:263:LEU:HD11	1:a:425:TYR:HD2	1.74	0.52
1:d:23:VAL:HG13	3:d:601:TA1:C41	2.39	0.52
1:j:227:HIS:HB3	3:j:601:TA1:HC71	1.91	0.52
2:C:262:TYR:CB	2:C:263:PRO:HD2	2.25	0.52
2:J:200:CYS:HG	2:J:202:PHE:HE1	1.57	0.52
2:M:297:GLU:HG3	2:M:299:ALA:H	1.75	0.52
1:p:86:ARG:HG3	1:q:281:TYR:HB3	1.91	0.52
1:e:218:THR:O	2:E:326:LYS:NZ	2.32	0.52
2:Q:306:ASP:C	2:Q:308:ARG:H	2.17	0.52
2:Y:45:GLY:HA2	2:Y:48:SER:HA	1.91	0.52
2:I:306:ASP:C	2:I:308:ARG:H	2.17	0.52
1:b:138:SER:HB2	4:b:602:GDP:N3	2.25	0.52
2:S:297:GLU:HG3	2:S:299:ALA:H	1.75	0.52
2:Z:297:GLU:HG3	2:Z:299:ALA:H	1.75	0.52
2:C:306:ASP:C	2:C:308:ARG:H	2.17	0.52
2:D:306:ASP:C	2:D:308:ARG:H	2.17	0.52
2:D:353:VAL:HG12	2:D:354:GLY:N	2.25	0.52
2:F:297:GLU:HG3	2:F:299:ALA:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:263:LEU:HD11	1:p:425:TYR:HD2	1.74	0.52
1:b:169:VAL:HG11	4:b:602:GDP:C2	2.44	0.52
1:j:222:TYR:CD2	4:j:602:GDP:C6	2.98	0.52
1:j:263:LEU:HD11	1:j:425:TYR:HD2	1.74	0.52
2:P:306:ASP:C	2:P:308:ARG:H	2.17	0.52
2:V:306:ASP:C	2:V:308:ARG:H	2.17	0.52
2:X:224:TYR:CG	6:X:502:GTP:O6	2.62	0.52
2:E:297:GLU:HG3	2:E:299:ALA:H	1.75	0.52
1:r:86:ARG:HG2	1:r:88:ASP:H	1.74	0.52
1:w:12:CYS:O	1:w:16:ILE:HG13	2.10	0.52
1:w:263:LEU:HD11	1:w:425:TYR:HD2	1.75	0.52
1:b:11:GLN:H	4:b:602:GDP:C4'	2.23	0.52
1:b:263:LEU:HD11	1:b:425:TYR:HD2	1.74	0.52
1:c:12:CYS:CB	4:c:602:GDP:C5	2.93	0.52
2:Q:224:TYR:CE2	6:Q:502:GTP:N3	2.77	0.52
2:T:439:SER:O	1:t:390:ARG:NH2	2.43	0.52
2:V:171:ILE:HD11	6:V:502:GTP:N2	2.19	0.52
2:D:89:PRO:HD3	2:E:283:HIS:CG	2.44	0.52
2:D:128:GLN:CD	2:E:285:GLN:HG3	2.35	0.52
1:v:87:PRO:CG	1:w:281:TYR:CE2	2.90	0.52
1:w:131:GLN:HE22	1:w:249:ASP:HB3	1.75	0.52
1:f:263:LEU:HD11	1:f:425:TYR:HD2	1.75	0.52
1:l:220:PRO:HD2	2:L:326:LYS:CG	2.23	0.52
1:m:23:VAL:HG13	3:m:601:TA1:C41	2.40	0.52
1:m:263:LEU:HD11	1:m:425:TYR:HD2	1.74	0.52
2:N:353:VAL:HG12	2:N:354:GLY:N	2.25	0.52
2:O:353:VAL:HG12	2:O:354:GLY:N	2.25	0.52
2:P:297:GLU:HG3	2:P:299:ALA:H	1.75	0.52
2:R:11:GLN:N	6:R:502:GTP:O1B	2.34	0.52
2:V:297:GLU:HG3	2:V:299:ALA:H	1.75	0.52
2:B:297:GLU:HG3	2:B:299:ALA:H	1.75	0.52
2:E:353:VAL:HG12	2:E:354:GLY:N	2.24	0.52
2:H:88:HIS:CA	2:I:283:HIS:CD2	2.72	0.52
2:I:89:PRO:HD3	2:J:283:HIS:CG	2.44	0.52
1:s:322:SER:O	1:s:326:VAL:HG23	2.09	0.52
1:u:263:LEU:HD11	1:u:425:TYR:HD2	1.74	0.52
1:g:263:LEU:HD11	1:g:425:TYR:HD2	1.75	0.52
2:O:326:LYS:NZ	1:o:218:THR:O	2.37	0.52
2:R:297:GLU:HG3	2:R:299:ALA:H	1.75	0.52
1:a:256:ASN:HA	2:N:404:PHE:HE1	1.75	0.51
1:b:138:SER:CB	4:b:602:GDP:O2'	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:601:TA1:H463	3:c:601:TA1:H261	1.91	0.51
1:e:23:VAL:HG13	3:e:601:TA1:C41	2.40	0.51
1:k:263:LEU:HD11	1:k:425:TYR:HD2	1.74	0.51
2:Q:98:ASP:HB2	6:Q:502:GTP:O2G	2.10	0.51
2:V:326:LYS:HE2	1:v:218:THR:O	2.09	0.51
2:C:297:GLU:HG3	2:C:299:ALA:H	1.75	0.51
2:G:89:PRO:HD3	2:H:283:HIS:NE2	2.16	0.51
2:I:297:GLU:HG3	2:I:299:ALA:H	1.75	0.51
2:L:297:GLU:HG3	2:L:299:ALA:H	1.75	0.51
1:q:263:LEU:HD11	1:q:425:TYR:HD2	1.75	0.51
1:v:263:LEU:HD11	1:v:425:TYR:HD2	1.75	0.51
1:c:322:SER:O	1:c:326:VAL:HG23	2.09	0.51
1:h:263:LEU:HD11	1:h:425:TYR:HD2	1.75	0.51
2:U:297:GLU:HG3	2:U:299:ALA:H	1.75	0.51
2:U:353:VAL:HG12	2:U:354:GLY:N	2.25	0.51
2:W:297:GLU:HG3	2:W:299:ALA:H	1.75	0.51
2:Y:297:GLU:HG3	2:Y:299:ALA:H	1.75	0.51
2:H:297:GLU:HG3	2:H:299:ALA:H	1.75	0.51
2:J:297:GLU:HG3	2:J:299:ALA:H	1.75	0.51
2:M:75:ILE:HD12	2:M:94:THR:HG22	1.91	0.51
1:v:12:CYS:O	1:v:16:ILE:HG13	2.10	0.51
1:x:131:GLN:HE22	1:x:249:ASP:HB3	1.75	0.51
1:e:222:TYR:OH	4:e:602:GDP:C2'	2.58	0.51
1:g:11:GLN:HB3	4:g:602:GDP:O2B	2.11	0.51
2:Q:353:VAL:HG12	2:Q:354:GLY:N	2.26	0.51
2:U:171:ILE:HD12	6:U:502:GTP:N3	2.25	0.51
2:U:224:TYR:CE1	6:U:502:GTP:C5	2.99	0.51
2:V:353:VAL:HG12	2:V:354:GLY:N	2.25	0.51
2:B:262:TYR:CB	2:B:263:PRO:HD2	2.25	0.51
2:J:306:ASP:C	2:J:308:ARG:H	2.17	0.51
1:p:12:CYS:O	1:p:16:ILE:HG13	2.10	0.51
1:s:87:PRO:HG3	1:t:281:TYR:HE2	1.65	0.51
1:x:12:CYS:O	1:x:16:ILE:HG13	2.10	0.51
1:f:220:PRO:HD2	2:F:326:LYS:CG	2.25	0.51
1:g:131:GLN:HE22	1:g:249:ASP:HB3	1.75	0.51
1:j:358:PRO:CB	3:j:601:TA1:C28	2.89	0.51
3:k:601:TA1:H463	3:k:601:TA1:C26	2.41	0.51
2:W:306:ASP:C	2:W:308:ARG:H	2.17	0.51
1:n:12:CYS:O	1:n:16:ILE:HG13	2.10	0.51
1:q:87:PRO:CG	1:r:281:TYR:CE2	2.74	0.51
1:a:218:THR:O	2:A:326:LYS:HE2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:12:CYS:O	1:i:16:ILE:HG13	2.11	0.51
1:i:131:GLN:HE22	1:i:249:ASP:HB3	1.76	0.51
1:j:358:PRO:CB	3:j:601:TA1:H281	2.39	0.51
2:O:297:GLU:HG3	2:O:299:ALA:H	1.75	0.51
2:Q:297:GLU:O	2:Q:301:GLN:NE2	2.40	0.51
2:S:75:ILE:HD12	2:S:94:THR:HG22	1.93	0.51
2:X:297:GLU:HG3	2:X:299:ALA:H	1.75	0.51
2:D:297:GLU:O	2:D:301:GLN:NE2	2.40	0.51
2:F:297:GLU:O	2:F:301:GLN:NE2	2.40	0.51
2:K:297:GLU:HG3	2:K:299:ALA:H	1.75	0.51
1:q:12:CYS:O	1:q:16:ILE:HG13	2.11	0.51
1:z:12:CYS:O	1:z:16:ILE:HG13	2.10	0.51
1:a:212:PHE:CZ	2:A:326:LYS:HD3	2.44	0.51
3:f:601:TA1:H463	3:f:601:TA1:C26	2.41	0.51
1:i:263:LEU:HD11	1:i:425:TYR:HD2	1.75	0.51
1:j:55:THR:OG1	1:k:283:ALA:CA	2.38	0.51
2:R:353:VAL:HG12	2:R:354:GLY:N	2.25	0.51
2:A:353:VAL:HG12	2:A:354:GLY:N	2.26	0.51
1:r:12:CYS:O	1:r:16:ILE:HG13	2.11	0.51
1:r:131:GLN:HE22	1:r:249:ASP:HB3	1.76	0.51
1:u:12:CYS:O	1:u:16:ILE:HG13	2.10	0.51
1:a:10:GLY:HA3	4:a:602:GDP:HO3'	1.72	0.51
1:d:12:CYS:CB	4:d:602:GDP:C5	2.94	0.51
1:d:263:LEU:HD11	1:d:425:TYR:HD2	1.75	0.51
1:g:141:GLY:CA	4:g:602:GDP:O5'	2.58	0.51
2:P:224:TYR:OH	6:P:502:GTP:C8	2.64	0.51
2:R:75:ILE:HD12	2:R:94:THR:HG22	1.92	0.51
2:S:297:GLU:O	2:S:301:GLN:NE2	2.40	0.51
2:X:171:ILE:HD13	6:X:502:GTP:HN22	1.72	0.51
2:B:353:VAL:HG12	2:B:354:GLY:N	2.26	0.51
2:F:339:ARG:O	2:F:342:GLN:NE2	2.42	0.51
2:G:88:HIS:NE2	2:H:283:HIS:O	2.42	0.51
2:H:297:GLU:O	2:H:301:GLN:NE2	2.40	0.51
1:n:263:LEU:HD11	1:n:425:TYR:HD2	1.76	0.51
1:q:322:SER:O	1:q:326:VAL:HG23	2.10	0.51
1:s:263:LEU:HD11	1:s:425:TYR:HD2	1.75	0.51
1:b:218:THR:O	2:B:326:LYS:HE2	2.10	0.51
1:b:360:GLY:HA3	3:b:601:TA1:H443	1.92	0.51
2:Q:297:GLU:HG3	2:Q:299:ALA:H	1.75	0.51
2:U:75:ILE:HD12	2:U:94:THR:HG22	1.93	0.51
2:U:326:LYS:HE2	1:u:218:THR:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W:353:VAL:HG12	2:W:354:GLY:N	2.24	0.51
2:B:75:ILE:HD12	2:B:94:THR:HG22	1.93	0.51
2:F:306:ASP:C	2:F:308:ARG:H	2.17	0.51
2:G:306:ASP:C	2:G:308:ARG:H	2.17	0.51
1:t:263:LEU:HD11	1:t:425:TYR:HD2	1.75	0.51
1:c:23:VAL:HG13	3:c:601:TA1:H421	1.92	0.51
1:c:131:GLN:HE22	1:c:249:ASP:HB3	1.76	0.51
1:e:263:LEU:HD11	1:e:425:TYR:HD2	1.76	0.51
2:P:88:HIS:HD2	2:Q:283:HIS:HB3	1.75	0.51
2:Q:171:ILE:CD1	6:Q:502:GTP:HN22	2.23	0.51
2:R:11:GLN:HB3	6:R:502:GTP:O2A	2.11	0.51
2:T:75:ILE:HD12	2:T:94:THR:HG22	1.93	0.51
2:T:306:ASP:C	2:T:308:ARG:H	2.17	0.51
2:T:353:VAL:HG12	2:T:354:GLY:N	2.25	0.51
2:U:297:GLU:O	2:U:301:GLN:NE2	2.40	0.51
2:U:306:ASP:C	2:U:308:ARG:H	2.17	0.51
2:Y:171:ILE:HD13	6:Y:502:GTP:N3	2.26	0.51
2:L:353:VAL:HG12	2:L:354:GLY:N	2.26	0.51
1:z:263:LEU:HD11	1:z:425:TYR:HD2	1.76	0.51
1:b:144:GLY:HA3	4:b:602:GDP:H3'	1.93	0.51
1:c:12:CYS:SG	4:c:602:GDP:C5	3.04	0.51
1:f:131:GLN:HE22	1:f:249:ASP:HB3	1.76	0.51
1:h:12:CYS:O	1:h:16:ILE:HG13	2.11	0.51
1:h:131:GLN:HE22	1:h:249:ASP:HB3	1.76	0.51
1:h:222:TYR:CD2	4:h:602:GDP:C6	2.99	0.51
1:m:15:GLN:HG3	4:m:602:GDP:C6	2.46	0.51
1:m:141:GLY:CA	4:m:602:GDP:H4'	2.40	0.51
2:N:171:ILE:CD1	6:N:502:GTP:N2	2.70	0.51
2:Q:171:ILE:HD11	6:Q:502:GTP:HN22	1.75	0.51
2:S:306:ASP:C	2:S:308:ARG:H	2.17	0.51
2:T:88:HIS:CD2	2:U:283:HIS:HB2	2.46	0.51
2:A:297:GLU:HG3	2:A:299:ALA:H	1.75	0.51
2:E:306:ASP:C	2:E:308:ARG:H	2.17	0.51
2:I:200:CYS:HG	2:I:202:PHE:HE1	1.59	0.51
1:o:12:CYS:O	1:o:16:ILE:HG13	2.11	0.51
1:s:12:CYS:O	1:s:16:ILE:HG13	2.11	0.51
1:j:222:TYR:CD1	4:j:602:GDP:N1	2.79	0.50
2:R:306:ASP:C	2:R:308:ARG:H	2.17	0.50
2:W:241:SER:OG	2:W:250:VAL:O	2.30	0.50
2:A:283:HIS:ND1	2:M:89:PRO:HD2	2.26	0.50
2:D:205:ASP:O	2:D:209:ILE:HG13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:297:GLU:HG3	2:D:299:ALA:H	1.75	0.50
2:G:297:GLU:HG3	2:G:299:ALA:H	1.75	0.50
1:p:86:ARG:HG2	1:p:88:ASP:H	1.76	0.50
1:p:86:ARG:CD	1:q:281:TYR:HB3	2.40	0.50
1:q:86:ARG:HG3	1:r:281:TYR:HB3	1.92	0.50
1:a:12:CYS:O	1:a:16:ILE:HG13	2.11	0.50
1:e:12:CYS:HB2	4:e:602:GDP:N9	2.25	0.50
1:f:231:ALA:HB1	3:f:601:TA1:C39	2.40	0.50
1:h:215:LEU:HD22	3:h:601:TA1:C14	2.40	0.50
1:k:141:GLY:HA3	4:k:602:GDP:O5'	2.11	0.50
1:m:12:CYS:O	1:m:16:ILE:HG13	2.11	0.50
2:N:297:GLU:HG3	2:N:299:ALA:H	1.75	0.50
2:P:353:VAL:HG12	2:P:354:GLY:N	2.26	0.50
2:Q:262:TYR:CB	2:Q:263:PRO:HD2	2.25	0.50
2:A:75:ILE:HD12	2:A:94:THR:HG22	1.93	0.50
2:C:353:VAL:HG12	2:C:354:GLY:N	2.26	0.50
2:G:241:SER:OG	2:G:250:VAL:O	2.29	0.50
2:H:306:ASP:C	2:H:308:ARG:H	2.17	0.50
2:I:353:VAL:HG12	2:I:354:GLY:N	2.26	0.50
2:K:353:VAL:HG12	2:K:354:GLY:N	2.26	0.50
1:c:86:ARG:HG2	1:c:88:ASP:H	1.77	0.50
1:j:12:CYS:O	1:j:16:ILE:HG13	2.12	0.50
1:l:263:LEU:HD11	1:l:425:TYR:HD2	1.75	0.50
2:Q:75:ILE:HD12	2:Q:94:THR:HG22	1.94	0.50
2:T:297:GLU:HG3	2:T:299:ALA:H	1.75	0.50
2:Z:171:ILE:HD13	6:Z:502:GTP:HN22	1.76	0.50
2:D:75:ILE:HD12	2:D:94:THR:HG22	1.94	0.50
2:H:75:ILE:HD12	2:H:94:THR:HG22	1.93	0.50
2:J:241:SER:OG	2:J:250:VAL:O	2.30	0.50
2:M:353:VAL:HG12	2:M:354:GLY:N	2.26	0.50
1:t:12:CYS:O	1:t:16:ILE:HG13	2.10	0.50
1:b:12:CYS:CA	4:b:602:GDP:C1'	2.86	0.50
1:b:131:GLN:HE22	1:b:249:ASP:HB3	1.76	0.50
1:c:286:VAL:HG23	1:c:363:MET:HE3	1.93	0.50
1:d:12:CYS:HB2	4:d:602:GDP:C8	2.47	0.50
1:i:222:TYR:CD1	4:i:602:GDP:N1	2.79	0.50
2:S:353:VAL:HG12	2:S:354:GLY:N	2.26	0.50
2:U:241:SER:OG	2:U:250:VAL:O	2.30	0.50
2:H:241:SER:OG	2:H:250:VAL:O	2.30	0.50
1:o:263:LEU:HD11	1:o:425:TYR:HD2	1.76	0.50
1:t:86:ARG:HG2	1:t:88:ASP:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:w:86:ARG:HG2	1:w:88:ASP:H	1.76	0.50
1:x:263:LEU:HD11	1:x:425:TYR:HD2	1.75	0.50
1:b:12:CYS:O	1:b:16:ILE:HG13	2.11	0.50
1:d:87:PRO:HD3	1:e:281:TYR:CD2	2.46	0.50
1:g:11:GLN:CB	4:g:602:GDP:O2B	2.60	0.50
1:g:12:CYS:O	1:g:16:ILE:HG13	2.11	0.50
1:g:358:PRO:HB2	3:g:601:TA1:H281	1.93	0.50
2:D:262:TYR:CB	2:D:263:PRO:HD2	2.25	0.50
2:E:241:SER:OG	2:E:250:VAL:O	2.30	0.50
2:H:353:VAL:HG12	2:H:354:GLY:N	2.26	0.50
2:L:297:GLU:O	2:L:301:GLN:NE2	2.40	0.50
2:M:241:SER:OG	2:M:250:VAL:O	2.30	0.50
1:p:86:ARG:CG	1:q:281:TYR:HB3	2.42	0.50
1:v:86:ARG:HG2	1:v:88:ASP:H	1.76	0.50
1:v:131:GLN:HE22	1:v:249:ASP:HB3	1.76	0.50
1:z:86:ARG:HG2	1:z:88:ASP:H	1.77	0.50
1:a:99:ASN:OD1	4:a:602:GDP:C8	2.64	0.50
2:T:241:SER:OG	2:T:250:VAL:O	2.30	0.50
2:U:224:TYR:CZ	6:U:502:GTP:C8	2.99	0.50
2:Z:241:SER:OG	2:Z:250:VAL:O	2.30	0.50
2:C:286:LEU:HB3	2:C:291:ILE:HD11	1.93	0.50
2:F:194:THR:O	2:F:198:SER:OG	2.30	0.50
2:L:241:SER:OG	2:L:250:VAL:O	2.30	0.50
1:c:12:CYS:O	1:c:16:ILE:HG13	2.12	0.50
1:c:263:LEU:HD11	1:c:425:TYR:HD2	1.76	0.50
1:m:23:VAL:CG1	3:m:601:TA1:C41	2.89	0.50
2:G:75:ILE:HD12	2:G:94:THR:HG22	1.94	0.50
1:q:86:ARG:HG2	1:q:88:ASP:H	1.77	0.50
1:y:263:LEU:HD11	1:y:425:TYR:HD2	1.76	0.50
1:e:131:GLN:HE22	1:e:249:ASP:HB3	1.77	0.50
1:j:131:GLN:HE22	1:j:249:ASP:HB3	1.76	0.50
1:m:193:VAL:HG13	1:m:262:ARG:HG3	1.94	0.50
2:P:75:ILE:HD12	2:P:94:THR:HG22	1.94	0.50
2:R:171:ILE:HD11	6:R:502:GTP:N2	2.27	0.50
2:Y:297:GLU:O	2:Y:301:GLN:NE2	2.40	0.50
1:a:131:GLN:HE22	1:a:249:ASP:HB3	1.76	0.50
1:a:390:ARG:NH2	2:A:439:SER:O	2.44	0.50
1:f:179:VAL:N	2:F:258:ASN:ND2	2.48	0.50
2:R:241:SER:OG	2:R:250:VAL:O	2.30	0.50
2:X:241:SER:OG	2:X:250:VAL:O	2.30	0.50
2:D:286:LEU:HB3	2:D:291:ILE:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:353:VAL:HG12	2:F:354:GLY:N	2.26	0.50
1:e:12:CYS:O	1:e:16:ILE:HG13	2.12	0.49
1:f:12:CYS:O	1:f:16:ILE:HG13	2.11	0.49
1:f:23:VAL:HG13	3:f:601:TA1:C42	2.42	0.49
1:h:256:ASN:HA	2:U:404:PHE:HE1	1.75	0.49
1:m:131:GLN:HE22	1:m:249:ASP:HB3	1.76	0.49
2:V:171:ILE:CD1	6:V:502:GTP:N2	2.75	0.49
2:W:75:ILE:HD12	2:W:94:THR:HG22	1.94	0.49
2:Y:88:HIS:CD2	2:Z:283:HIS:HB2	2.46	0.49
2:C:75:ILE:HD12	2:C:94:THR:HG22	1.94	0.49
2:J:75:ILE:HD12	2:J:94:THR:HG22	1.94	0.49
2:K:241:SER:OG	2:K:250:VAL:O	2.30	0.49
1:y:131:GLN:HE22	1:y:249:ASP:HB3	1.76	0.49
2:O:75:ILE:HD12	2:O:94:THR:HG22	1.94	0.49
2:O:241:SER:OG	2:O:250:VAL:O	2.30	0.49
2:B:241:SER:OG	2:B:250:VAL:O	2.30	0.49
2:F:89:PRO:HD3	2:G:283:HIS:NE2	2.21	0.49
2:I:241:SER:OG	2:I:250:VAL:O	2.30	0.49
1:y:12:CYS:O	1:y:16:ILE:HG13	2.11	0.49
1:e:86:ARG:HG2	1:e:88:ASP:H	1.77	0.49
1:l:193:VAL:HG13	1:l:262:ARG:HG3	1.94	0.49
3:m:601:TA1:H463	3:m:601:TA1:C26	2.41	0.49
2:C:26:LEU:HD13	2:C:364:PRO:HD3	1.94	0.49
2:D:26:LEU:HD13	2:D:364:PRO:HD3	1.95	0.49
2:G:353:VAL:HG12	2:G:354:GLY:N	2.26	0.49
1:r:263:LEU:HD11	1:r:425:TYR:HD2	1.78	0.49
1:u:86:ARG:HG2	1:u:88:ASP:H	1.77	0.49
1:x:86:ARG:HG2	1:x:88:ASP:H	1.77	0.49
1:a:208:TYR:CE1	2:A:326:LYS:HB3	2.47	0.49
1:d:12:CYS:O	1:d:16:ILE:HG13	2.12	0.49
1:h:143:THR:HB	4:h:602:GDP:O1B	2.13	0.49
1:j:222:TYR:CD1	4:j:602:GDP:C6	3.00	0.49
2:O:297:GLU:O	2:O:301:GLN:NE2	2.40	0.49
2:S:258:ASN:ND2	1:s:179:VAL:N	2.48	0.49
2:F:75:ILE:HD12	2:F:94:THR:HG22	1.95	0.49
2:F:241:SER:OG	2:F:250:VAL:O	2.29	0.49
2:I:297:GLU:O	2:I:301:GLN:NE2	2.40	0.49
1:b:193:VAL:HG13	1:b:262:ARG:HG3	1.94	0.49
3:e:601:TA1:H463	3:e:601:TA1:C26	2.42	0.49
1:j:88:ASP:OD2	1:k:282:ARG:NH2	2.45	0.49
2:O:12:ALA:HB2	6:O:502:GTP:N9	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:200:CYS:HG	2:Q:202:PHE:HE1	1.59	0.49
2:X:75:ILE:HD12	2:X:94:THR:HG22	1.93	0.49
2:B:297:GLU:O	2:B:301:GLN:NE2	2.40	0.49
2:J:353:VAL:HG12	2:J:354:GLY:N	2.26	0.49
2:L:75:ILE:HD12	2:L:94:THR:HG22	1.93	0.49
1:n:131:GLN:HE22	1:n:249:ASP:HB3	1.76	0.49
1:b:86:ARG:HG2	1:b:88:ASP:H	1.77	0.49
1:d:131:GLN:HE22	1:d:249:ASP:HB3	1.77	0.49
1:d:358:PRO:HB2	3:d:601:TA1:H281	1.93	0.49
1:g:86:ARG:HG2	1:g:88:ASP:H	1.78	0.49
1:h:358:PRO:CB	3:h:601:TA1:H281	2.41	0.49
2:N:75:ILE:HD12	2:N:94:THR:HG22	1.94	0.49
2:N:255:PHE:O	2:N:259:LEU:N	2.46	0.49
2:O:224:TYR:CE1	6:O:502:GTP:C5	3.01	0.49
2:V:224:TYR:OH	6:V:502:GTP:C8	2.65	0.49
2:X:255:PHE:O	2:X:259:LEU:N	2.46	0.49
2:Y:255:PHE:O	2:Y:259:LEU:N	2.46	0.49
2:E:75:ILE:HD12	2:E:94:THR:HG22	1.95	0.49
2:I:75:ILE:HD12	2:I:94:THR:HG22	1.94	0.49
1:z:131:GLN:HE22	1:z:249:ASP:HB3	1.77	0.49
3:a:601:TA1:H463	3:a:601:TA1:C26	2.43	0.49
1:e:169:VAL:HG21	4:e:602:GDP:HN22	1.78	0.49
1:f:347:ASN:O	2:S:181:VAL:HG21	2.04	0.49
1:k:12:CYS:O	1:k:16:ILE:HG13	2.12	0.49
1:k:131:GLN:HE22	1:k:249:ASP:HB3	1.77	0.49
2:N:171:ILE:HD13	6:N:502:GTP:N3	2.27	0.49
2:P:224:TYR:CD2	6:P:502:GTP:C6	3.01	0.49
2:V:75:ILE:HD12	2:V:94:THR:HG22	1.95	0.49
2:Y:75:ILE:HD12	2:Y:94:THR:HG22	1.94	0.49
2:Z:75:ILE:HD12	2:Z:94:THR:HG22	1.93	0.49
2:Z:194:THR:O	2:Z:198:SER:OG	2.30	0.49
2:A:255:PHE:O	2:A:259:LEU:N	2.46	0.49
2:C:241:SER:OG	2:C:250:VAL:O	2.30	0.49
2:M:194:THR:O	2:M:198:SER:OG	2.30	0.49
1:o:86:ARG:HG2	1:o:88:ASP:H	1.77	0.49
1:k:347:ASN:O	2:X:181:VAL:HG21	2.04	0.49
1:l:215:LEU:CD2	3:l:601:TA1:C14	2.90	0.49
2:S:241:SER:OG	2:S:250:VAL:O	2.30	0.49
2:V:297:GLU:O	2:V:301:GLN:NE2	2.40	0.49
2:K:75:ILE:HD12	2:K:94:THR:HG22	1.94	0.49
2:L:128:GLN:CD	2:M:285:GLN:HG3	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:87:PRO:CG	1:o:281:TYR:HE2	2.26	0.49
1:c:220:PRO:HD2	2:C:326:LYS:CG	2.24	0.49
1:i:86:ARG:HG2	1:i:88:ASP:H	1.77	0.49
1:m:67:ASP:HB2	1:m:73:MET:CE	2.43	0.49
2:R:331:ALA:O	2:R:335:ILE:HG12	2.13	0.49
2:T:154:MET:HE1	2:T:166:LYS:HB3	1.94	0.49
2:W:331:ALA:O	2:W:335:ILE:HG12	2.13	0.49
2:Y:331:ALA:O	2:Y:335:ILE:HG12	2.13	0.49
2:D:200:CYS:HG	2:D:202:PHE:HE1	1.60	0.49
2:E:331:ALA:O	2:E:335:ILE:HG12	2.13	0.49
2:F:128:GLN:CD	2:G:285:GLN:HG3	2.37	0.49
2:L:255:PHE:O	2:L:259:LEU:N	2.46	0.49
1:n:86:ARG:HG2	1:n:88:ASP:H	1.77	0.49
1:t:131:GLN:HE22	1:t:249:ASP:HB3	1.78	0.49
1:y:86:ARG:HG2	1:y:88:ASP:H	1.77	0.49
1:a:86:ARG:HG2	1:a:88:ASP:H	1.77	0.49
1:g:67:ASP:HB2	1:g:73:MET:CE	2.43	0.49
1:g:141:GLY:HA3	4:g:602:GDP:O5'	2.12	0.49
1:h:12:CYS:CB	4:h:602:GDP:C5	2.95	0.49
1:l:12:CYS:O	1:l:16:ILE:HG13	2.12	0.49
1:m:86:ARG:HG2	1:m:88:ASP:H	1.78	0.49
2:N:331:ALA:O	2:N:335:ILE:HG12	2.13	0.49
2:O:26:LEU:HD13	2:O:364:PRO:HD3	1.95	0.49
2:O:286:LEU:HB3	2:O:291:ILE:HD11	1.94	0.49
2:P:241:SER:OG	2:P:250:VAL:O	2.30	0.49
2:Q:331:ALA:O	2:Q:335:ILE:HG12	2.13	0.49
2:V:255:PHE:O	2:V:259:LEU:N	2.46	0.49
2:W:326:LYS:NZ	1:w:218:THR:O	2.43	0.49
2:E:194:THR:O	2:E:198:SER:OG	2.30	0.49
2:F:26:LEU:HD13	2:F:364:PRO:HD3	1.95	0.49
2:K:255:PHE:O	2:K:259:LEU:N	2.46	0.49
1:z:193:VAL:HG13	1:z:262:ARG:HG3	1.94	0.49
1:e:193:VAL:HG13	1:e:262:ARG:HG3	1.94	0.48
1:g:67:ASP:HB2	1:g:73:MET:HE2	1.93	0.48
1:g:164:MET:HE3	1:g:164:MET:HB2	1.72	0.48
1:h:86:ARG:HG2	1:h:88:ASP:H	1.78	0.48
1:i:222:TYR:CG	4:i:602:GDP:O6	2.65	0.48
1:j:67:ASP:HB2	1:j:73:MET:CE	2.43	0.48
1:l:131:GLN:HE22	1:l:249:ASP:HB3	1.77	0.48
2:Q:26:LEU:HD13	2:Q:364:PRO:HD3	1.95	0.48
2:R:194:THR:O	2:R:198:SER:OG	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:154:MET:HE1	2:S:166:LYS:HB3	1.95	0.48
2:T:171:ILE:HD12	6:T:502:GTP:N3	2.28	0.48
2:T:224:TYR:HD2	6:T:502:GTP:C2	2.11	0.48
2:V:286:LEU:HB3	2:V:291:ILE:HD11	1.95	0.48
2:Z:26:LEU:HD13	2:Z:364:PRO:HD3	1.95	0.48
1:q:131:GLN:HE22	1:q:249:ASP:HB3	1.78	0.48
1:s:86:ARG:HG2	1:s:88:ASP:H	1.78	0.48
1:u:67:ASP:HB2	1:u:73:MET:CE	2.43	0.48
1:a:193:VAL:HG13	1:a:262:ARG:HG3	1.95	0.48
1:f:358:PRO:CB	3:f:601:TA1:H281	2.43	0.48
1:i:67:ASP:HB2	1:i:73:MET:CE	2.43	0.48
2:O:194:THR:O	2:O:198:SER:OG	2.30	0.48
2:U:26:LEU:HD13	2:U:364:PRO:HD3	1.94	0.48
2:Y:262:TYR:CB	2:Y:263:PRO:HD2	2.25	0.48
2:Y:286:LEU:HB3	2:Y:291:ILE:HD11	1.95	0.48
2:Z:255:PHE:O	2:Z:259:LEU:N	2.46	0.48
2:Z:262:TYR:CB	2:Z:263:PRO:HD2	2.25	0.48
2:Z:353:VAL:CG1	2:Z:354:GLY:N	2.76	0.48
2:A:88:HIS:N	2:B:283:HIS:CD2	2.80	0.48
2:A:331:ALA:O	2:A:335:ILE:HG12	2.14	0.48
2:K:286:LEU:HB3	2:K:291:ILE:HD11	1.95	0.48
1:v:67:ASP:HB2	1:v:73:MET:CE	2.43	0.48
1:w:67:ASP:HB2	1:w:73:MET:CE	2.43	0.48
1:z:67:ASP:HB2	1:z:73:MET:CE	2.43	0.48
1:a:216:LYS:HB2	1:a:275:SER:HB3	1.95	0.48
1:f:86:ARG:HG2	1:f:88:ASP:H	1.78	0.48
3:h:601:TA1:H472	3:h:601:TA1:C20	2.43	0.48
1:i:222:TYR:CD2	4:i:602:GDP:C6	3.01	0.48
1:j:86:ARG:HG2	1:j:88:ASP:H	1.78	0.48
1:k:216:LYS:HB2	1:k:275:SER:HB3	1.95	0.48
1:l:216:LYS:HB2	1:l:275:SER:HB3	1.95	0.48
2:S:140:SER:OG	6:S:502:GTP:C4'	2.61	0.48
2:U:286:LEU:HB3	2:U:291:ILE:HD11	1.95	0.48
2:V:331:ALA:O	2:V:335:ILE:HG12	2.13	0.48
2:X:262:TYR:CB	2:X:263:PRO:HD2	2.25	0.48
2:I:255:PHE:O	2:I:259:LEU:N	2.46	0.48
1:o:131:GLN:HE22	1:o:249:ASP:HB3	1.77	0.48
1:p:193:VAL:HG13	1:p:262:ARG:HG3	1.94	0.48
1:s:131:GLN:HE22	1:s:249:ASP:HB3	1.78	0.48
1:t:67:ASP:HB2	1:t:73:MET:CE	2.43	0.48
1:c:231:ALA:CB	3:c:601:TA1:C39	2.89	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:67:ASP:HB2	1:f:73:MET:HE2	1.94	0.48
1:m:216:LYS:HB2	1:m:275:SER:HB3	1.96	0.48
2:N:88:HIS:HD2	2:O:283:HIS:HB3	1.76	0.48
2:S:331:ALA:O	2:S:335:ILE:HG12	2.13	0.48
2:T:224:TYR:CD2	6:T:502:GTP:C5	2.85	0.48
2:T:255:PHE:O	2:T:259:LEU:N	2.46	0.48
2:W:286:LEU:HB3	2:W:291:ILE:HD11	1.95	0.48
2:A:241:SER:OG	2:A:250:VAL:O	2.30	0.48
2:J:286:LEU:HB3	2:J:291:ILE:HD11	1.95	0.48
2:L:331:ALA:O	2:L:335:ILE:HG12	2.14	0.48
1:t:193:VAL:HG13	1:t:262:ARG:HG3	1.94	0.48
1:x:67:ASP:HB2	1:x:73:MET:CE	2.43	0.48
1:y:216:LYS:HB2	1:y:275:SER:HB3	1.96	0.48
1:a:67:ASP:HB2	1:a:73:MET:CE	2.43	0.48
1:b:67:ASP:HB2	1:b:73:MET:CE	2.43	0.48
1:k:67:ASP:HB2	1:k:73:MET:CE	2.43	0.48
1:k:222:TYR:CD1	4:k:602:GDP:C6	3.01	0.48
2:N:241:SER:OG	2:N:250:VAL:O	2.30	0.48
2:R:255:PHE:O	2:R:259:LEU:N	2.46	0.48
2:J:331:ALA:O	2:J:335:ILE:HG12	2.14	0.48
1:r:193:VAL:HG13	1:r:262:ARG:HG3	1.94	0.48
1:u:193:VAL:HG13	1:u:262:ARG:HG3	1.95	0.48
1:f:87:PRO:HD3	1:g:281:TYR:CD2	2.48	0.48
1:g:359:ARG:N	3:g:601:TA1:O13	2.44	0.48
1:j:216:LYS:HB2	1:j:275:SER:HB3	1.95	0.48
1:l:67:ASP:HB2	1:l:73:MET:CE	2.43	0.48
2:O:331:ALA:O	2:O:335:ILE:HG12	2.14	0.48
2:S:224:TYR:CD1	6:S:502:GTP:C6	3.01	0.48
2:U:331:ALA:O	2:U:335:ILE:HG12	2.14	0.48
2:Y:353:VAL:CG1	2:Y:354:GLY:N	2.76	0.48
2:Z:286:LEU:HB3	2:Z:291:ILE:HD11	1.94	0.48
2:E:205:ASP:O	2:E:209:ILE:HG13	2.13	0.48
2:F:331:ALA:O	2:F:335:ILE:HG12	2.14	0.48
2:H:286:LEU:HB3	2:H:291:ILE:HD11	1.95	0.48
2:I:286:LEU:HB3	2:I:291:ILE:HD11	1.96	0.48
2:J:88:HIS:CA	2:K:283:HIS:CD2	2.87	0.48
2:L:242:LEU:HD11	2:L:252:LEU:HG	1.96	0.48
2:M:26:LEU:HD13	2:M:364:PRO:HD3	1.96	0.48
1:x:193:VAL:HG13	1:x:262:ARG:HG3	1.94	0.48
1:y:67:ASP:HB2	1:y:73:MET:CE	2.43	0.48
1:e:67:ASP:HB2	1:e:73:MET:CE	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:164:MET:HE3	1:f:164:MET:HB2	1.72	0.48
1:h:12:CYS:SG	4:h:602:GDP:C5	3.06	0.48
2:O:224:TYR:HE2	6:O:502:GTP:N3	1.98	0.48
2:V:241:SER:OG	2:V:250:VAL:O	2.30	0.48
2:W:224:TYR:CE1	6:W:502:GTP:C5	3.02	0.48
2:X:331:ALA:O	2:X:335:ILE:HG12	2.13	0.48
2:Z:171:ILE:HD13	6:Z:502:GTP:C2	2.43	0.48
2:B:194:THR:O	2:B:198:SER:OG	2.30	0.48
2:B:331:ALA:O	2:B:335:ILE:HG12	2.14	0.48
2:C:255:PHE:O	2:C:259:LEU:N	2.46	0.48
1:s:193:VAL:HG13	1:s:262:ARG:HG3	1.94	0.48
1:v:193:VAL:HG13	1:v:262:ARG:HG3	1.95	0.48
1:y:193:VAL:HG13	1:y:262:ARG:HG3	1.95	0.48
1:e:329:GLN:O	1:e:333:VAL:HG23	2.14	0.48
1:f:67:ASP:HB2	1:f:73:MET:CE	2.43	0.48
1:f:169:VAL:HG21	4:f:602:GDP:N2	2.29	0.48
1:l:12:CYS:HB2	4:l:602:GDP:C4	2.49	0.48
2:O:171:ILE:HD11	6:O:502:GTP:N2	2.18	0.48
2:P:255:PHE:O	2:P:259:LEU:N	2.46	0.48
1:o:67:ASP:HB2	1:o:73:MET:CE	2.44	0.48
1:s:67:ASP:HB2	1:s:73:MET:CE	2.43	0.48
1:b:102:ALA:HB1	1:b:401:GLU:HB2	1.96	0.48
1:b:256:ASN:HA	2:O:404:PHE:HE1	1.77	0.48
1:d:86:ARG:HG2	1:d:88:ASP:H	1.78	0.48
2:O:353:VAL:CG1	2:O:354:GLY:N	2.77	0.48
2:Q:255:PHE:O	2:Q:259:LEU:N	2.46	0.48
2:S:255:PHE:O	2:S:259:LEU:N	2.46	0.48
2:W:353:VAL:CG1	2:W:354:GLY:N	2.77	0.48
2:D:331:ALA:O	2:D:335:ILE:HG12	2.14	0.48
2:E:255:PHE:O	2:E:259:LEU:N	2.46	0.48
2:G:128:GLN:CD	2:H:285:GLN:HG3	2.36	0.48
2:I:26:LEU:HD13	2:I:364:PRO:HD3	1.94	0.48
2:I:331:ALA:O	2:I:335:ILE:HG12	2.14	0.48
2:L:26:LEU:HD13	2:L:364:PRO:HD3	1.96	0.48
2:M:255:PHE:O	2:M:259:LEU:N	2.46	0.48
1:n:67:ASP:HB2	1:n:73:MET:CE	2.44	0.48
1:n:216:LYS:HB2	1:n:275:SER:HB3	1.96	0.48
1:p:67:ASP:HB2	1:p:73:MET:CE	2.44	0.48
1:a:102:ALA:HB1	1:a:401:GLU:HB2	1.96	0.48
1:c:67:ASP:HB2	1:c:73:MET:CE	2.44	0.48
1:g:193:VAL:HG13	1:g:262:ARG:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:193:VAL:HG13	1:k:262:ARG:HG3	1.95	0.48
2:N:26:LEU:HD13	2:N:364:PRO:HD3	1.96	0.48
2:P:26:LEU:HD13	2:P:364:PRO:HD3	1.96	0.48
2:R:286:LEU:HB3	2:R:291:ILE:HD11	1.95	0.48
2:T:286:LEU:HB3	2:T:291:ILE:HD11	1.95	0.48
2:V:224:TYR:CD1	6:V:502:GTP:C6	3.02	0.48
2:W:154:MET:HE1	2:W:166:LYS:HB3	1.95	0.48
2:X:286:LEU:HB3	2:X:291:ILE:HD11	1.96	0.48
2:Y:26:LEU:HD13	2:Y:364:PRO:HD3	1.95	0.48
2:Z:331:ALA:O	2:Z:335:ILE:HG12	2.13	0.48
2:D:353:VAL:CG1	2:D:354:GLY:N	2.77	0.48
2:G:255:PHE:O	2:G:259:LEU:N	2.46	0.48
2:L:286:LEU:HB3	2:L:291:ILE:HD11	1.95	0.48
2:L:353:VAL:CG1	2:L:354:GLY:N	2.77	0.48
2:M:242:LEU:HD11	2:M:252:LEU:HG	1.96	0.48
1:o:102:ALA:HB1	1:o:401:GLU:HB2	1.96	0.48
1:r:67:ASP:HB2	1:r:73:MET:CE	2.43	0.48
1:x:216:LYS:HB2	1:x:275:SER:HB3	1.96	0.48
1:b:358:PRO:CB	3:b:601:TA1:H281	2.41	0.47
1:c:102:ALA:HB1	1:c:401:GLU:HB2	1.96	0.47
1:d:23:VAL:HG13	3:d:601:TA1:H421	1.95	0.47
1:f:193:VAL:HG13	1:f:262:ARG:HG3	1.95	0.47
1:h:193:VAL:HG13	1:h:262:ARG:HG3	1.95	0.47
2:Q:286:LEU:HB3	2:Q:291:ILE:HD11	1.95	0.47
2:Q:353:VAL:CG1	2:Q:354:GLY:N	2.77	0.47
2:T:331:ALA:O	2:T:335:ILE:HG12	2.13	0.47
2:V:26:LEU:HD13	2:V:364:PRO:HD3	1.95	0.47
2:W:326:LYS:HE2	1:w:218:THR:O	2.14	0.47
2:B:353:VAL:CG1	2:B:354:GLY:N	2.77	0.47
2:C:154:MET:HE1	2:C:166:LYS:HB3	1.96	0.47
2:E:26:LEU:HD13	2:E:364:PRO:HD3	1.96	0.47
2:F:286:LEU:HB3	2:F:291:ILE:HD11	1.95	0.47
2:G:26:LEU:HD13	2:G:364:PRO:HD3	1.94	0.47
2:G:297:GLU:O	2:G:301:GLN:NE2	2.40	0.47
2:J:353:VAL:CG1	2:J:354:GLY:N	2.77	0.47
2:L:238:ILE:HG23	2:L:255:PHE:CE2	2.50	0.47
2:M:244:PHE:HB2	2:M:356:ASN:HD21	1.80	0.47
1:p:102:ALA:HB1	1:p:401:GLU:HB2	1.96	0.47
1:w:193:VAL:HG13	1:w:262:ARG:HG3	1.95	0.47
1:b:212:PHE:CE1	2:B:326:LYS:HD3	2.48	0.47
3:b:601:TA1:H441	3:b:601:TA1:C27	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:281:TYR:HD2	1:o:87:PRO:HD2	1.79	0.47
1:e:397:TRP:CH2	2:E:256:GLN:HB3	2.49	0.47
1:i:193:VAL:HG13	1:i:262:ARG:HG3	1.95	0.47
1:k:12:CYS:SG	4:k:602:GDP:N3	2.87	0.47
1:l:222:TYR:OH	4:l:602:GDP:C2'	2.62	0.47
2:N:286:LEU:HB3	2:N:291:ILE:HD11	1.95	0.47
2:N:353:VAL:CG1	2:N:354:GLY:N	2.77	0.47
2:T:26:LEU:HD13	2:T:364:PRO:HD3	1.95	0.47
2:W:255:PHE:O	2:W:259:LEU:N	2.46	0.47
2:X:200:CYS:HG	2:X:202:PHE:HE1	1.63	0.47
2:Y:224:TYR:CE1	6:Y:502:GTP:C5	3.01	0.47
2:A:244:PHE:HB2	2:A:356:ASN:HD21	1.79	0.47
2:C:200:CYS:HG	2:C:202:PHE:HE1	1.61	0.47
2:D:255:PHE:O	2:D:259:LEU:N	2.46	0.47
2:J:88:HIS:NE2	2:K:283:HIS:HB2	2.13	0.47
2:M:353:VAL:CG1	2:M:354:GLY:N	2.77	0.47
1:n:102:ALA:HB1	1:n:401:GLU:HB2	1.96	0.47
1:p:131:GLN:HE22	1:p:249:ASP:HB3	1.79	0.47
1:b:216:LYS:HB2	1:b:275:SER:HB3	1.96	0.47
3:c:601:TA1:C20	3:c:601:TA1:H472	2.45	0.47
1:d:227:HIS:HB3	3:d:601:TA1:HC71	1.96	0.47
1:i:216:LYS:HB2	1:i:275:SER:HB3	1.96	0.47
1:j:193:VAL:HG13	1:j:262:ARG:HG3	1.95	0.47
1:m:23:VAL:CG1	3:m:601:TA1:H411	2.44	0.47
2:S:26:LEU:HD13	2:S:364:PRO:HD3	1.95	0.47
2:T:101:ASN:N	6:T:502:GTP:O3G	2.40	0.47
2:U:255:PHE:O	2:U:259:LEU:N	2.46	0.47
2:X:154:MET:HE1	2:X:166:LYS:HB3	1.96	0.47
2:Z:244:PHE:HB2	2:Z:356:ASN:HD21	1.80	0.47
2:A:353:VAL:CG1	2:A:354:GLY:N	2.77	0.47
2:B:26:LEU:HD13	2:B:364:PRO:HD3	1.97	0.47
2:D:244:PHE:HB2	2:D:356:ASN:HD21	1.79	0.47
2:G:331:ALA:O	2:G:335:ILE:HG12	2.14	0.47
2:J:194:THR:O	2:J:198:SER:OG	2.30	0.47
2:K:242:LEU:HD11	2:K:252:LEU:HG	1.96	0.47
2:K:331:ALA:O	2:K:335:ILE:HG12	2.14	0.47
1:n:193:VAL:HG13	1:n:262:ARG:HG3	1.95	0.47
1:o:216:LYS:HB2	1:o:275:SER:HB3	1.96	0.47
1:q:164:MET:HE3	1:q:164:MET:HB2	1.73	0.47
1:q:193:VAL:HG13	1:q:262:ARG:HG3	1.94	0.47
1:b:138:SER:CA	4:b:602:GDP:H2'	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:67:ASP:OD2	1:d:72:THR:OG1	2.32	0.47
1:d:193:VAL:HG13	1:d:262:ARG:HG3	1.95	0.47
2:N:244:PHE:HB2	2:N:356:ASN:HD21	1.80	0.47
2:R:26:LEU:HD13	2:R:364:PRO:HD3	1.96	0.47
2:A:205:ASP:O	2:A:209:ILE:HG13	2.15	0.47
2:E:244:PHE:HB2	2:E:356:ASN:HD21	1.79	0.47
2:F:255:PHE:O	2:F:259:LEU:N	2.46	0.47
2:G:286:LEU:HB3	2:G:291:ILE:HD11	1.96	0.47
2:M:286:LEU:HB3	2:M:291:ILE:HD11	1.96	0.47
1:r:164:MET:HE3	1:r:164:MET:HB2	1.73	0.47
1:u:11:GLN:O	1:u:15:GLN:HG2	2.14	0.47
1:v:11:GLN:O	1:v:15:GLN:HG2	2.14	0.47
1:w:216:LYS:HB2	1:w:275:SER:HB3	1.97	0.47
1:i:23:VAL:HG13	3:i:601:TA1:C42	2.44	0.47
2:N:224:TYR:OH	6:N:502:GTP:C1'	2.62	0.47
2:P:331:ALA:O	2:P:335:ILE:HG12	2.13	0.47
2:S:286:LEU:HB3	2:S:291:ILE:HD11	1.95	0.47
2:T:297:GLU:O	2:T:301:GLN:NE2	2.40	0.47
2:W:171:ILE:CD1	6:W:502:GTP:C2	2.97	0.47
2:W:194:THR:O	2:W:198:SER:OG	2.30	0.47
2:Z:171:ILE:HD11	6:Z:502:GTP:C2	2.49	0.47
2:A:26:LEU:HD13	2:A:364:PRO:HD3	1.97	0.47
2:A:242:LEU:HD11	2:A:252:LEU:HG	1.96	0.47
2:B:205:ASP:O	2:B:209:ILE:HG13	2.15	0.47
2:C:244:PHE:HB2	2:C:356:ASN:HD21	1.79	0.47
2:D:241:SER:OG	2:D:250:VAL:O	2.30	0.47
2:H:262:TYR:CB	2:H:263:PRO:HD2	2.25	0.47
2:H:331:ALA:O	2:H:335:ILE:HG12	2.14	0.47
1:u:164:MET:HE3	1:u:164:MET:HB2	1.72	0.47
1:v:164:MET:HB2	1:v:164:MET:HE3	1.72	0.47
1:w:102:ALA:HB1	1:w:401:GLU:HB2	1.96	0.47
1:z:216:LYS:HB2	1:z:275:SER:HB3	1.97	0.47
1:h:164:MET:HE3	1:h:164:MET:HB2	1.72	0.47
1:i:164:MET:HB2	1:i:164:MET:HE3	1.72	0.47
1:l:345:ILE:CG2	2:Y:181:VAL:HG11	2.44	0.47
2:N:171:ILE:CD1	6:N:502:GTP:C2	2.98	0.47
2:V:262:TYR:CB	2:V:263:PRO:HD2	2.25	0.47
2:Y:244:PHE:HB2	2:Y:356:ASN:HD21	1.80	0.47
2:F:154:MET:HE1	2:F:166:LYS:HB3	1.96	0.47
2:G:154:MET:HE1	2:G:166:LYS:HB3	1.96	0.47
2:H:255:PHE:O	2:H:259:LEU:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:89:PRO:HD3	2:J:283:HIS:CD2	2.50	0.47
2:L:244:PHE:HB2	2:L:356:ASN:HD21	1.80	0.47
1:q:67:ASP:OD2	1:q:72:THR:OG1	2.32	0.47
1:q:102:ALA:HB1	1:q:401:GLU:HB2	1.96	0.47
1:s:102:ALA:HB1	1:s:401:GLU:HB2	1.96	0.47
1:u:131:GLN:HE22	1:u:249:ASP:HB3	1.79	0.47
1:c:5:VAL:HB	1:c:133:PHE:CD1	2.50	0.47
1:c:193:VAL:HG13	1:c:262:ARG:HG3	1.95	0.47
1:c:216:LYS:HB2	1:c:275:SER:HB3	1.95	0.47
1:c:281:TYR:HD2	1:o:87:PRO:CD	2.28	0.47
1:d:5:VAL:HB	1:d:133:PHE:CD1	2.50	0.47
1:d:67:ASP:HB2	1:d:73:MET:CE	2.43	0.47
1:d:359:ARG:N	3:d:601:TA1:O13	2.44	0.47
1:h:67:ASP:HB2	1:h:73:MET:CE	2.43	0.47
1:j:102:ALA:HB1	1:j:401:GLU:HB2	1.96	0.47
1:k:102:ALA:HB1	1:k:401:GLU:HB2	1.96	0.47
1:l:5:VAL:HB	1:l:133:PHE:CD1	2.50	0.47
1:l:86:ARG:HG2	1:l:88:ASP:H	1.79	0.47
1:m:102:ALA:HB1	1:m:401:GLU:HB2	1.96	0.47
2:N:205:ASP:O	2:N:209:ILE:HG13	2.15	0.47
2:O:205:ASP:O	2:O:209:ILE:HG13	2.15	0.47
2:O:244:PHE:HB2	2:O:356:ASN:HD21	1.79	0.47
2:O:255:PHE:O	2:O:259:LEU:N	2.46	0.47
2:Q:241:SER:OG	2:Q:250:VAL:O	2.30	0.47
2:R:244:PHE:HB2	2:R:356:ASN:HD21	1.80	0.47
2:R:353:VAL:CG1	2:R:354:GLY:N	2.77	0.47
2:T:224:TYR:CZ	6:T:502:GTP:C8	3.03	0.47
2:T:353:VAL:CG1	2:T:354:GLY:N	2.77	0.47
2:U:262:TYR:CB	2:U:263:PRO:HD2	2.25	0.47
2:U:326:LYS:CE	1:u:218:THR:O	2.62	0.47
2:V:154:MET:HE1	2:V:166:LYS:HB3	1.96	0.47
2:X:244:PHE:HB2	2:X:356:ASN:HD21	1.80	0.47
2:Y:241:SER:OG	2:Y:250:VAL:O	2.30	0.47
2:Z:205:ASP:O	2:Z:209:ILE:HG13	2.15	0.47
2:B:273:ALA:HB3	2:B:291:ILE:HG23	1.97	0.47
2:E:154:MET:HE1	2:E:166:LYS:HB3	1.97	0.47
2:E:286:LEU:HB3	2:E:291:ILE:HD11	1.95	0.47
2:E:353:VAL:CG1	2:E:354:GLY:N	2.77	0.47
2:F:244:PHE:HB2	2:F:356:ASN:HD21	1.80	0.47
2:J:26:LEU:HD13	2:J:364:PRO:HD3	1.95	0.47
2:J:264:ARG:HA	2:J:266:HIS:ND1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:154:MET:HE1	2:K:166:LYS:HB3	1.96	0.47
2:K:353:VAL:CG1	2:K:354:GLY:N	2.77	0.47
2:M:205:ASP:O	2:M:209:ILE:HG13	2.15	0.47
2:M:331:ALA:O	2:M:335:ILE:HG12	2.14	0.47
1:q:67:ASP:HB2	1:q:73:MET:CE	2.44	0.47
1:v:102:ALA:HB1	1:v:401:GLU:HB2	1.96	0.47
1:w:11:GLN:O	1:w:15:GLN:HG2	2.15	0.47
1:x:102:ALA:HB1	1:x:401:GLU:HB2	1.96	0.47
1:y:5:VAL:HB	1:y:133:PHE:CD1	2.50	0.47
1:c:12:CYS:CB	4:c:602:GDP:C4	2.97	0.47
1:c:360:GLY:CA	3:c:601:TA1:H443	2.29	0.47
1:d:102:ALA:HB1	1:d:401:GLU:HB2	1.97	0.47
1:d:222:TYR:CZ	4:d:602:GDP:N3	2.82	0.47
1:f:216:LYS:HB2	1:f:275:SER:HB3	1.96	0.47
1:g:216:LYS:HB2	1:g:275:SER:HB3	1.96	0.47
1:k:5:VAL:HB	1:k:133:PHE:CD1	2.50	0.47
1:k:86:ARG:HG2	1:k:88:ASP:H	1.79	0.47
2:S:244:PHE:HB2	2:S:356:ASN:HD21	1.80	0.47
2:U:21:TRP:CZ2	2:U:65:ALA:HB2	2.50	0.47
2:U:353:VAL:CG1	2:U:354:GLY:N	2.77	0.47
2:V:21:TRP:CZ2	2:V:65:ALA:HB2	2.50	0.47
2:V:326:LYS:NZ	1:v:218:THR:O	2.47	0.47
2:V:353:VAL:CG1	2:V:354:GLY:N	2.77	0.47
2:W:21:TRP:CZ2	2:W:65:ALA:HB2	2.50	0.47
2:Z:171:ILE:HD13	6:Z:502:GTP:N2	2.27	0.47
2:C:331:ALA:O	2:C:335:ILE:HG12	2.14	0.47
2:C:353:VAL:CG1	2:C:354:GLY:N	2.77	0.47
2:D:154:MET:HE1	2:D:166:LYS:HB3	1.97	0.47
2:E:297:GLU:O	2:E:301:GLN:NE2	2.40	0.47
2:H:88:HIS:HA	2:I:283:HIS:CG	2.39	0.47
2:K:264:ARG:HA	2:K:266:HIS:ND1	2.30	0.47
2:M:297:GLU:O	2:M:301:GLN:NE2	2.40	0.47
1:v:216:LYS:HB2	1:v:275:SER:HB3	1.97	0.47
1:v:286:VAL:HG23	1:v:363:MET:HE3	1.96	0.47
1:z:102:ALA:HB1	1:z:401:GLU:HB2	1.96	0.47
1:a:310:TYR:HA	1:a:371:SER:HA	1.97	0.47
3:d:601:TA1:H463	3:d:601:TA1:C26	2.44	0.47
1:h:216:LYS:HB2	1:h:275:SER:HB3	1.95	0.47
1:i:11:GLN:O	1:i:15:GLN:HG2	2.15	0.47
3:j:601:TA1:H441	3:j:601:TA1:C27	2.44	0.47
1:k:23:VAL:HG11	3:k:601:TA1:H411	1.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:m:12:CYS:HB2	4:m:602:GDP:N3	2.28	0.47
1:m:12:CYS:HB2	4:m:602:GDP:N9	2.28	0.47
1:m:222:TYR:CD2	4:m:602:GDP:C6	3.03	0.47
2:P:353:VAL:CG1	2:P:354:GLY:N	2.77	0.47
2:Q:205:ASP:O	2:Q:209:ILE:HG13	2.15	0.47
2:Q:326:LYS:HE2	1:q:218:THR:O	2.15	0.47
2:R:297:GLU:O	2:R:301:GLN:NE2	2.40	0.47
2:T:136:LEU:HD23	2:T:167:LEU:HB2	1.97	0.47
2:U:224:TYR:CE2	6:U:502:GTP:C6	2.91	0.47
2:X:353:VAL:CG1	2:X:354:GLY:N	2.77	0.47
2:Y:154:MET:HE1	2:Y:166:LYS:HB3	1.96	0.47
2:B:255:PHE:O	2:B:259:LEU:N	2.46	0.47
2:G:89:PRO:HD3	2:H:283:HIS:CD2	2.49	0.47
2:J:128:GLN:CD	2:K:285:GLN:HG3	2.39	0.47
2:J:255:PHE:O	2:J:259:LEU:N	2.46	0.47
1:n:310:TYR:HA	1:n:371:SER:HA	1.97	0.47
1:o:193:VAL:HG13	1:o:262:ARG:HG3	1.95	0.47
1:t:102:ALA:HB1	1:t:401:GLU:HB2	1.96	0.47
1:u:102:ALA:HB1	1:u:401:GLU:HB2	1.96	0.47
1:x:5:VAL:HB	1:x:133:PHE:CD1	2.50	0.47
1:x:395:LEU:HD12	1:x:395:LEU:HA	1.82	0.47
1:b:310:TYR:HA	1:b:371:SER:HA	1.97	0.47
1:d:216:LYS:HB2	1:d:275:SER:HB3	1.96	0.47
1:f:67:ASP:OD2	1:f:72:THR:OG1	2.32	0.47
1:f:88:ASP:OD2	1:g:282:ARG:NH2	2.47	0.47
1:h:231:ALA:HB1	3:h:601:TA1:C39	2.45	0.47
1:i:102:ALA:HB1	1:i:401:GLU:HB2	1.96	0.47
2:S:353:VAL:CG1	2:S:354:GLY:N	2.77	0.47
2:U:228:ASN:HD21	6:U:502:GTP:HN1	1.62	0.47
2:G:244:PHE:HB2	2:G:356:ASN:HD21	1.80	0.47
2:G:353:VAL:CG1	2:G:354:GLY:N	2.77	0.47
2:I:353:VAL:CG1	2:I:354:GLY:N	2.77	0.47
2:K:26:LEU:HD13	2:K:364:PRO:HD3	1.96	0.47
1:p:5:VAL:HB	1:p:133:PHE:CD1	2.50	0.47
1:p:11:GLN:O	1:p:15:GLN:HG2	2.14	0.47
1:q:11:GLN:O	1:q:15:GLN:HG2	2.15	0.47
1:q:310:TYR:HA	1:q:371:SER:HA	1.98	0.47
1:w:5:VAL:HB	1:w:133:PHE:CD1	2.50	0.47
1:z:310:TYR:HA	1:z:371:SER:HA	1.97	0.47
1:e:216:LYS:HB2	1:e:275:SER:HB3	1.96	0.46
1:g:5:VAL:HB	1:g:133:PHE:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:i:601:TA1:H441	3:i:601:TA1:C27	2.45	0.46
1:j:361:LEU:HD23	3:j:601:TA1:C44	2.40	0.46
1:k:310:TYR:HA	1:k:371:SER:HA	1.97	0.46
1:l:310:TYR:HA	1:l:371:SER:HA	1.97	0.46
1:m:310:TYR:HA	1:m:371:SER:HA	1.98	0.46
2:P:205:ASP:O	2:P:209:ILE:HG13	2.16	0.46
2:P:224:TYR:CE2	6:P:502:GTP:C6	3.03	0.46
2:T:273:ALA:HB3	2:T:291:ILE:HG23	1.97	0.46
2:U:154:MET:HE1	2:U:166:LYS:HB3	1.96	0.46
2:W:26:LEU:HD13	2:W:364:PRO:HD3	1.96	0.46
2:X:264:ARG:HA	2:X:266:HIS:ND1	2.30	0.46
2:B:244:PHE:HB2	2:B:356:ASN:HD21	1.80	0.46
2:F:353:VAL:CG1	2:F:354:GLY:N	2.77	0.46
2:G:194:THR:O	2:G:198:SER:OG	2.30	0.46
2:H:154:MET:HE1	2:H:166:LYS:HB3	1.96	0.46
2:H:244:PHE:HB2	2:H:356:ASN:HD21	1.80	0.46
2:J:8:HIS:CE1	2:J:138:PHE:CD2	3.03	0.46
2:K:8:HIS:CE1	2:K:138:PHE:CD2	3.04	0.46
2:L:205:ASP:O	2:L:209:ILE:HG13	2.15	0.46
1:o:310:TYR:HA	1:o:371:SER:HA	1.97	0.46
1:t:11:GLN:O	1:t:15:GLN:HG2	2.15	0.46
1:d:310:TYR:HA	1:d:371:SER:HA	1.98	0.46
1:f:5:VAL:HB	1:f:133:PHE:CD1	2.50	0.46
1:i:231:ALA:HB1	3:i:601:TA1:H391	1.97	0.46
1:j:67:ASP:OD2	1:j:72:THR:OG1	2.32	0.46
2:O:154:MET:HE1	2:O:166:LYS:HB3	1.96	0.46
2:O:224:TYR:CE2	6:O:502:GTP:C5	3.03	0.46
2:Q:244:PHE:HB2	2:Q:356:ASN:HD21	1.80	0.46
2:R:35:GLN:NE2	2:R:59:GLY:O	2.48	0.46
2:S:205:ASP:O	2:S:209:ILE:HG13	2.15	0.46
2:T:244:PHE:HB2	2:T:356:ASN:HD21	1.80	0.46
2:T:285:GLN:O	2:T:287:SER:N	2.46	0.46
2:X:8:HIS:CE1	2:X:138:PHE:CD2	3.04	0.46
2:X:21:TRP:CZ2	2:X:65:ALA:HB2	2.50	0.46
2:X:26:LEU:HD13	2:X:364:PRO:HD3	1.96	0.46
2:Y:205:ASP:O	2:Y:209:ILE:HG13	2.15	0.46
2:Y:224:TYR:CD2	6:Y:502:GTP:C2	2.84	0.46
2:Z:326:LYS:NZ	1:z:218:THR:O	2.41	0.46
2:A:273:ALA:HB3	2:A:291:ILE:HG23	1.98	0.46
2:B:154:MET:HE1	2:B:166:LYS:HB3	1.96	0.46
2:B:286:LEU:HB3	2:B:291:ILE:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:264:ARG:HA	2:G:266:HIS:ND1	2.30	0.46
2:I:194:THR:O	2:I:198:SER:OG	2.30	0.46
2:J:297:GLU:O	2:J:301:GLN:NE2	2.40	0.46
2:K:244:PHE:HB2	2:K:356:ASN:HD21	1.80	0.46
2:L:8:HIS:CE1	2:L:138:PHE:CD2	3.04	0.46
2:M:238:ILE:HG23	2:M:255:PHE:CE2	2.50	0.46
1:q:5:VAL:HB	1:q:133:PHE:CD1	2.50	0.46
1:s:155:ILE:CG2	1:s:164:MET:HE1	2.45	0.46
1:w:67:ASP:OD2	1:w:72:THR:OG1	2.32	0.46
1:x:310:TYR:HA	1:x:371:SER:HA	1.98	0.46
1:y:310:TYR:HA	1:y:371:SER:HA	1.98	0.46
1:y:322:SER:HG	1:y:325:GLU:HB2	1.79	0.46
1:z:5:VAL:HB	1:z:133:PHE:CD1	2.50	0.46
1:e:5:VAL:HB	1:e:133:PHE:CD1	2.50	0.46
1:f:102:ALA:HB1	1:f:401:GLU:HB2	1.96	0.46
1:g:11:GLN:O	1:g:15:GLN:HG2	2.15	0.46
1:h:23:VAL:HG13	3:h:601:TA1:H421	1.97	0.46
1:h:102:ALA:HB1	1:h:401:GLU:HB2	1.96	0.46
1:i:274:THR:H	3:i:601:TA1:H162	1.79	0.46
1:m:5:VAL:HB	1:m:133:PHE:CD1	2.50	0.46
2:N:21:TRP:CZ2	2:N:65:ALA:HB2	2.50	0.46
2:O:8:HIS:CE1	2:O:138:PHE:CD2	3.04	0.46
2:P:244:PHE:HB2	2:P:356:ASN:HD21	1.80	0.46
2:Q:273:ALA:HB3	2:Q:291:ILE:HG23	1.98	0.46
2:R:205:ASP:O	2:R:209:ILE:HG13	2.15	0.46
2:S:285:GLN:NE2	1:r:53:GLU:O	2.36	0.46
2:X:224:TYR:CD1	6:X:502:GTP:C6	3.04	0.46
2:Y:273:ALA:HB3	2:Y:291:ILE:HG23	1.97	0.46
2:A:238:ILE:HG23	2:A:255:PHE:CE2	2.50	0.46
2:A:286:LEU:HB3	2:A:291:ILE:HD11	1.96	0.46
2:D:194:THR:O	2:D:198:SER:OG	2.30	0.46
2:E:21:TRP:CZ2	2:E:65:ALA:HB2	2.50	0.46
2:H:21:TRP:CZ2	2:H:65:ALA:HB2	2.51	0.46
2:J:154:MET:HE1	2:J:166:LYS:HB3	1.96	0.46
2:L:194:THR:O	2:L:198:SER:OG	2.30	0.46
1:r:310:TYR:HA	1:r:371:SER:HA	1.98	0.46
1:u:216:LYS:HB2	1:u:275:SER:HB3	1.97	0.46
1:z:322:SER:HG	1:z:325:GLU:HB2	1.79	0.46
1:b:13:GLY:N	4:b:602:GDP:O3'	2.49	0.46
1:b:137:HIS:HA	4:b:602:GDP:C3'	2.45	0.46
1:c:310:TYR:HA	1:c:371:SER:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:310:TYR:HA	1:f:371:SER:HA	1.97	0.46
1:g:310:TYR:HA	1:g:371:SER:HA	1.97	0.46
1:h:5:VAL:HB	1:h:133:PHE:CD1	2.50	0.46
1:h:11:GLN:O	1:h:15:GLN:HG2	2.15	0.46
1:i:5:VAL:HB	1:i:133:PHE:CD1	2.50	0.46
1:j:67:ASP:HB2	1:j:73:MET:HE2	1.97	0.46
1:m:222:TYR:CD1	4:m:602:GDP:N2	2.83	0.46
2:Q:5:ILE:HD12	2:Q:135:PHE:CE1	2.51	0.46
2:R:21:TRP:CZ2	2:R:65:ALA:HB2	2.51	0.46
2:V:194:THR:O	2:V:198:SER:OG	2.30	0.46
2:V:205:ASP:O	2:V:209:ILE:HG13	2.15	0.46
2:W:264:ARG:HA	2:W:266:HIS:ND1	2.30	0.46
2:X:326:LYS:NZ	1:x:218:THR:O	2.41	0.46
2:Y:8:HIS:CE1	2:Y:138:PHE:CD2	3.04	0.46
2:Z:297:GLU:O	2:Z:301:GLN:NE2	2.40	0.46
2:C:8:HIS:CE1	2:C:138:PHE:CD2	3.04	0.46
2:C:205:ASP:O	2:C:209:ILE:HG13	2.16	0.46
2:D:89:PRO:HD3	2:E:283:HIS:NE2	2.24	0.46
2:F:88:HIS:HD2	2:G:283:HIS:CA	2.19	0.46
2:H:205:ASP:O	2:H:209:ILE:HG13	2.15	0.46
2:L:264:ARG:HA	2:L:266:HIS:ND1	2.30	0.46
1:o:5:VAL:HB	1:o:133:PHE:CD1	2.50	0.46
1:p:216:LYS:HB2	1:p:275:SER:HB3	1.97	0.46
1:p:310:TYR:HA	1:p:371:SER:HA	1.98	0.46
1:r:11:GLN:O	1:r:15:GLN:HG2	2.14	0.46
1:r:102:ALA:HB1	1:r:401:GLU:HB2	1.97	0.46
1:t:5:VAL:HB	1:t:133:PHE:CD1	2.50	0.46
1:e:102:ALA:HB1	1:e:401:GLU:HB2	1.97	0.46
1:e:310:TYR:HA	1:e:371:SER:HA	1.98	0.46
1:e:358:PRO:CB	3:e:601:TA1:H281	2.45	0.46
1:g:88:ASP:OD2	1:h:282:ARG:NH2	2.48	0.46
1:g:102:ALA:HB1	1:g:401:GLU:HB2	1.96	0.46
1:h:310:TYR:HA	1:h:371:SER:HA	1.97	0.46
1:j:5:VAL:HB	1:j:133:PHE:CD1	2.50	0.46
1:l:102:ALA:HB1	1:l:401:GLU:HB2	1.96	0.46
2:N:154:MET:HE1	2:N:166:LYS:HB3	1.96	0.46
2:R:5:ILE:HD12	2:R:135:PHE:CE1	2.51	0.46
2:U:205:ASP:O	2:U:209:ILE:HG13	2.15	0.46
2:U:244:PHE:HB2	2:U:356:ASN:HD21	1.80	0.46
2:U:273:ALA:HB3	2:U:291:ILE:HG23	1.97	0.46
2:W:8:HIS:CE1	2:W:138:PHE:CD2	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W:205:ASP:O	2:W:209:ILE:HG13	2.15	0.46
2:W:244:PHE:HB2	2:W:356:ASN:HD21	1.80	0.46
2:X:285:GLN:O	2:X:287:SER:N	2.46	0.46
2:Y:194:THR:O	2:Y:198:SER:OG	2.30	0.46
2:Y:264:ARG:HA	2:Y:266:HIS:ND1	2.30	0.46
2:F:205:ASP:O	2:F:209:ILE:HG13	2.15	0.46
2:G:273:ALA:HB3	2:G:291:ILE:HG23	1.98	0.46
2:H:26:LEU:HD13	2:H:364:PRO:HD3	1.96	0.46
2:H:353:VAL:CG1	2:H:354:GLY:N	2.77	0.46
2:I:205:ASP:O	2:I:209:ILE:HG13	2.15	0.46
2:J:238:ILE:HG23	2:J:255:PHE:CE2	2.51	0.46
2:J:242:LEU:HD11	2:J:252:LEU:HG	1.97	0.46
2:K:238:ILE:HG23	2:K:255:PHE:CE2	2.51	0.46
2:L:262:TYR:CB	2:L:263:PRO:HD2	2.26	0.46
1:w:395:LEU:HD12	1:w:395:LEU:HA	1.82	0.46
1:y:102:ALA:HB1	1:y:401:GLU:HB2	1.97	0.46
1:z:67:ASP:HB2	1:z:73:MET:HE2	1.98	0.46
1:b:5:VAL:HB	1:b:133:PHE:CD1	2.50	0.46
1:d:11:GLN:O	1:d:15:GLN:HG2	2.15	0.46
1:j:11:GLN:O	1:j:15:GLN:HG2	2.15	0.46
2:O:21:TRP:CZ2	2:O:65:ALA:HB2	2.50	0.46
2:P:8:HIS:CE1	2:P:138:PHE:CD2	3.04	0.46
2:P:286:LEU:HB3	2:P:291:ILE:HD11	1.97	0.46
2:Q:194:THR:O	2:Q:198:SER:OG	2.30	0.46
2:R:273:ALA:HB3	2:R:291:ILE:HG23	1.97	0.46
2:T:21:TRP:CZ2	2:T:65:ALA:HB2	2.51	0.46
2:T:194:THR:O	2:T:198:SER:OG	2.30	0.46
2:G:205:ASP:O	2:G:209:ILE:HG13	2.15	0.46
2:G:312:TYR:HB2	2:G:343:PHE:HD1	1.81	0.46
2:H:264:ARG:HA	2:H:266:HIS:ND1	2.30	0.46
2:J:89:PRO:CD	2:K:283:HIS:ND1	2.75	0.46
2:J:244:PHE:HB2	2:J:356:ASN:HD21	1.80	0.46
2:K:205:ASP:O	2:K:209:ILE:HG13	2.15	0.46
1:n:11:GLN:O	1:n:15:GLN:HG2	2.15	0.46
1:o:11:GLN:O	1:o:15:GLN:HG2	2.15	0.46
1:r:5:VAL:HB	1:r:133:PHE:CD1	2.50	0.46
1:s:5:VAL:HB	1:s:133:PHE:CD1	2.50	0.46
1:s:310:TYR:HA	1:s:371:SER:HA	1.98	0.46
1:u:310:TYR:HA	1:u:371:SER:HA	1.97	0.46
1:v:5:VAL:HB	1:v:133:PHE:CD1	2.50	0.46
1:v:395:LEU:HD12	1:v:395:LEU:HA	1.82	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:5:ILE:HD12	2:P:135:PHE:CE1	2.51	0.46
2:S:21:TRP:CZ2	2:S:65:ALA:HB2	2.51	0.46
2:S:100:ALA:N	6:S:502:GTP:O2G	2.46	0.46
2:V:285:GLN:O	2:V:287:SER:N	2.46	0.46
2:W:273:ALA:HB3	2:W:291:ILE:HG23	1.97	0.46
2:W:297:GLU:O	2:W:301:GLN:NE2	2.40	0.46
2:B:238:ILE:HG23	2:B:255:PHE:CE2	2.50	0.46
2:C:5:ILE:HD12	2:C:135:PHE:CE1	2.51	0.46
2:C:21:TRP:CZ2	2:C:65:ALA:HB2	2.50	0.46
2:E:5:ILE:HD12	2:E:135:PHE:CE1	2.51	0.46
2:H:8:HIS:CE1	2:H:138:PHE:CD2	3.03	0.46
2:J:205:ASP:O	2:J:209:ILE:HG13	2.15	0.46
2:M:262:TYR:CB	2:M:263:PRO:HD2	2.26	0.46
1:q:46:ARG:HB2	1:q:241:ARG:O	2.16	0.46
1:q:119:VAL:O	1:q:119:VAL:HG12	2.16	0.46
1:t:310:TYR:HA	1:t:371:SER:HA	1.98	0.46
1:w:310:TYR:HA	1:w:371:SER:HA	1.98	0.46
1:d:222:TYR:CG	4:d:602:GDP:C6	3.02	0.46
1:j:310:TYR:HA	1:j:371:SER:HA	1.98	0.46
2:O:273:ALA:HB3	2:O:291:ILE:HG23	1.98	0.46
2:P:21:TRP:CZ2	2:P:65:ALA:HB2	2.50	0.46
2:P:326:LYS:CE	1:p:219:THR:HA	2.32	0.46
2:Q:242:LEU:HD11	2:Q:252:LEU:HG	1.97	0.46
2:R:285:GLN:O	2:R:287:SER:N	2.46	0.46
2:T:205:ASP:O	2:T:209:ILE:HG13	2.15	0.46
2:V:242:LEU:HD11	2:V:252:LEU:HG	1.98	0.46
2:X:205:ASP:O	2:X:209:ILE:HG13	2.15	0.46
2:B:242:LEU:HD11	2:B:252:LEU:HG	1.97	0.46
2:E:238:ILE:HG23	2:E:255:PHE:CE2	2.51	0.46
2:F:238:ILE:HG23	2:F:255:PHE:CE2	2.51	0.46
2:F:264:ARG:HA	2:F:266:HIS:ND1	2.30	0.46
2:G:8:HIS:CE1	2:G:138:PHE:CD2	3.03	0.46
2:G:88:HIS:CG	2:H:283:HIS:CB	2.79	0.46
2:G:242:LEU:HD11	2:G:252:LEU:HG	1.97	0.46
2:I:8:HIS:CE1	2:I:138:PHE:CD2	3.03	0.46
2:I:154:MET:HE1	2:I:166:LYS:HB3	1.96	0.46
2:J:21:TRP:CZ2	2:J:65:ALA:HB2	2.51	0.46
2:K:262:TYR:CB	2:K:263:PRO:HD2	2.26	0.46
2:L:154:MET:HE1	2:L:166:LYS:HB3	1.97	0.46
1:r:216:LYS:HB2	1:r:275:SER:HB3	1.96	0.46
1:s:67:ASP:HB2	1:s:73:MET:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:s:86:ARG:HG3	1:t:281:TYR:CB	2.42	0.46
1:v:310:TYR:HA	1:v:371:SER:HA	1.97	0.46
1:b:218:THR:O	2:B:326:LYS:NZ	2.47	0.46
1:c:11:GLN:CB	4:c:602:GDP:O2B	2.63	0.46
1:c:347:ASN:O	2:P:181:VAL:HG21	2.05	0.46
1:h:12:CYS:SG	4:h:602:GDP:C6	3.09	0.46
1:i:215:LEU:CD2	3:i:601:TA1:O06	2.64	0.46
1:i:215:LEU:HD22	3:i:601:TA1:C14	2.46	0.46
1:i:310:TYR:HA	1:i:371:SER:HA	1.97	0.46
1:i:395:LEU:HD12	1:i:395:LEU:HA	1.83	0.46
1:l:215:LEU:CD2	3:l:601:TA1:O06	2.62	0.46
2:T:5:ILE:HD12	2:T:135:PHE:CE1	2.51	0.46
2:T:264:ARG:HA	2:T:266:HIS:ND1	2.31	0.46
2:Y:21:TRP:CZ2	2:Y:65:ALA:HB2	2.50	0.46
2:Z:154:MET:HE1	2:Z:166:LYS:HB3	1.97	0.46
2:Z:285:GLN:O	2:Z:287:SER:N	2.46	0.46
2:A:8:HIS:CE1	2:A:138:PHE:CD2	3.04	0.46
2:A:154:MET:HE1	2:A:166:LYS:HB3	1.96	0.46
2:B:8:HIS:CE1	2:B:138:PHE:CD2	3.04	0.46
2:D:5:ILE:HD12	2:D:135:PHE:CE1	2.51	0.46
2:D:264:ARG:HA	2:D:266:HIS:ND1	2.30	0.46
2:E:242:LEU:HD11	2:E:252:LEU:HG	1.97	0.46
2:F:8:HIS:CE1	2:F:138:PHE:CD2	3.03	0.46
2:G:5:ILE:HD12	2:G:135:PHE:CE1	2.51	0.46
2:H:5:ILE:HD12	2:H:135:PHE:CE1	2.51	0.46
2:I:21:TRP:CZ2	2:I:65:ALA:HB2	2.51	0.46
2:K:21:TRP:CZ2	2:K:65:ALA:HB2	2.51	0.46
2:K:180:ALA:HB3	2:K:183:GLU:HB2	1.97	0.46
1:o:67:ASP:HB2	1:o:73:MET:HE2	1.97	0.46
1:o:274:THR:HG22	1:o:282:ARG:HD2	1.98	0.46
1:o:322:SER:HG	1:o:325:GLU:HB2	1.78	0.46
1:u:5:VAL:HB	1:u:133:PHE:CD1	2.50	0.46
1:v:67:ASP:OD2	1:v:72:THR:OG1	2.32	0.46
1:a:5:VAL:HB	1:a:133:PHE:CD1	2.50	0.46
1:e:11:GLN:CB	4:e:602:GDP:O2B	2.64	0.46
1:h:67:ASP:OD2	1:h:72:THR:OG1	2.32	0.46
1:h:87:PRO:HD3	1:i:281:TYR:CD2	2.51	0.46
1:i:403:MET:HE2	1:i:403:MET:HB3	1.87	0.46
1:l:11:GLN:O	1:l:15:GLN:HG2	2.15	0.46
2:N:8:HIS:CE1	2:N:138:PHE:CD2	3.04	0.46
2:R:242:LEU:HD11	2:R:252:LEU:HG	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:171:ILE:HD11	6:T:502:GTP:HN22	1.81	0.46
2:U:8:HIS:CE1	2:U:138:PHE:CD2	3.04	0.46
2:V:244:PHE:HB2	2:V:356:ASN:HD21	1.80	0.46
2:Z:8:HIS:CE1	2:Z:138:PHE:CD2	3.04	0.46
2:C:238:ILE:HG23	2:C:255:PHE:CE2	2.51	0.46
2:I:5:ILE:HD12	2:I:135:PHE:CE1	2.51	0.46
2:I:238:ILE:HG23	2:I:255:PHE:CE2	2.50	0.46
2:I:242:LEU:HD11	2:I:252:LEU:HG	1.98	0.46
2:I:264:ARG:HA	2:I:266:HIS:ND1	2.30	0.46
2:L:273:ALA:HB3	2:L:291:ILE:HG23	1.98	0.46
2:M:273:ALA:HB3	2:M:291:ILE:HG23	1.97	0.46
1:n:106:TYR:HE2	1:n:403:MET:HG2	1.81	0.46
1:w:403:MET:HE2	1:w:403:MET:HB3	1.88	0.46
1:y:11:GLN:O	1:y:15:GLN:HG2	2.15	0.46
1:j:121:ARG:O	1:j:125:GLU:HG2	2.17	0.45
1:m:256:ASN:HA	2:Z:404:PHE:HE1	1.80	0.45
1:m:322:SER:HG	1:m:325:GLU:HB2	1.80	0.45
2:N:242:LEU:HD11	2:N:252:LEU:HG	1.98	0.45
2:O:224:TYR:OH	6:O:502:GTP:C1'	2.64	0.45
2:U:5:ILE:HD12	2:U:135:PHE:CE1	2.51	0.45
2:U:264:ARG:HA	2:U:266:HIS:ND1	2.30	0.45
2:A:21:TRP:CZ2	2:A:65:ALA:HB2	2.51	0.45
2:B:21:TRP:CZ2	2:B:65:ALA:HB2	2.50	0.45
2:C:264:ARG:HA	2:C:266:HIS:ND1	2.30	0.45
2:J:273:ALA:HB3	2:J:291:ILE:HG23	1.97	0.45
2:M:8:HIS:CE1	2:M:138:PHE:CD2	3.04	0.45
1:n:322:SER:HG	1:n:325:GLU:HB2	1.80	0.45
1:p:164:MET:HB2	1:p:164:MET:HE3	1.73	0.45
1:s:164:MET:HE3	1:s:164:MET:HB2	1.79	0.45
1:t:216:LYS:HB2	1:t:275:SER:HB3	1.96	0.45
1:w:164:MET:HE3	1:w:164:MET:HB2	1.72	0.45
1:e:99:ASN:OD1	4:e:602:GDP:H5'	2.16	0.45
1:i:67:ASP:OD2	1:i:72:THR:OG1	2.32	0.45
1:k:395:LEU:HD12	1:k:395:LEU:HA	1.82	0.45
2:Q:21:TRP:CZ2	2:Q:65:ALA:HB2	2.50	0.45
2:R:256:GLN:HB3	1:r:397:TRP:CH2	2.51	0.45
2:S:5:ILE:HD12	2:S:135:PHE:CE1	2.51	0.45
2:S:8:HIS:CE1	2:S:138:PHE:CD2	3.04	0.45
2:T:8:HIS:CE1	2:T:138:PHE:CD2	3.04	0.45
2:Z:326:LYS:HG2	1:z:220:PRO:CD	2.22	0.45
2:A:89:PRO:HD2	2:B:283:HIS:ND1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:8:HIS:CE1	2:D:138:PHE:CD2	3.04	0.45
2:D:21:TRP:CZ2	2:D:65:ALA:HB2	2.51	0.45
2:F:5:ILE:HD12	2:F:135:PHE:CE1	2.51	0.45
2:H:242:LEU:HD11	2:H:252:LEU:HG	1.98	0.45
1:q:121:ARG:O	1:q:125:GLU:HG2	2.16	0.45
1:r:46:ARG:HB2	1:r:241:ARG:O	2.17	0.45
1:s:11:GLN:O	1:s:15:GLN:HG2	2.15	0.45
1:u:46:ARG:HB2	1:u:241:ARG:O	2.17	0.45
1:w:121:ARG:O	1:w:125:GLU:HG2	2.17	0.45
1:a:23:VAL:HG13	3:a:601:TA1:C42	2.46	0.45
1:a:134:GLN:HA	1:a:165:ASN:O	2.17	0.45
1:b:11:GLN:O	1:b:15:GLN:HG2	2.16	0.45
1:c:11:GLN:O	1:c:15:GLN:HG2	2.15	0.45
1:d:121:ARG:O	1:d:125:GLU:HG2	2.16	0.45
1:g:169:VAL:HG21	4:g:602:GDP:N2	2.31	0.45
1:k:218:THR:O	2:K:326:LYS:NZ	2.43	0.45
1:l:390:ARG:NH2	2:L:439:SER:O	2.49	0.45
2:N:194:THR:O	2:N:198:SER:OG	2.30	0.45
2:O:5:ILE:HD12	2:O:135:PHE:CE1	2.51	0.45
2:Q:8:HIS:CE1	2:Q:138:PHE:CD2	3.04	0.45
2:Q:209:ILE:O	2:Q:213:CYS:SG	2.67	0.45
2:V:5:ILE:HD12	2:V:135:PHE:CE1	2.51	0.45
2:Z:21:TRP:CZ2	2:Z:65:ALA:HB2	2.51	0.45
2:Z:273:ALA:HB3	2:Z:291:ILE:HG23	1.98	0.45
2:A:264:ARG:HA	2:A:266:HIS:ND1	2.30	0.45
2:D:238:ILE:HG23	2:D:255:PHE:CE2	2.51	0.45
2:D:242:LEU:HD11	2:D:252:LEU:HG	1.97	0.45
2:E:62:VAL:O	2:E:62:VAL:HG13	2.15	0.45
2:F:21:TRP:CZ2	2:F:65:ALA:HB2	2.51	0.45
2:F:242:LEU:HD11	2:F:252:LEU:HG	1.97	0.45
2:F:273:ALA:HB3	2:F:291:ILE:HG23	1.98	0.45
2:H:238:ILE:HG23	2:H:255:PHE:CE2	2.51	0.45
2:J:5:ILE:HD12	2:J:135:PHE:CE1	2.51	0.45
1:u:67:ASP:HB2	1:u:73:MET:HE2	1.98	0.45
1:u:67:ASP:OD2	1:u:72:THR:OG1	2.32	0.45
1:w:322:SER:HG	1:w:325:GLU:HB2	1.80	0.45
1:z:11:GLN:O	1:z:15:GLN:HG2	2.15	0.45
1:a:11:GLN:O	1:a:15:GLN:HG2	2.16	0.45
1:a:121:ARG:O	1:a:125:GLU:HG2	2.16	0.45
1:a:281:TYR:CD2	1:m:87:PRO:HD3	2.50	0.45
1:f:222:TYR:OH	4:f:602:GDP:C2'	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:222:TYR:CE1	4:i:602:GDP:C2	3.05	0.45
1:j:134:GLN:HA	1:j:165:ASN:O	2.17	0.45
1:j:164:MET:HB2	1:j:164:MET:HE3	1.72	0.45
1:j:395:LEU:HD12	1:j:395:LEU:HA	1.82	0.45
1:k:134:GLN:HA	1:k:165:ASN:O	2.17	0.45
1:l:322:SER:HG	1:l:325:GLU:HB2	1.82	0.45
2:P:285:GLN:O	2:P:287:SER:N	2.47	0.45
2:P:297:GLU:O	2:P:301:GLN:NE2	2.40	0.45
2:S:264:ARG:HA	2:S:266:HIS:ND1	2.31	0.45
2:U:49:PHE:HE2	2:U:55:GLU:HB2	1.81	0.45
2:U:171:ILE:HD12	6:U:502:GTP:N2	2.27	0.45
2:V:8:HIS:CE1	2:V:138:PHE:CD2	3.04	0.45
2:X:273:ALA:HB3	2:X:291:ILE:HG23	1.98	0.45
2:I:244:PHE:HB2	2:I:356:ASN:HD21	1.80	0.45
2:K:273:ALA:HB3	2:K:291:ILE:HG23	1.98	0.45
1:n:5:VAL:HB	1:n:133:PHE:CD1	2.50	0.45
1:r:106:TYR:HE2	1:r:403:MET:HG2	1.81	0.45
1:v:67:ASP:HB2	1:v:73:MET:HE2	1.99	0.45
1:x:11:GLN:O	1:x:15:GLN:HG2	2.15	0.45
1:z:121:ARG:O	1:z:125:GLU:HG2	2.16	0.45
1:c:87:PRO:HD3	1:d:281:TYR:CE2	2.50	0.45
1:c:256:ASN:HA	2:P:404:PHE:HE1	1.79	0.45
1:e:11:GLN:O	1:e:15:GLN:HG2	2.15	0.45
1:e:106:TYR:HE2	1:e:403:MET:HG2	1.82	0.45
1:f:121:ARG:O	1:f:125:GLU:HG2	2.17	0.45
1:g:215:LEU:CD2	3:g:601:TA1:O06	2.65	0.45
1:i:121:ARG:O	1:i:125:GLU:HG2	2.17	0.45
1:m:11:GLN:O	1:m:15:GLN:HG2	2.15	0.45
1:m:121:ARG:O	1:m:125:GLU:HG2	2.17	0.45
2:N:264:ARG:HA	2:N:266:HIS:ND1	2.30	0.45
2:O:264:ARG:HA	2:O:266:HIS:ND1	2.31	0.45
2:P:273:ALA:HB3	2:P:291:ILE:HG23	1.98	0.45
2:P:395:PHE:CD2	2:P:422:ARG:HD3	2.52	0.45
2:Q:395:PHE:CD2	2:Q:422:ARG:HD3	2.52	0.45
2:R:395:PHE:CD2	2:R:422:ARG:HD3	2.52	0.45
2:U:242:LEU:HD11	2:U:252:LEU:HG	1.98	0.45
2:W:171:ILE:HD11	6:W:502:GTP:HN22	1.79	0.45
2:A:194:THR:O	2:A:198:SER:OG	2.30	0.45
2:C:395:PHE:CD2	2:C:422:ARG:HD3	2.52	0.45
2:D:10:GLY:O	2:D:14:VAL:HG23	2.17	0.45
2:E:10:GLY:O	2:E:14:VAL:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:21:TRP:CZ2	2:G:65:ALA:HB2	2.51	0.45
2:K:5:ILE:HD12	2:K:135:PHE:CE1	2.51	0.45
1:n:121:ARG:O	1:n:125:GLU:HG2	2.16	0.45
1:q:216:LYS:HB2	1:q:275:SER:HB3	1.97	0.45
1:v:403:MET:HE2	1:v:403:MET:HB3	1.87	0.45
1:w:67:ASP:HB2	1:w:73:MET:HE2	1.98	0.45
1:w:86:ARG:HG3	1:x:281:TYR:CD2	2.52	0.45
1:w:106:TYR:HE2	1:w:403:MET:HG2	1.82	0.45
1:a:106:TYR:HE2	1:a:403:MET:HG2	1.82	0.45
1:a:322:SER:HG	1:a:325:GLU:HB2	1.80	0.45
1:b:121:ARG:O	1:b:125:GLU:HG2	2.17	0.45
1:d:12:CYS:SG	4:d:602:GDP:N1	2.87	0.45
1:e:46:ARG:HB2	1:e:241:ARG:O	2.17	0.45
1:f:23:VAL:HG13	3:f:601:TA1:H421	1.98	0.45
1:g:67:ASP:OD2	1:g:72:THR:OG1	2.32	0.45
1:g:121:ARG:O	1:g:125:GLU:HG2	2.17	0.45
1:j:322:SER:HG	1:j:325:GLU:HB2	1.81	0.45
1:m:345:ILE:CG2	2:Z:181:VAL:HG11	2.47	0.45
2:N:273:ALA:HB3	2:N:291:ILE:HG23	1.99	0.45
2:O:242:LEU:HD11	2:O:252:LEU:HG	1.97	0.45
2:P:264:ARG:HA	2:P:266:HIS:ND1	2.31	0.45
2:T:49:PHE:HE2	2:T:55:GLU:HB2	1.81	0.45
2:V:264:ARG:HA	2:V:266:HIS:ND1	2.31	0.45
2:W:5:ILE:HD12	2:W:135:PHE:CE1	2.51	0.45
2:D:395:PHE:CD2	2:D:422:ARG:HD3	2.52	0.45
2:H:194:THR:O	2:H:198:SER:OG	2.30	0.45
2:M:21:TRP:CZ2	2:M:65:ALA:HB2	2.51	0.45
1:o:121:ARG:O	1:o:125:GLU:HG2	2.17	0.45
1:o:256:ASN:ND2	1:o:350:LYS:HD2	2.30	0.45
1:s:216:LYS:HB2	1:s:275:SER:HB3	1.97	0.45
1:z:106:TYR:HE2	1:z:403:MET:HG2	1.82	0.45
1:c:106:TYR:HE2	1:c:403:MET:HG2	1.82	0.45
1:h:403:MET:HE2	1:h:403:MET:HB3	1.88	0.45
1:i:134:GLN:HA	1:i:165:ASN:O	2.17	0.45
1:k:358:PRO:HB2	3:k:601:TA1:H281	1.98	0.45
1:l:67:ASP:HB2	1:l:73:MET:HE2	1.99	0.45
1:l:164:MET:HE3	1:l:164:MET:HB2	1.71	0.45
1:l:347:ASN:O	2:Y:181:VAL:HG21	2.02	0.45
2:N:5:ILE:HD12	2:N:135:PHE:CE1	2.51	0.45
2:Q:264:ARG:HA	2:Q:266:HIS:ND1	2.31	0.45
2:S:326:LYS:HD3	1:s:212:PHE:HE1	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:56:THR:HA	2:Z:285:GLN:NE2	2.32	0.45
2:B:5:ILE:HD12	2:B:135:PHE:CE1	2.52	0.45
2:G:238:ILE:HG23	2:G:255:PHE:CE2	2.51	0.45
2:H:273:ALA:HB3	2:H:291:ILE:HG23	1.99	0.45
2:I:312:TYR:HB2	2:I:343:PHE:HD1	1.82	0.45
2:M:264:ARG:HA	2:M:266:HIS:ND1	2.30	0.45
1:n:134:GLN:HA	1:n:165:ASN:O	2.17	0.45
1:q:322:SER:HG	1:q:325:GLU:HB2	1.81	0.45
1:v:46:ARG:HB2	1:v:241:ARG:O	2.17	0.45
1:v:121:ARG:O	1:v:125:GLU:HG2	2.17	0.45
1:y:395:LEU:HD12	1:y:395:LEU:HA	1.82	0.45
1:a:179:VAL:N	2:A:258:ASN:HD22	2.05	0.45
1:a:261:PRO:O	1:a:262:ARG:CB	2.65	0.45
1:d:46:ARG:HB2	1:d:241:ARG:O	2.17	0.45
1:d:134:GLN:HA	1:d:165:ASN:O	2.17	0.45
1:m:106:TYR:HE2	1:m:403:MET:HG2	1.82	0.45
1:m:361:LEU:HD23	3:m:601:TA1:H171	1.97	0.45
2:R:10:GLY:O	2:R:14:VAL:HG23	2.17	0.45
2:S:10:GLY:O	2:S:14:VAL:HG23	2.17	0.45
2:T:202:PHE:HE2	2:T:238:ILE:HD13	1.82	0.45
2:U:88:HIS:CD2	2:V:283:HIS:HB2	2.51	0.45
2:X:242:LEU:HD11	2:X:252:LEU:HG	1.99	0.45
2:C:242:LEU:HD11	2:C:252:LEU:HG	1.98	0.45
2:C:297:GLU:O	2:C:301:GLN:NE2	2.40	0.45
2:E:8:HIS:CE1	2:E:138:PHE:CD2	3.04	0.45
2:E:395:PHE:CD2	2:E:422:ARG:HD3	2.52	0.45
2:F:10:GLY:O	2:F:14:VAL:HG23	2.17	0.45
2:I:262:TYR:CB	2:I:263:PRO:HD2	2.26	0.45
2:L:5:ILE:HD12	2:L:135:PHE:CE1	2.51	0.45
1:n:261:PRO:O	1:n:262:ARG:CB	2.65	0.45
1:o:261:PRO:O	1:o:262:ARG:CB	2.65	0.45
1:t:67:ASP:OD2	1:t:72:THR:OG1	2.32	0.45
1:x:121:ARG:O	1:x:125:GLU:HG2	2.17	0.45
1:y:67:ASP:HB2	1:y:73:MET:HE2	1.99	0.45
1:b:134:GLN:HA	1:b:165:ASN:O	2.17	0.45
1:c:46:ARG:HB2	1:c:241:ARG:O	2.17	0.45
1:e:121:ARG:O	1:e:125:GLU:HG2	2.16	0.45
1:f:12:CYS:CB	4:f:602:GDP:C5	3.00	0.45
1:f:134:GLN:HA	1:f:165:ASN:O	2.17	0.45
1:f:222:TYR:OH	4:f:602:GDP:C1'	2.64	0.45
1:g:261:PRO:O	1:g:262:ARG:CB	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:11:GLN:O	1:k:15:GLN:HG2	2.15	0.45
1:k:121:ARG:O	1:k:125:GLU:HG2	2.17	0.45
1:l:121:ARG:O	1:l:125:GLU:HG2	2.16	0.45
1:m:256:ASN:ND2	2:Z:180:ALA:HA	2.32	0.45
2:P:238:ILE:HG23	2:P:255:PHE:CE2	2.52	0.45
2:P:256:GLN:HB3	1:p:397:TRP:CH2	2.52	0.45
2:Q:10:GLY:O	2:Q:14:VAL:HG23	2.17	0.45
2:U:11:GLN:N	6:U:502:GTP:O1B	2.48	0.45
2:U:194:THR:O	2:U:198:SER:OG	2.30	0.45
2:X:395:PHE:CD2	2:X:422:ARG:HD3	2.52	0.45
2:Y:242:LEU:HD11	2:Y:252:LEU:HG	1.98	0.45
2:Z:264:ARG:HA	2:Z:266:HIS:ND1	2.31	0.45
2:B:264:ARG:HA	2:B:266:HIS:ND1	2.31	0.45
2:C:273:ALA:HB3	2:C:291:ILE:HG23	1.98	0.45
2:E:264:ARG:HA	2:E:266:HIS:ND1	2.31	0.45
2:G:49:PHE:HE2	2:G:55:GLU:HB2	1.82	0.45
2:K:10:GLY:O	2:K:14:VAL:HG23	2.17	0.45
2:K:312:TYR:HB2	2:K:343:PHE:HD1	1.82	0.45
2:L:21:TRP:CZ2	2:L:65:ALA:HB2	2.51	0.45
2:L:89:PRO:HD3	2:M:283:HIS:CG	2.51	0.45
2:M:154:MET:HE1	2:M:166:LYS:HB3	1.97	0.45
1:o:134:GLN:HA	1:o:165:ASN:O	2.17	0.45
1:p:46:ARG:HB2	1:p:241:ARG:O	2.17	0.45
1:q:134:GLN:HA	1:q:165:ASN:O	2.17	0.45
1:s:134:GLN:HA	1:s:165:ASN:O	2.17	0.45
1:v:134:GLN:HA	1:v:165:ASN:O	2.17	0.45
1:x:322:SER:HG	1:x:325:GLU:HB2	1.80	0.45
1:y:164:MET:HB2	1:y:164:MET:HE3	1.71	0.45
1:a:23:VAL:CG1	3:a:601:TA1:C41	2.95	0.45
1:h:12:CYS:CB	4:h:602:GDP:C4	3.00	0.45
1:h:274:THR:H	3:h:601:TA1:H162	1.82	0.45
1:h:395:LEU:HD12	1:h:395:LEU:HA	1.82	0.45
1:j:261:PRO:O	1:j:262:ARG:CB	2.65	0.45
1:l:134:GLN:HA	1:l:165:ASN:O	2.17	0.45
1:m:134:GLN:HA	1:m:165:ASN:O	2.17	0.45
2:P:312:TYR:HB2	2:P:343:PHE:HD1	1.82	0.45
2:P:439:SER:O	1:p:390:ARG:NH2	2.50	0.45
2:R:8:HIS:CE1	2:R:138:PHE:CD2	3.04	0.45
2:R:154:MET:HE1	2:R:166:LYS:HB3	1.98	0.45
2:R:238:ILE:HG23	2:R:255:PHE:CE2	2.52	0.45
2:R:312:TYR:HB2	2:R:343:PHE:HD1	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:348:PRO:HG3	1:s:384:GLN:HA	1.98	0.45
2:T:10:GLY:O	2:T:14:VAL:HG23	2.17	0.45
2:U:20:CYS:SG	2:U:138:PHE:HE2	2.40	0.45
2:Z:49:PHE:HE2	2:Z:55:GLU:HB2	1.82	0.45
2:A:5:ILE:HD12	2:A:135:PHE:CE1	2.51	0.45
2:B:395:PHE:CD2	2:B:422:ARG:HD3	2.52	0.45
2:E:312:TYR:HB2	2:E:343:PHE:HD1	1.82	0.45
2:M:49:PHE:HE2	2:M:55:GLU:HB2	1.82	0.45
1:u:403:MET:HE2	1:u:403:MET:HB3	1.87	0.45
1:w:261:PRO:O	1:w:262:ARG:CB	2.65	0.45
1:x:356:ILE:HA	1:x:357:PRO:HD2	1.91	0.45
1:y:121:ARG:O	1:y:125:GLU:HG2	2.16	0.45
1:b:222:TYR:OH	4:b:602:GDP:N1	2.48	0.44
1:b:261:PRO:O	1:b:262:ARG:CB	2.65	0.44
1:b:322:SER:HG	1:b:325:GLU:HB2	1.80	0.44
1:d:222:TYR:CE1	4:d:602:GDP:C5	2.95	0.44
1:g:106:TYR:HE2	1:g:403:MET:HG2	1.82	0.44
1:g:360:GLY:HA3	3:g:601:TA1:H443	1.99	0.44
1:g:403:MET:HE2	1:g:403:MET:HB3	1.87	0.44
1:h:134:GLN:HA	1:h:165:ASN:O	2.17	0.44
1:j:356:ILE:HA	1:j:357:PRO:HD2	1.91	0.44
1:l:12:CYS:SG	4:l:602:GDP:C4	3.09	0.44
1:m:67:ASP:HB2	1:m:73:MET:HE2	1.99	0.44
1:m:261:PRO:O	1:m:262:ARG:CB	2.65	0.44
2:O:395:PHE:CD2	2:O:422:ARG:HD3	2.52	0.44
2:Q:326:LYS:CE	1:q:218:THR:O	2.65	0.44
2:R:171:ILE:CD1	6:R:502:GTP:C2	3.01	0.44
2:T:326:LYS:CD	1:t:220:PRO:HD2	2.46	0.44
2:Y:5:ILE:HD12	2:Y:135:PHE:CE1	2.51	0.44
2:A:312:TYR:HB2	2:A:343:PHE:HD1	1.82	0.44
2:C:285:GLN:O	2:C:287:SER:N	2.47	0.44
2:C:312:TYR:HB2	2:C:343:PHE:HD1	1.83	0.44
2:E:306:ASP:C	2:E:308:ARG:N	2.75	0.44
2:F:157:LEU:HD23	2:F:157:LEU:HA	1.86	0.44
2:H:49:PHE:HE2	2:H:55:GLU:HB2	1.82	0.44
2:I:395:PHE:CD2	2:I:422:ARG:HD3	2.52	0.44
1:o:106:TYR:HE2	1:o:403:MET:HG2	1.81	0.44
1:p:322:SER:HG	1:p:325:GLU:HB2	1.80	0.44
1:r:121:ARG:O	1:r:125:GLU:HG2	2.16	0.44
1:s:46:ARG:HB2	1:s:241:ARG:O	2.17	0.44
1:a:361:LEU:CD2	3:a:601:TA1:C17	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:67:ASP:HB2	1:b:73:MET:HE2	1.98	0.44
1:c:134:GLN:HA	1:c:165:ASN:O	2.17	0.44
1:d:172:SER:HA	1:d:173:PRO:HD3	1.89	0.44
1:d:256:ASN:ND2	2:Q:180:ALA:HA	2.32	0.44
1:d:356:ILE:HA	1:d:357:PRO:HD2	1.91	0.44
1:g:345:ILE:CG2	2:T:181:VAL:HG11	2.47	0.44
1:g:395:LEU:HD12	1:g:395:LEU:HA	1.83	0.44
1:j:106:TYR:HE2	1:j:403:MET:HG2	1.83	0.44
1:k:67:ASP:OD2	1:k:72:THR:OG1	2.32	0.44
1:l:67:ASP:OD2	1:l:72:THR:OG1	2.32	0.44
1:l:222:TYR:CE2	4:l:602:GDP:C5	3.05	0.44
2:P:258:ASN:ND2	1:p:179:VAL:N	2.51	0.44
2:V:49:PHE:HE2	2:V:55:GLU:HB2	1.81	0.44
2:V:395:PHE:CD2	2:V:422:ARG:HD3	2.52	0.44
2:W:224:TYR:OH	6:W:502:GTP:C8	2.69	0.44
2:C:10:GLY:O	2:C:14:VAL:HG23	2.17	0.44
2:F:395:PHE:CD2	2:F:422:ARG:HD3	2.52	0.44
2:J:183:GLU:HB3	2:J:184:PRO:HD3	1.99	0.44
2:K:395:PHE:CD2	2:K:422:ARG:HD3	2.52	0.44
1:s:322:SER:HG	1:s:325:GLU:HB2	1.81	0.44
1:t:67:ASP:HB2	1:t:73:MET:HE2	1.97	0.44
1:u:121:ARG:O	1:u:125:GLU:HG2	2.17	0.44
1:w:134:GLN:HA	1:w:165:ASN:O	2.18	0.44
1:x:67:ASP:OD2	1:x:72:THR:OG1	2.32	0.44
3:a:601:TA1:H441	3:a:601:TA1:C27	2.46	0.44
1:c:121:ARG:O	1:c:125:GLU:HG2	2.16	0.44
1:d:322:SER:O	1:d:326:VAL:CG2	2.65	0.44
1:e:134:GLN:HA	1:e:165:ASN:O	2.17	0.44
1:f:322:SER:O	1:f:326:VAL:CG2	2.65	0.44
1:g:391:ARG:NH1	2:G:346:TRP:CD1	2.85	0.44
1:i:23:VAL:CG1	3:i:601:TA1:C41	2.95	0.44
1:j:141:GLY:HA3	4:j:602:GDP:O5'	2.18	0.44
1:k:234:SER:HB3	3:k:601:TA1:H401	1.98	0.44
2:N:297:GLU:O	2:N:301:GLN:NE2	2.40	0.44
2:S:262:TYR:CB	2:S:263:PRO:HD2	2.25	0.44
2:S:273:ALA:HB3	2:S:291:ILE:HG23	1.99	0.44
2:S:395:PHE:CD2	2:S:422:ARG:HD3	2.52	0.44
2:U:202:PHE:HE2	2:U:238:ILE:HD13	1.83	0.44
2:U:238:ILE:HG23	2:U:255:PHE:CE2	2.52	0.44
2:V:312:TYR:HB2	2:V:343:PHE:HD1	1.83	0.44
2:X:5:ILE:HD12	2:X:135:PHE:CE1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:213:CYS:O	2:X:217:LEU:HB3	2.18	0.44
2:X:312:TYR:HB2	2:X:343:PHE:HD1	1.83	0.44
2:Y:49:PHE:HE2	2:Y:55:GLU:HB2	1.82	0.44
2:Y:183:GLU:HB3	2:Y:184:PRO:HD3	1.99	0.44
2:Z:5:ILE:HD12	2:Z:135:PHE:CE1	2.51	0.44
2:B:306:ASP:C	2:B:308:ARG:N	2.75	0.44
2:E:273:ALA:HB3	2:E:291:ILE:HG23	1.99	0.44
2:H:312:TYR:HB2	2:H:343:PHE:HD1	1.82	0.44
2:I:273:ALA:HB3	2:I:291:ILE:HG23	1.98	0.44
2:J:395:PHE:CD2	2:J:422:ARG:HD3	2.52	0.44
2:M:5:ILE:HD12	2:M:135:PHE:CE1	2.52	0.44
1:r:134:GLN:HA	1:r:165:ASN:O	2.17	0.44
1:s:403:MET:HE2	1:s:403:MET:HB3	1.87	0.44
1:t:134:GLN:HA	1:t:165:ASN:O	2.17	0.44
1:t:164:MET:HE3	1:t:164:MET:HB2	1.72	0.44
1:x:46:ARG:HB2	1:x:241:ARG:O	2.17	0.44
1:x:106:TYR:HE2	1:x:403:MET:HG2	1.82	0.44
1:y:322:SER:O	1:y:326:VAL:CG2	2.65	0.44
1:z:261:PRO:O	1:z:262:ARG:CB	2.65	0.44
1:d:67:ASP:HB2	1:d:73:MET:HE2	1.98	0.44
1:d:106:TYR:HE2	1:d:403:MET:HG2	1.82	0.44
1:h:227:HIS:HB3	3:h:601:TA1:C07	2.31	0.44
1:i:23:VAL:CG1	3:i:601:TA1:H411	2.46	0.44
1:k:46:ARG:HB2	1:k:241:ARG:O	2.17	0.44
1:k:106:TYR:HE2	1:k:403:MET:HG2	1.82	0.44
2:N:306:ASP:C	2:N:308:ARG:N	2.75	0.44
2:P:154:MET:HE1	2:P:166:LYS:HB3	1.98	0.44
2:Q:183:GLU:HB3	2:Q:184:PRO:HD3	1.99	0.44
2:Q:224:TYR:CE2	6:Q:502:GTP:C6	3.05	0.44
2:R:264:ARG:HA	2:R:266:HIS:ND1	2.31	0.44
2:S:49:PHE:HE2	2:S:55:GLU:HB2	1.81	0.44
2:T:183:GLU:HB3	2:T:184:PRO:HD3	1.99	0.44
2:T:228:ASN:OD1	6:T:502:GTP:N2	2.25	0.44
2:X:20:CYS:SG	2:X:138:PHE:HE2	2.41	0.44
2:Z:306:ASP:C	2:Z:308:ARG:N	2.75	0.44
2:A:49:PHE:HE2	2:A:55:GLU:HB2	1.81	0.44
2:B:49:PHE:HE2	2:B:55:GLU:HB2	1.81	0.44
2:F:312:TYR:HB2	2:F:343:PHE:HD1	1.82	0.44
2:G:10:GLY:O	2:G:14:VAL:HG23	2.17	0.44
2:G:395:PHE:CD2	2:G:422:ARG:HD3	2.52	0.44
2:L:49:PHE:HE2	2:L:55:GLU:HB2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:306:ASP:C	2:M:308:ARG:N	2.75	0.44
2:M:312:TYR:HB2	2:M:343:PHE:HD1	1.82	0.44
1:p:106:TYR:HE2	1:p:403:MET:HG2	1.82	0.44
1:p:134:GLN:HA	1:p:165:ASN:O	2.17	0.44
1:r:67:ASP:HB2	1:r:73:MET:HE2	1.98	0.44
1:r:322:SER:O	1:r:326:VAL:CG2	2.65	0.44
1:t:46:ARG:HB2	1:t:241:ARG:O	2.17	0.44
1:t:403:MET:HE2	1:t:403:MET:HB3	1.87	0.44
1:u:134:GLN:HA	1:u:165:ASN:O	2.17	0.44
1:w:356:ILE:HA	1:w:357:PRO:HD2	1.91	0.44
1:z:67:ASP:OD2	1:z:72:THR:OG1	2.32	0.44
1:z:134:GLN:HA	1:z:165:ASN:O	2.17	0.44
1:a:164:MET:HB2	1:a:164:MET:HE3	1.71	0.44
1:e:55:THR:CG2	2:F:284:GLU:OE2	2.57	0.44
1:e:67:ASP:HB2	1:e:73:MET:HE2	1.98	0.44
1:f:11:GLN:O	1:f:15:GLN:HG2	2.16	0.44
1:f:403:MET:HE2	1:f:403:MET:HB3	1.87	0.44
1:g:134:GLN:HA	1:g:165:ASN:O	2.17	0.44
1:h:121:ARG:O	1:h:125:GLU:HG2	2.17	0.44
1:j:222:TYR:CG	4:j:602:GDP:O6	2.70	0.44
1:l:234:SER:HB3	3:l:601:TA1:H401	2.00	0.44
1:l:322:SER:O	1:l:326:VAL:CG2	2.66	0.44
1:m:322:SER:O	1:m:326:VAL:CG2	2.65	0.44
2:N:10:GLY:O	2:N:14:VAL:HG23	2.17	0.44
2:N:49:PHE:HE2	2:N:55:GLU:HB2	1.82	0.44
2:N:395:PHE:CD2	2:N:422:ARG:HD3	2.52	0.44
2:P:10:GLY:O	2:P:14:VAL:HG23	2.17	0.44
2:S:183:GLU:HB3	2:S:184:PRO:HD3	1.99	0.44
2:S:202:PHE:HE2	2:S:238:ILE:HD13	1.82	0.44
2:S:213:CYS:O	2:S:217:LEU:HB3	2.18	0.44
2:S:326:LYS:HE2	1:s:220:PRO:CD	2.48	0.44
2:T:312:TYR:HB2	2:T:343:PHE:HD1	1.83	0.44
2:W:395:PHE:CD2	2:W:422:ARG:HD3	2.52	0.44
2:X:10:GLY:O	2:X:14:VAL:HG23	2.18	0.44
2:Z:213:CYS:O	2:Z:217:LEU:HB3	2.18	0.44
2:Z:242:LEU:HD11	2:Z:252:LEU:HG	1.99	0.44
2:A:20:CYS:SG	2:A:138:PHE:HE2	2.41	0.44
2:C:62:VAL:HG13	2:C:62:VAL:O	2.17	0.44
2:I:49:PHE:HE2	2:I:55:GLU:HB2	1.81	0.44
2:J:49:PHE:HE2	2:J:55:GLU:HB2	1.82	0.44
2:J:157:LEU:HD23	2:J:157:LEU:HA	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:10:GLY:O	2:M:14:VAL:HG23	2.17	0.44
1:n:67:ASP:HB2	1:n:73:MET:HE2	1.98	0.44
1:v:106:TYR:HE2	1:v:403:MET:HG2	1.82	0.44
1:v:356:ILE:HA	1:v:357:PRO:HD2	1.91	0.44
1:y:134:GLN:HA	1:y:165:ASN:O	2.17	0.44
1:y:329:GLN:O	1:y:333:VAL:HG23	2.18	0.44
1:z:322:SER:O	1:z:326:VAL:CG2	2.66	0.44
1:a:347:ASN:O	2:N:181:VAL:HG21	2.02	0.44
1:b:359:ARG:N	3:b:601:TA1:O13	2.49	0.44
1:c:329:GLN:O	1:c:333:VAL:HG23	2.18	0.44
1:d:329:GLN:O	1:d:333:VAL:HG23	2.18	0.44
1:e:172:SER:HA	1:e:173:PRO:HD3	1.89	0.44
1:e:322:SER:HG	1:e:325:GLU:HB2	1.83	0.44
1:g:329:GLN:O	1:g:333:VAL:HG23	2.18	0.44
1:i:274:THR:O	3:i:601:TA1:C19	2.66	0.44
1:m:227:HIS:HB3	3:m:601:TA1:HC71	2.00	0.44
1:m:246:LEU:HD11	1:m:323:MET:HE1	2.00	0.44
2:O:183:GLU:HB3	2:O:184:PRO:HD3	1.99	0.44
2:Q:136:LEU:HD23	2:Q:167:LEU:HB2	2.00	0.44
2:Q:154:MET:HE1	2:Q:166:LYS:HB3	1.98	0.44
2:Q:238:ILE:HG23	2:Q:255:PHE:CE2	2.52	0.44
2:S:171:ILE:CD1	6:S:502:GTP:N3	2.81	0.44
2:V:273:ALA:HB3	2:V:291:ILE:HG23	1.98	0.44
2:W:242:LEU:HD11	2:W:252:LEU:HG	1.99	0.44
2:Y:213:CYS:O	2:Y:217:LEU:HB3	2.18	0.44
2:Y:306:ASP:C	2:Y:308:ARG:N	2.75	0.44
2:Z:157:LEU:HD23	2:Z:157:LEU:HA	1.85	0.44
2:Z:395:PHE:CD2	2:Z:422:ARG:HD3	2.52	0.44
2:A:306:ASP:C	2:A:308:ARG:N	2.75	0.44
2:B:312:TYR:HB2	2:B:343:PHE:HD1	1.82	0.44
2:G:136:LEU:HD23	2:G:167:LEU:HB2	2.00	0.44
2:H:395:PHE:CD2	2:H:422:ARG:HD3	2.52	0.44
2:I:10:GLY:O	2:I:14:VAL:HG23	2.17	0.44
2:I:136:LEU:HD23	2:I:167:LEU:HB2	2.00	0.44
2:K:213:CYS:O	2:K:217:LEU:HB3	2.18	0.44
2:L:306:ASP:C	2:L:308:ARG:N	2.75	0.44
2:M:213:CYS:O	2:M:217:LEU:HB3	2.18	0.44
1:p:155:ILE:CG2	1:p:164:MET:HE1	2.48	0.44
1:q:155:ILE:CG2	1:q:164:MET:HE1	2.47	0.44
1:x:67:ASP:HB2	1:x:73:MET:HE2	1.99	0.44
1:x:134:GLN:HA	1:x:165:ASN:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:67:ASP:HB2	1:a:73:MET:HE2	1.98	0.44
1:a:67:ASP:OD2	1:a:72:THR:OG1	2.32	0.44
1:c:67:ASP:HB2	1:c:73:MET:HE2	1.99	0.44
1:h:106:TYR:HE2	1:h:403:MET:HG2	1.83	0.44
1:i:106:TYR:HE2	1:i:403:MET:HG2	1.83	0.44
1:k:322:SER:O	1:k:326:VAL:CG2	2.65	0.44
1:m:67:ASP:OD2	1:m:72:THR:OG1	2.32	0.44
2:N:213:CYS:O	2:N:217:LEU:HB3	2.18	0.44
2:N:312:TYR:HB2	2:N:343:PHE:HD1	1.83	0.44
2:O:49:PHE:HE2	2:O:55:GLU:HB2	1.82	0.44
2:P:304:LYS:HD2	2:P:304:LYS:HA	1.89	0.44
2:S:312:TYR:HB2	2:S:343:PHE:HD1	1.82	0.44
2:T:20:CYS:SG	2:T:138:PHE:HE2	2.41	0.44
2:T:395:PHE:CD2	2:T:422:ARG:HD3	2.52	0.44
2:U:312:TYR:HB2	2:U:343:PHE:HD1	1.83	0.44
2:X:183:GLU:HB3	2:X:184:PRO:HD3	1.99	0.44
2:Y:10:GLY:O	2:Y:14:VAL:HG23	2.17	0.44
2:Y:395:PHE:CD2	2:Y:422:ARG:HD3	2.52	0.44
2:A:62:VAL:O	2:A:62:VAL:HG13	2.18	0.44
2:A:297:GLU:O	2:A:301:GLN:NE2	2.40	0.44
2:A:395:PHE:CD2	2:A:422:ARG:HD3	2.52	0.44
2:B:10:GLY:O	2:B:14:VAL:HG23	2.17	0.44
2:C:49:PHE:HE2	2:C:55:GLU:HB2	1.82	0.44
2:C:304:LYS:HD2	2:C:304:LYS:HA	1.89	0.44
2:D:273:ALA:HB3	2:D:291:ILE:HG23	2.00	0.44
2:F:20:CYS:SG	2:F:138:PHE:HE2	2.40	0.44
2:H:21:TRP:CZ3	2:H:63:PRO:HB3	2.53	0.44
2:J:213:CYS:O	2:J:217:LEU:HB3	2.18	0.44
2:L:10:GLY:O	2:L:14:VAL:HG23	2.17	0.44
2:L:62:VAL:O	2:L:62:VAL:HG13	2.18	0.44
2:L:213:CYS:O	2:L:217:LEU:HB3	2.18	0.44
2:M:395:PHE:CD2	2:M:422:ARG:HD3	2.52	0.44
1:n:322:SER:O	1:n:326:VAL:CG2	2.65	0.44
1:p:121:ARG:O	1:p:125:GLU:HG2	2.17	0.44
1:w:46:ARG:HB2	1:w:241:ARG:O	2.18	0.44
1:c:397:TRP:CH2	2:C:256:GLN:HB3	2.52	0.44
1:d:164:MET:HE3	1:d:164:MET:HB2	1.72	0.44
1:h:222:TYR:CD1	4:h:602:GDP:N1	2.86	0.44
1:k:322:SER:HG	1:k:325:GLU:HB2	1.80	0.44
1:l:106:TYR:HE2	1:l:403:MET:HG2	1.82	0.44
1:l:395:LEU:HD12	1:l:395:LEU:HA	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:m:46:ARG:HB2	1:m:241:ARG:O	2.17	0.44
2:O:213:CYS:O	2:O:217:LEU:HB3	2.18	0.44
2:O:306:ASP:C	2:O:308:ARG:N	2.75	0.44
2:S:140:SER:HG	6:S:502:GTP:C4'	2.31	0.44
2:S:224:TYR:CZ	6:S:502:GTP:C8	3.06	0.44
2:U:224:TYR:HD2	6:U:502:GTP:C2	2.28	0.44
2:V:20:CYS:SG	2:V:138:PHE:HE2	2.41	0.44
2:V:238:ILE:HG23	2:V:255:PHE:CE2	2.53	0.44
2:W:213:CYS:O	2:W:217:LEU:HB3	2.18	0.44
2:A:285:GLN:O	2:A:287:SER:N	2.47	0.44
2:F:213:CYS:O	2:F:217:LEU:HB3	2.18	0.44
2:G:21:TRP:CZ3	2:G:63:PRO:HB3	2.53	0.44
2:H:10:GLY:O	2:H:14:VAL:HG23	2.17	0.44
2:I:21:TRP:CZ3	2:I:63:PRO:HB3	2.53	0.44
2:J:20:CYS:SG	2:J:138:PHE:HE2	2.41	0.44
2:K:20:CYS:SG	2:K:138:PHE:HE2	2.41	0.44
2:L:395:PHE:CD2	2:L:422:ARG:HD3	2.52	0.44
1:u:395:LEU:HD12	1:u:395:LEU:HA	1.82	0.44
1:b:329:GLN:O	1:b:333:VAL:HG23	2.18	0.44
1:e:164:MET:HB2	1:e:164:MET:HE3	1.72	0.44
1:i:46:ARG:HB2	1:i:241:ARG:O	2.18	0.44
1:l:46:ARG:HB2	1:l:241:ARG:O	2.17	0.44
1:l:222:TYR:CZ	4:l:602:GDP:C5	3.06	0.44
1:l:261:PRO:O	1:l:262:ARG:CB	2.65	0.44
1:l:329:GLN:O	1:l:333:VAL:HG23	2.18	0.44
2:O:238:ILE:HG23	2:O:255:PHE:CE2	2.53	0.44
2:P:183:GLU:HB3	2:P:184:PRO:HD3	1.99	0.44
2:R:136:LEU:HD23	2:R:167:LEU:HB2	2.00	0.44
2:R:183:GLU:HB3	2:R:184:PRO:HD3	1.99	0.44
2:S:194:THR:O	2:S:198:SER:OG	2.30	0.44
2:S:238:ILE:HG23	2:S:255:PHE:CE2	2.53	0.44
2:S:326:LYS:HE2	1:s:220:PRO:HD3	1.98	0.44
2:T:49:PHE:CE2	2:T:55:GLU:HB2	2.53	0.44
2:T:213:CYS:O	2:T:217:LEU:HB3	2.18	0.44
2:V:136:LEU:HD23	2:V:167:LEU:HB2	2.00	0.44
2:V:183:GLU:HB3	2:V:184:PRO:HD3	1.99	0.44
2:W:49:PHE:HE2	2:W:55:GLU:HB2	1.82	0.44
2:W:183:GLU:HB3	2:W:184:PRO:HD3	2.00	0.44
2:W:202:PHE:HE2	2:W:238:ILE:HD13	1.83	0.44
2:X:171:ILE:CD1	6:X:502:GTP:N3	2.81	0.44
2:X:306:ASP:C	2:X:308:ARG:N	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:10:GLY:O	2:Z:14:VAL:HG23	2.18	0.44
2:A:10:GLY:O	2:A:14:VAL:HG23	2.17	0.44
2:C:183:GLU:HB3	2:C:184:PRO:HD3	2.00	0.44
2:H:20:CYS:SG	2:H:138:PHE:HE2	2.41	0.44
2:I:20:CYS:SG	2:I:138:PHE:HE2	2.41	0.44
2:I:213:CYS:O	2:I:217:LEU:HB3	2.18	0.44
2:L:183:GLU:HB3	2:L:184:PRO:HD3	2.00	0.44
1:o:329:GLN:O	1:o:333:VAL:HG23	2.18	0.44
1:p:67:ASP:HB2	1:p:73:MET:HE2	1.99	0.44
1:r:274:THR:HG22	1:r:282:ARG:HD2	2.00	0.44
1:y:67:ASP:OD2	1:y:72:THR:OG1	2.32	0.44
1:y:106:TYR:HE2	1:y:403:MET:HG2	1.82	0.44
1:a:46:ARG:HB2	1:a:241:ARG:O	2.17	0.43
1:a:329:GLN:O	1:a:333:VAL:HG23	2.18	0.43
1:c:67:ASP:OD2	1:c:72:THR:OG1	2.32	0.43
1:e:86:ARG:HG3	2:F:283:HIS:HB2	2.00	0.43
1:e:256:ASN:HA	2:R:404:PHE:HE1	1.80	0.43
1:g:99:ASN:ND2	2:G:254:GLU:OE2	2.50	0.43
1:g:322:SER:O	1:g:326:VAL:CG2	2.65	0.43
1:j:255:VAL:HA	2:W:407:TRP:CE2	2.53	0.43
1:k:67:ASP:HB2	1:k:73:MET:HE2	1.99	0.43
2:N:62:VAL:O	2:N:62:VAL:HG13	2.18	0.43
2:T:258:ASN:ND2	1:t:179:VAL:N	2.53	0.43
2:U:49:PHE:CE2	2:U:55:GLU:HB2	2.53	0.43
2:U:395:PHE:CD2	2:U:422:ARG:HD3	2.52	0.43
2:V:213:CYS:O	2:V:217:LEU:HB3	2.18	0.43
2:X:49:PHE:HE2	2:X:55:GLU:HB2	1.82	0.43
2:Z:202:PHE:HE2	2:Z:238:ILE:HD13	1.83	0.43
2:Z:312:TYR:HB2	2:Z:343:PHE:HD1	1.83	0.43
2:B:183:GLU:HB3	2:B:184:PRO:HD3	2.00	0.43
2:E:20:CYS:SG	2:E:138:PHE:HE2	2.41	0.43
2:F:49:PHE:HE2	2:F:55:GLU:HB2	1.82	0.43
2:G:20:CYS:SG	2:G:138:PHE:HE2	2.41	0.43
2:H:62:VAL:O	2:H:62:VAL:HG13	2.18	0.43
2:H:136:LEU:HD23	2:H:167:LEU:HB2	2.00	0.43
2:K:49:PHE:HE2	2:K:55:GLU:HB2	1.82	0.43
2:K:128:GLN:CD	2:L:285:GLN:HG3	2.41	0.43
2:K:306:ASP:C	2:K:308:ARG:N	2.75	0.43
1:n:67:ASP:OD2	1:n:72:THR:OG1	2.32	0.43
1:n:329:GLN:O	1:n:333:VAL:HG23	2.18	0.43
1:q:86:ARG:HG3	1:r:281:TYR:CB	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:329:GLN:O	1:q:333:VAL:HG23	2.18	0.43
1:x:164:MET:HB2	1:x:164:MET:HE3	1.71	0.43
1:y:261:PRO:O	1:y:262:ARG:CB	2.65	0.43
1:z:46:ARG:HB2	1:z:241:ARG:O	2.18	0.43
1:b:46:ARG:HB2	1:b:241:ARG:O	2.17	0.43
1:b:106:TYR:HE2	1:b:403:MET:HG2	1.83	0.43
1:f:329:GLN:O	1:f:333:VAL:HG23	2.18	0.43
1:j:46:ARG:HB2	1:j:241:ARG:O	2.18	0.43
1:j:329:GLN:O	1:j:333:VAL:HG23	2.18	0.43
1:j:391:ARG:NH1	2:J:346:TRP:CD1	2.86	0.43
2:P:262:TYR:HE1	1:p:393:ALA:HA	1.83	0.43
2:R:49:PHE:HE2	2:R:55:GLU:HB2	1.82	0.43
2:V:10:GLY:O	2:V:14:VAL:HG23	2.17	0.43
2:C:213:CYS:O	2:C:217:LEU:HB3	2.18	0.43
2:E:49:PHE:HE2	2:E:55:GLU:HB2	1.82	0.43
2:F:21:TRP:CZ3	2:F:63:PRO:HB3	2.53	0.43
2:H:213:CYS:O	2:H:217:LEU:HB3	2.18	0.43
2:L:304:LYS:HD2	2:L:304:LYS:HA	1.89	0.43
1:n:164:MET:HB2	1:n:164:MET:HE3	1.71	0.43
1:o:322:SER:O	1:o:326:VAL:CG2	2.65	0.43
1:p:329:GLN:O	1:p:333:VAL:HG23	2.18	0.43
1:q:67:ASP:HB2	1:q:73:MET:HE2	1.99	0.43
1:s:121:ARG:O	1:s:125:GLU:HG2	2.18	0.43
1:t:121:ARG:O	1:t:125:GLU:HG2	2.18	0.43
1:t:155:ILE:CG2	1:t:164:MET:HE1	2.48	0.43
1:t:329:GLN:O	1:t:333:VAL:HG23	2.18	0.43
1:w:322:SER:O	1:w:326:VAL:CG2	2.66	0.43
1:w:329:GLN:O	1:w:333:VAL:HG23	2.18	0.43
1:x:322:SER:O	1:x:326:VAL:CG2	2.66	0.43
1:b:169:VAL:CG2	4:b:602:GDP:N2	2.58	0.43
1:g:140:GLY:C	4:g:602:GDP:H4'	2.43	0.43
1:h:46:ARG:HB2	1:h:241:ARG:O	2.19	0.43
1:h:141:GLY:HA2	4:h:602:GDP:O5'	2.17	0.43
1:h:322:SER:O	1:h:326:VAL:CG2	2.66	0.43
1:i:23:VAL:HG13	3:i:601:TA1:C41	2.49	0.43
1:i:179:VAL:N	2:I:258:ASN:ND2	2.54	0.43
1:i:329:GLN:O	1:i:333:VAL:HG23	2.18	0.43
1:k:12:CYS:SG	4:k:602:GDP:C2	3.11	0.43
2:O:10:GLY:O	2:O:14:VAL:HG23	2.17	0.43
2:P:49:PHE:HE2	2:P:55:GLU:HB2	1.82	0.43
2:P:306:ASP:C	2:P:308:ARG:N	2.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:21:TRP:CZ3	2:R:63:PRO:HB3	2.53	0.43
2:S:49:PHE:CE2	2:S:55:GLU:HB2	2.54	0.43
2:W:157:LEU:HD23	2:W:157:LEU:HA	1.86	0.43
2:X:221:ARG:HE	2:X:221:ARG:HB2	1.70	0.43
2:Y:62:VAL:O	2:Y:62:VAL:HG13	2.18	0.43
2:A:213:CYS:O	2:A:217:LEU:HB3	2.18	0.43
2:B:20:CYS:SG	2:B:138:PHE:HE2	2.41	0.43
2:C:136:LEU:HD23	2:C:167:LEU:HB2	2.01	0.43
2:C:306:ASP:C	2:C:308:ARG:N	2.75	0.43
2:D:49:PHE:HE2	2:D:55:GLU:HB2	1.82	0.43
2:J:10:GLY:O	2:J:14:VAL:HG23	2.17	0.43
2:J:136:LEU:HD23	2:J:167:LEU:HB2	2.00	0.43
2:K:136:LEU:HD23	2:K:167:LEU:HB2	2.00	0.43
2:M:136:LEU:HD23	2:M:167:LEU:HB2	2.01	0.43
2:M:157:LEU:HD23	2:M:157:LEU:HA	1.85	0.43
1:r:356:ILE:HA	1:r:357:PRO:HD2	1.91	0.43
1:b:179:VAL:HG22	2:B:351:PHE:HA	1.99	0.43
1:e:403:MET:HE2	1:e:403:MET:HB3	1.88	0.43
1:f:256:ASN:HA	2:S:404:PHE:HE1	1.79	0.43
1:i:322:SER:O	1:i:326:VAL:CG2	2.66	0.43
2:N:202:PHE:HE2	2:N:238:ILE:HD13	1.83	0.43
2:O:312:TYR:HB2	2:O:343:PHE:HD1	1.83	0.43
2:P:136:LEU:HD23	2:P:167:LEU:HB2	2.01	0.43
2:R:213:CYS:O	2:R:217:LEU:HB3	2.18	0.43
2:S:20:CYS:SG	2:S:138:PHE:HE2	2.41	0.43
2:U:183:GLU:HB3	2:U:184:PRO:HD3	1.99	0.43
2:V:88:HIS:CD2	2:W:283:HIS:HB2	2.52	0.43
2:Y:136:LEU:HD23	2:Y:167:LEU:HB2	2.00	0.43
2:Y:238:ILE:HG23	2:Y:255:PHE:CE2	2.53	0.43
2:Z:11:GLN:N	6:Z:502:GTP:O1B	2.47	0.43
2:A:136:LEU:HD23	2:A:167:LEU:HB2	2.01	0.43
2:D:183:GLU:HB3	2:D:184:PRO:HD3	2.00	0.43
2:G:213:CYS:O	2:G:217:LEU:HB3	2.18	0.43
2:H:285:GLN:O	2:H:287:SER:N	2.47	0.43
2:L:312:TYR:HB2	2:L:343:PHE:HD1	1.82	0.43
2:M:20:CYS:SG	2:M:138:PHE:HE2	2.41	0.43
2:M:183:GLU:HB3	2:M:184:PRO:HD3	2.00	0.43
1:n:403:MET:HE2	1:n:403:MET:HB3	1.88	0.43
1:q:86:ARG:HD3	1:r:281:TYR:HB3	2.01	0.43
1:s:329:GLN:O	1:s:333:VAL:HG23	2.18	0.43
1:t:46:ARG:HD3	1:t:46:ARG:HA	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:322:SER:HG	1:v:325:GLU:HB2	1.83	0.43
1:v:329:GLN:O	1:v:333:VAL:HG23	2.18	0.43
1:y:46:ARG:HB2	1:y:241:ARG:O	2.18	0.43
1:a:172:SER:HA	1:a:173:PRO:HD3	1.89	0.43
1:a:322:SER:O	1:a:326:VAL:CG2	2.66	0.43
1:e:67:ASP:OD2	1:e:72:THR:OG1	2.32	0.43
1:e:360:GLY:CA	3:e:601:TA1:H443	2.34	0.43
1:f:46:ARG:HB2	1:f:241:ARG:O	2.18	0.43
1:h:274:THR:O	3:h:601:TA1:C19	2.67	0.43
1:i:274:THR:O	3:i:601:TA1:H192	2.19	0.43
1:j:220:PRO:HD2	2:J:326:LYS:CG	2.29	0.43
2:O:202:PHE:HE2	2:O:238:ILE:HD13	1.83	0.43
2:P:62:VAL:O	2:P:62:VAL:HG13	2.18	0.43
2:P:213:CYS:O	2:P:217:LEU:HB3	2.18	0.43
6:P:502:GTP:H2'	6:P:502:GTP:H5''	1.64	0.43
2:Q:49:PHE:HE2	2:Q:55:GLU:HB2	1.82	0.43
2:Q:213:CYS:O	2:Q:217:LEU:HB3	2.18	0.43
2:R:20:CYS:SG	2:R:138:PHE:HE2	2.42	0.43
2:U:10:GLY:O	2:U:14:VAL:HG23	2.18	0.43
2:V:49:PHE:CE2	2:V:55:GLU:HB2	2.54	0.43
2:W:238:ILE:HG23	2:W:255:PHE:CE2	2.54	0.43
2:X:202:PHE:HE2	2:X:238:ILE:HD13	1.83	0.43
2:Y:143:GLY:HA3	6:Y:502:GTP:O2B	2.19	0.43
2:Y:256:GLN:HB3	1:y:397:TRP:CH2	2.53	0.43
2:Z:183:GLU:HB3	2:Z:184:PRO:HD3	2.00	0.43
2:B:49:PHE:CE2	2:B:55:GLU:HB2	2.54	0.43
2:C:202:PHE:HE2	2:C:238:ILE:HD13	1.84	0.43
2:D:136:LEU:HD23	2:D:167:LEU:HB2	2.01	0.43
2:E:183:GLU:HB3	2:E:184:PRO:HD3	2.00	0.43
2:F:136:LEU:HD23	2:F:167:LEU:HB2	2.00	0.43
2:J:312:TYR:HB2	2:J:343:PHE:HD1	1.82	0.43
1:q:106:TYR:HE2	1:q:403:MET:HG2	1.83	0.43
1:r:172:SER:HA	1:r:173:PRO:HD3	1.90	0.43
1:u:87:PRO:HG2	1:v:281:TYR:HE2	1.79	0.43
1:w:46:ARG:HD3	1:w:46:ARG:HA	1.88	0.43
1:b:322:SER:O	1:b:326:VAL:CG2	2.65	0.43
1:e:179:VAL:N	2:E:258:ASN:ND2	2.49	0.43
1:f:322:SER:HG	1:f:325:GLU:HB2	1.84	0.43
1:h:155:ILE:CG2	1:h:164:MET:HE1	2.49	0.43
1:j:322:SER:O	1:j:326:VAL:CG2	2.66	0.43
1:k:141:GLY:CA	4:k:602:GDP:O5'	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:136:LEU:HD23	2:N:167:LEU:HB2	2.01	0.43
2:N:238:ILE:HG23	2:N:255:PHE:CE2	2.53	0.43
2:O:62:VAL:O	2:O:62:VAL:HG13	2.18	0.43
2:T:21:TRP:CZ3	2:T:63:PRO:HB3	2.54	0.43
2:U:136:LEU:HD23	2:U:167:LEU:HB2	2.01	0.43
2:W:10:GLY:O	2:W:14:VAL:HG23	2.17	0.43
2:W:20:CYS:SG	2:W:138:PHE:HE2	2.41	0.43
2:X:238:ILE:HG23	2:X:255:PHE:CE2	2.54	0.43
2:X:262:TYR:CB	2:X:263:PRO:CD	2.97	0.43
2:Z:136:LEU:HD23	2:Z:167:LEU:HB2	2.01	0.43
2:Z:238:ILE:HG23	2:Z:255:PHE:CE2	2.53	0.43
2:D:202:PHE:HE2	2:D:238:ILE:HD13	1.84	0.43
2:F:62:VAL:HG13	2:F:62:VAL:O	2.18	0.43
2:G:202:PHE:HE2	2:G:238:ILE:HD13	1.84	0.43
2:K:62:VAL:O	2:K:62:VAL:HG13	2.18	0.43
2:L:136:LEU:HD23	2:L:167:LEU:HB2	2.01	0.43
2:M:62:VAL:O	2:M:62:VAL:HG13	2.18	0.43
1:n:293:MET:HB3	1:n:367:PHE:HB2	2.01	0.43
1:o:46:ARG:HB2	1:o:241:ARG:O	2.18	0.43
1:r:155:ILE:CG2	1:r:164:MET:HE1	2.48	0.43
1:r:322:SER:HG	1:r:325:GLU:HB2	1.84	0.43
1:u:155:ILE:CG2	1:u:164:MET:HE1	2.49	0.43
1:v:155:ILE:CG2	1:v:164:MET:HE1	2.49	0.43
1:c:322:SER:O	1:c:326:VAL:CG2	2.66	0.43
1:e:23:VAL:HG13	3:e:601:TA1:H421	2.00	0.43
1:l:87:PRO:HD3	1:m:281:TYR:CD2	2.53	0.43
1:m:329:GLN:O	1:m:333:VAL:HG23	2.18	0.43
2:N:283:HIS:CB	2:Z:88:HIS:CD2	3.01	0.43
2:Q:202:PHE:HE2	2:Q:238:ILE:HD13	1.84	0.43
2:Q:312:TYR:HB2	2:Q:343:PHE:HD1	1.83	0.43
2:R:202:PHE:HE2	2:R:238:ILE:HD13	1.84	0.43
2:S:136:LEU:HD23	2:S:167:LEU:HB2	2.00	0.43
2:U:21:TRP:CZ3	2:U:63:PRO:HB3	2.54	0.43
2:U:213:CYS:O	2:U:217:LEU:HB3	2.18	0.43
2:W:312:TYR:HB2	2:W:343:PHE:HD1	1.83	0.43
2:X:136:LEU:HD23	2:X:167:LEU:HB2	2.01	0.43
2:Y:100:ALA:N	6:Y:502:GTP:O2G	2.44	0.43
2:Y:304:LYS:HA	2:Y:304:LYS:HD2	1.89	0.43
2:Z:62:VAL:O	2:Z:62:VAL:HG13	2.18	0.43
2:C:221:ARG:HE	2:C:221:ARG:HB2	1.70	0.43
2:D:89:PRO:HD3	2:E:283:HIS:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:312:TYR:HB2	2:D:343:PHE:HD1	1.83	0.43
2:E:157:LEU:HD23	2:E:157:LEU:HA	1.85	0.43
2:G:49:PHE:CE2	2:G:55:GLU:HB2	2.54	0.43
2:L:20:CYS:SG	2:L:138:PHE:HE2	2.41	0.43
1:p:67:ASP:OD2	1:p:72:THR:OG1	2.32	0.43
1:p:293:MET:HB3	1:p:367:PHE:HB2	2.01	0.43
1:r:67:ASP:OD2	1:r:72:THR:OG1	2.32	0.43
1:s:172:SER:HA	1:s:173:PRO:HD3	1.89	0.43
1:x:329:GLN:O	1:x:333:VAL:HG23	2.18	0.43
1:z:329:GLN:O	1:z:333:VAL:HG23	2.18	0.43
1:b:293:MET:HB3	1:b:367:PHE:HB2	2.01	0.43
1:e:322:SER:O	1:e:326:VAL:CG2	2.66	0.43
1:g:143:THR:HB	4:g:602:GDP:O1B	2.17	0.43
1:g:155:ILE:CG2	1:g:164:MET:HE1	2.49	0.43
1:i:155:ILE:CG2	1:i:164:MET:HE1	2.49	0.43
1:j:215:LEU:CD2	3:j:601:TA1:C14	2.97	0.43
1:k:261:PRO:O	1:k:262:ARG:CB	2.65	0.43
1:k:329:GLN:O	1:k:333:VAL:HG23	2.18	0.43
1:l:359:ARG:N	3:l:601:TA1:O13	2.50	0.43
1:m:208:TYR:CE1	2:M:326:LYS:HB3	2.53	0.43
1:m:293:MET:HB3	1:m:367:PHE:HB2	2.01	0.43
2:N:183:GLU:HB3	2:N:184:PRO:HD3	1.99	0.43
2:R:62:VAL:O	2:R:62:VAL:HG13	2.18	0.43
2:W:306:ASP:C	2:W:308:ARG:N	2.75	0.43
2:A:49:PHE:CE2	2:A:55:GLU:HB2	2.54	0.43
2:A:88:HIS:CB	2:B:283:HIS:CG	2.98	0.43
2:E:136:LEU:HD23	2:E:167:LEU:HB2	2.01	0.43
2:G:221:ARG:HE	2:G:221:ARG:HB2	1.70	0.43
2:I:49:PHE:CE2	2:I:55:GLU:HB2	2.54	0.43
2:J:306:ASP:C	2:J:308:ARG:N	2.75	0.43
2:M:21:TRP:CZ3	2:M:63:PRO:HB3	2.54	0.43
2:M:202:PHE:HE2	2:M:238:ILE:HD13	1.84	0.43
1:n:46:ARG:HB2	1:n:241:ARG:O	2.18	0.43
1:t:322:SER:HG	1:t:325:GLU:HB2	1.82	0.43
1:v:322:SER:O	1:v:326:VAL:CG2	2.66	0.43
1:a:293:MET:HB3	1:a:367:PHE:HB2	2.01	0.43
1:d:129:CYS:SG	2:Q:97:GLU:OE2	2.76	0.43
1:d:261:PRO:O	1:d:262:ARG:CB	2.65	0.43
1:f:172:SER:HA	1:f:173:PRO:HD3	1.89	0.43
1:g:234:SER:CB	3:g:601:TA1:H411	2.49	0.43
2:O:136:LEU:HD23	2:O:167:LEU:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:109:THR:OG1	2:P:411:GLU:O	2.37	0.43
2:S:88:HIS:CD2	2:T:283:HIS:CB	3.01	0.43
2:W:136:LEU:HD23	2:W:167:LEU:HB2	2.01	0.43
2:A:183:GLU:HB3	2:A:184:PRO:HD3	1.99	0.43
2:C:49:PHE:CE2	2:C:55:GLU:HB2	2.54	0.43
2:C:109:THR:OG1	2:C:411:GLU:O	2.37	0.43
2:C:194:THR:O	2:C:198:SER:OG	2.30	0.43
2:E:213:CYS:O	2:E:217:LEU:HB3	2.18	0.43
2:J:62:VAL:O	2:J:62:VAL:HG13	2.18	0.43
2:K:183:GLU:HB3	2:K:184:PRO:HD3	2.00	0.43
2:L:285:GLN:O	2:L:287:SER:N	2.47	0.43
1:n:16:ILE:O	1:n:20:PHE:N	2.52	0.43
1:o:46:ARG:HD3	1:o:46:ARG:HA	1.88	0.43
1:q:261:PRO:O	1:q:262:ARG:CB	2.65	0.43
1:b:46:ARG:HD3	1:b:46:ARG:HA	1.88	0.43
1:b:169:VAL:HG11	4:b:602:GDP:N2	2.33	0.43
1:b:212:PHE:HZ	2:B:326:LYS:HD3	1.81	0.43
1:d:322:SER:HG	1:d:325:GLU:HB2	1.83	0.43
1:d:331:LEU:HD11	2:Q:176:GLN:HB3	1.99	0.43
1:f:106:TYR:HE2	1:f:403:MET:HG2	1.83	0.43
1:g:23:VAL:CG1	3:g:601:TA1:C42	2.93	0.43
1:g:179:VAL:N	2:G:258:ASN:ND2	2.53	0.43
1:g:255:VAL:HA	2:T:407:TRP:CE2	2.54	0.43
1:g:293:MET:HB3	1:g:367:PHE:HB2	2.01	0.43
1:h:293:MET:HB3	1:h:367:PHE:HB2	2.01	0.43
1:l:215:LEU:HD22	3:l:601:TA1:C14	2.49	0.43
2:Q:20:CYS:SG	2:Q:138:PHE:HE2	2.41	0.43
2:R:109:THR:OG1	2:R:411:GLU:O	2.37	0.43
2:U:62:VAL:O	2:U:62:VAL:HG13	2.18	0.43
2:A:21:TRP:CZ3	2:A:63:PRO:HB3	2.54	0.43
2:D:213:CYS:O	2:D:217:LEU:HB3	2.18	0.43
2:D:262:TYR:CB	2:D:263:PRO:CD	2.97	0.43
2:E:21:TRP:CZ3	2:E:63:PRO:HB3	2.54	0.43
2:E:109:THR:OG1	2:E:411:GLU:O	2.37	0.43
2:F:183:GLU:HB3	2:F:184:PRO:HD3	2.01	0.43
2:F:304:LYS:HD2	2:F:304:LYS:HA	1.89	0.43
2:H:49:PHE:CE2	2:H:55:GLU:HB2	2.54	0.43
2:J:285:GLN:O	2:J:287:SER:N	2.47	0.43
2:K:262:TYR:CB	2:K:263:PRO:CD	2.97	0.43
2:K:297:GLU:O	2:K:301:GLN:NE2	2.40	0.43
2:L:21:TRP:CZ3	2:L:63:PRO:HB3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:293:MET:HB3	1:o:367:PHE:HB2	2.01	0.43
1:s:293:MET:HB3	1:s:367:PHE:HB2	2.01	0.43
1:u:322:SER:HG	1:u:325:GLU:HB2	1.82	0.43
1:z:293:MET:HB3	1:z:367:PHE:HB2	2.01	0.43
1:c:46:ARG:HD3	1:c:46:ARG:HA	1.88	0.42
1:c:261:PRO:O	1:c:262:ARG:CB	2.64	0.42
1:f:46:ARG:HA	1:f:46:ARG:HD3	1.87	0.42
1:i:215:LEU:HD22	3:i:601:TA1:H142	2.01	0.42
1:l:256:ASN:HA	2:Y:404:PHE:HE1	1.83	0.42
2:P:88:HIS:CD2	2:Q:283:HIS:HB3	2.51	0.42
2:Q:12:ALA:HB2	6:Q:502:GTP:C4	2.53	0.42
2:Q:262:TYR:CB	2:Q:263:PRO:CD	2.97	0.42
2:R:306:ASP:C	2:R:308:ARG:N	2.75	0.42
2:S:21:TRP:CZ3	2:S:63:PRO:HB3	2.54	0.42
2:S:44:GLY:O	2:S:48:SER:N	2.52	0.42
2:S:109:THR:OG1	2:S:411:GLU:O	2.37	0.42
2:S:304:LYS:HD2	2:S:304:LYS:HA	1.89	0.42
2:U:224:TYR:OH	6:U:502:GTP:H2'	2.19	0.42
2:V:306:ASP:C	2:V:308:ARG:N	2.75	0.42
2:Z:21:TRP:CZ3	2:Z:63:PRO:HB3	2.54	0.42
2:B:304:LYS:HD2	2:B:304:LYS:HA	1.90	0.42
2:E:44:GLY:O	2:E:48:SER:N	2.52	0.42
2:F:109:THR:OG1	2:F:411:GLU:O	2.37	0.42
2:F:262:TYR:CB	2:F:263:PRO:HD2	2.26	0.42
2:G:62:VAL:O	2:G:62:VAL:HG13	2.18	0.42
2:J:21:TRP:CZ3	2:J:63:PRO:HB3	2.54	0.42
2:J:49:PHE:CE2	2:J:55:GLU:HB2	2.54	0.42
2:J:202:PHE:HE2	2:J:238:ILE:HD13	1.84	0.42
1:r:232:THR:O	1:r:236:VAL:HG23	2.19	0.42
1:r:329:GLN:O	1:r:333:VAL:HG23	2.18	0.42
1:y:293:MET:HB3	1:y:367:PHE:HB2	2.01	0.42
1:a:218:THR:O	2:A:326:LYS:NZ	2.50	0.42
1:h:220:PRO:HD2	2:H:326:LYS:CG	2.25	0.42
1:h:329:GLN:O	1:h:333:VAL:HG23	2.18	0.42
1:j:232:THR:O	1:j:236:VAL:HG23	2.19	0.42
1:j:293:MET:HB3	1:j:367:PHE:HB2	2.01	0.42
1:k:23:VAL:HG13	3:k:601:TA1:C42	2.49	0.42
1:l:232:THR:O	1:l:236:VAL:HG23	2.19	0.42
2:O:21:TRP:CZ3	2:O:63:PRO:HB3	2.54	0.42
2:P:194:THR:O	2:P:198:SER:OG	2.30	0.42
2:R:157:LEU:HD23	2:R:157:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:88:HIS:CD2	2:U:283:HIS:CB	3.02	0.42
2:U:109:THR:OG1	2:U:411:GLU:O	2.37	0.42
2:U:285:GLN:O	2:U:287:SER:N	2.46	0.42
2:V:21:TRP:CZ3	2:V:63:PRO:HB3	2.54	0.42
2:V:202:PHE:HE2	2:V:238:ILE:HD13	1.83	0.42
2:W:49:PHE:CE2	2:W:55:GLU:HB2	2.54	0.42
2:Y:20:CYS:SG	2:Y:138:PHE:HE2	2.42	0.42
2:Y:21:TRP:CZ3	2:Y:63:PRO:HB3	2.54	0.42
2:B:136:LEU:HD23	2:B:167:LEU:HB2	2.01	0.42
2:B:213:CYS:O	2:B:217:LEU:HB3	2.18	0.42
2:E:202:PHE:HE2	2:E:238:ILE:HD13	1.84	0.42
2:F:44:GLY:O	2:F:48:SER:N	2.52	0.42
2:H:109:THR:OG1	2:H:411:GLU:O	2.37	0.42
2:I:183:GLU:HB3	2:I:184:PRO:HD3	2.00	0.42
2:I:306:ASP:C	2:I:308:ARG:N	2.75	0.42
2:K:21:TRP:CZ3	2:K:63:PRO:HB3	2.54	0.42
1:n:155:ILE:CG2	1:n:164:MET:HE1	2.49	0.42
1:s:261:PRO:O	1:s:262:ARG:CB	2.65	0.42
1:t:106:TYR:HE2	1:t:403:MET:HG2	1.84	0.42
1:t:293:MET:HB3	1:t:367:PHE:HB2	2.01	0.42
1:t:395:LEU:HD12	1:t:395:LEU:HA	1.82	0.42
1:y:232:THR:O	1:y:236:VAL:HG23	2.19	0.42
1:z:16:ILE:O	1:z:20:PHE:N	2.52	0.42
1:b:403:MET:HE2	1:b:403:MET:HB3	1.87	0.42
1:c:293:MET:HB3	1:c:367:PHE:HB2	2.01	0.42
1:e:347:ASN:O	2:R:181:VAL:HG21	2.04	0.42
1:e:361:LEU:HD23	3:e:601:TA1:H171	2.01	0.42
1:f:232:THR:O	1:f:236:VAL:HG23	2.19	0.42
1:f:293:MET:HB3	1:f:367:PHE:HB2	2.01	0.42
1:g:397:TRP:CH2	2:G:256:GLN:HB3	2.54	0.42
1:k:232:THR:O	1:k:236:VAL:HG23	2.19	0.42
1:l:179:VAL:N	2:L:258:ASN:ND2	2.51	0.42
1:l:293:MET:HB3	1:l:367:PHE:HB2	2.01	0.42
2:O:49:PHE:CE2	2:O:55:GLU:HB2	2.55	0.42
2:S:285:GLN:O	2:S:287:SER:N	2.47	0.42
2:T:368:LEU:N	2:T:368:LEU:HD12	2.35	0.42
2:U:306:ASP:C	2:U:308:ARG:N	2.75	0.42
2:X:62:VAL:O	2:X:62:VAL:HG13	2.19	0.42
2:Z:20:CYS:SG	2:Z:138:PHE:HE2	2.42	0.42
2:D:49:PHE:CE2	2:D:55:GLU:HB2	2.54	0.42
2:F:49:PHE:CE2	2:F:55:GLU:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:183:GLU:HB3	2:G:184:PRO:HD3	2.01	0.42
1:p:46:ARG:HD3	1:p:46:ARG:HA	1.88	0.42
1:p:232:THR:O	1:p:236:VAL:HG23	2.19	0.42
1:r:261:PRO:O	1:r:262:ARG:CB	2.65	0.42
1:r:403:MET:HE2	1:r:403:MET:HB3	1.88	0.42
1:u:329:GLN:O	1:u:333:VAL:HG23	2.18	0.42
1:w:232:THR:O	1:w:236:VAL:HG23	2.19	0.42
1:x:232:THR:O	1:x:236:VAL:HG23	2.19	0.42
1:z:232:THR:O	1:z:236:VAL:HG23	2.19	0.42
1:a:16:ILE:O	1:a:20:PHE:N	2.53	0.42
1:e:261:PRO:O	1:e:262:ARG:CB	2.65	0.42
1:f:395:LEU:HD12	1:f:395:LEU:HA	1.83	0.42
2:N:21:TRP:CZ3	2:N:63:PRO:HB3	2.54	0.42
2:P:224:TYR:CZ	6:P:502:GTP:C4	3.07	0.42
2:Q:21:TRP:CZ3	2:Q:63:PRO:HB3	2.54	0.42
2:R:44:GLY:O	2:R:48:SER:N	2.53	0.42
2:T:44:GLY:O	2:T:48:SER:N	2.52	0.42
2:T:326:LYS:HB3	1:t:208:TYR:CE1	2.55	0.42
2:W:21:TRP:CZ3	2:W:63:PRO:HB3	2.54	0.42
2:X:12:ALA:HB2	6:X:502:GTP:C4	2.54	0.42
2:X:49:PHE:CE2	2:X:55:GLU:HB2	2.54	0.42
2:X:304:LYS:HA	2:X:304:LYS:HD2	1.89	0.42
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.54	0.42
2:D:62:VAL:HG13	2:D:62:VAL:O	2.18	0.42
2:G:44:GLY:O	2:G:48:SER:N	2.52	0.42
2:H:306:ASP:C	2:H:308:ARG:N	2.75	0.42
2:K:202:PHE:HE2	2:K:238:ILE:HD13	1.84	0.42
1:n:172:SER:HA	1:n:173:PRO:HD3	1.89	0.42
1:o:16:ILE:O	1:o:20:PHE:N	2.52	0.42
1:t:232:THR:O	1:t:236:VAL:HG23	2.19	0.42
1:u:232:THR:O	1:u:236:VAL:HG23	2.19	0.42
1:x:261:PRO:O	1:x:262:ARG:CB	2.65	0.42
1:b:16:ILE:O	1:b:20:PHE:N	2.53	0.42
3:c:601:TA1:H463	3:c:601:TA1:C26	2.49	0.42
1:d:360:GLY:HA3	3:d:601:TA1:C44	2.45	0.42
1:e:232:THR:O	1:e:236:VAL:HG23	2.19	0.42
1:g:220:PRO:HD2	2:G:326:LYS:CG	2.28	0.42
1:h:232:THR:O	1:h:236:VAL:HG23	2.19	0.42
1:i:322:SER:HG	1:i:325:GLU:HB2	1.84	0.42
1:m:232:THR:O	1:m:236:VAL:HG23	2.20	0.42
2:N:20:CYS:SG	2:N:138:PHE:HE2	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:285:GLN:O	2:N:287:SER:N	2.46	0.42
2:O:122:ILE:O	2:O:126:ALA:N	2.53	0.42
2:P:20:CYS:SG	2:P:138:PHE:HE2	2.41	0.42
2:Q:44:GLY:O	2:Q:48:SER:N	2.53	0.42
2:R:49:PHE:CE2	2:R:55:GLU:HB2	2.55	0.42
2:S:284:GLU:OE2	1:r:55:THR:CG2	2.62	0.42
2:U:122:ILE:O	2:U:126:ALA:N	2.53	0.42
2:U:140:SER:OG	6:U:502:GTP:C4'	2.66	0.42
2:V:12:ALA:HB2	6:V:502:GTP:C4	2.55	0.42
2:W:62:VAL:O	2:W:62:VAL:HG13	2.19	0.42
2:Y:202:PHE:HE2	2:Y:238:ILE:HD13	1.83	0.42
2:D:20:CYS:SG	2:D:138:PHE:HE2	2.42	0.42
2:D:44:GLY:O	2:D:48:SER:N	2.52	0.42
2:E:324:VAL:HA	2:E:325:PRO:HD3	1.94	0.42
2:F:88:HIS:CD2	2:G:283:HIS:CA	2.91	0.42
1:s:232:THR:O	1:s:236:VAL:HG23	2.19	0.42
1:c:232:THR:O	1:c:236:VAL:HG23	2.19	0.42
1:d:138:SER:OG	4:d:602:GDP:H1'	2.19	0.42
1:g:46:ARG:HB2	1:g:241:ARG:O	2.19	0.42
1:g:172:SER:HA	1:g:173:PRO:HD3	1.89	0.42
1:g:232:THR:O	1:g:236:VAL:HG23	2.19	0.42
1:i:293:MET:HB3	1:i:367:PHE:HB2	2.01	0.42
1:m:16:ILE:O	1:m:20:PHE:N	2.53	0.42
2:O:109:THR:OG1	2:O:411:GLU:O	2.37	0.42
2:O:304:LYS:HD2	2:O:304:LYS:HA	1.89	0.42
2:Q:49:PHE:CE2	2:Q:55:GLU:HB2	2.55	0.42
2:S:62:VAL:O	2:S:62:VAL:HG13	2.18	0.42
2:T:282:TYR:O	2:T:283:HIS:C	2.61	0.42
2:X:21:TRP:CZ3	2:X:63:PRO:HB3	2.54	0.42
2:X:297:GLU:O	2:X:301:GLN:NE2	2.40	0.42
2:Y:312:TYR:HB2	2:Y:343:PHE:HD1	1.83	0.42
2:Z:221:ARG:HE	2:Z:221:ARG:HB2	1.70	0.42
2:A:202:PHE:HE2	2:A:238:ILE:HD13	1.84	0.42
2:B:44:GLY:O	2:B:48:SER:N	2.52	0.42
2:E:49:PHE:CE2	2:E:55:GLU:HB2	2.55	0.42
2:F:285:GLN:O	2:F:287:SER:N	2.47	0.42
2:H:183:GLU:HB3	2:H:184:PRO:HD3	2.01	0.42
2:H:202:PHE:HE2	2:H:238:ILE:HD13	1.84	0.42
2:I:62:VAL:HG13	2:I:62:VAL:O	2.18	0.42
2:J:16:ILE:HD11	2:J:171:ILE:HD11	2.02	0.42
2:M:49:PHE:CE2	2:M:55:GLU:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:p:16:ILE:O	1:p:20:PHE:N	2.52	0.42
1:q:293:MET:HB3	1:q:367:PHE:HB2	2.01	0.42
1:v:69:GLU:HA	1:v:70:PRO:HD3	1.92	0.42
1:w:155:ILE:CG2	1:w:164:MET:HE1	2.49	0.42
1:x:293:MET:HB3	1:x:367:PHE:HB2	2.01	0.42
1:y:155:ILE:CG2	1:y:164:MET:HE1	2.49	0.42
1:c:16:ILE:O	1:c:20:PHE:N	2.53	0.42
1:d:293:MET:HB3	1:d:367:PHE:HB2	2.01	0.42
1:f:155:ILE:CG2	1:f:164:MET:HE1	2.49	0.42
1:j:255:VAL:HG22	2:W:407:TRP:CE3	2.54	0.42
2:N:49:PHE:CE2	2:N:55:GLU:HB2	2.55	0.42
2:O:285:GLN:O	2:O:287:SER:N	2.47	0.42
2:P:49:PHE:CE2	2:P:55:GLU:HB2	2.55	0.42
2:P:262:TYR:CB	2:P:263:PRO:CD	2.97	0.42
2:T:62:VAL:HG13	2:T:62:VAL:O	2.18	0.42
2:T:256:GLN:H	2:T:256:GLN:HG3	1.62	0.42
2:T:306:ASP:C	2:T:308:ARG:N	2.75	0.42
2:V:62:VAL:O	2:V:62:VAL:HG13	2.18	0.42
2:Z:16:ILE:HD11	2:Z:171:ILE:HD11	2.02	0.42
2:B:62:VAL:O	2:B:62:VAL:HG13	2.19	0.42
2:B:109:THR:OG1	2:B:411:GLU:O	2.37	0.42
2:H:122:ILE:O	2:H:126:ALA:N	2.53	0.42
2:I:202:PHE:HE2	2:I:238:ILE:HD13	1.84	0.42
2:L:202:PHE:HE2	2:L:238:ILE:HD13	1.84	0.42
1:s:67:ASP:OD2	1:s:72:THR:OG1	2.32	0.42
1:y:16:ILE:O	1:y:20:PHE:N	2.53	0.42
1:a:138:SER:HB3	4:a:602:GDP:O2'	2.20	0.42
1:b:12:CYS:SG	4:b:602:GDP:H1'	2.49	0.42
1:b:155:ILE:CG2	1:b:164:MET:HE1	2.50	0.42
1:b:214:THR:HG22	1:b:273:LEU:O	2.20	0.42
1:d:403:MET:HE2	1:d:403:MET:HB3	1.87	0.42
1:f:261:PRO:O	1:f:262:ARG:CB	2.65	0.42
1:h:222:TYR:CD1	4:h:602:GDP:C6	3.06	0.42
1:i:69:GLU:HA	1:i:70:PRO:HD3	1.92	0.42
1:l:256:ASN:ND2	2:Y:180:ALA:HA	2.34	0.42
1:m:395:LEU:HD12	1:m:395:LEU:HA	1.83	0.42
2:N:224:TYR:CG	6:N:502:GTP:C6	3.07	0.42
2:P:202:PHE:HE2	2:P:238:ILE:HD13	1.85	0.42
2:V:326:LYS:CE	1:v:218:THR:O	2.68	0.42
2:C:44:GLY:O	2:C:48:SER:N	2.52	0.42
2:D:109:THR:OG1	2:D:411:GLU:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:122:ILE:O	2:E:126:ALA:N	2.53	0.42
2:G:306:ASP:C	2:G:308:ARG:N	2.75	0.42
2:K:49:PHE:CE2	2:K:55:GLU:HB2	2.55	0.42
2:L:44:GLY:O	2:L:48:SER:N	2.52	0.42
2:L:256:GLN:H	2:L:256:GLN:HG3	1.62	0.42
1:q:286:VAL:HG23	1:q:363:MET:HE3	2.00	0.42
1:v:293:MET:HB3	1:v:367:PHE:HB2	2.01	0.42
1:z:155:ILE:CG2	1:z:164:MET:HE1	2.50	0.42
1:a:155:ILE:CG2	1:a:164:MET:HE1	2.50	0.42
1:c:222:TYR:CD1	4:c:602:GDP:O6	2.70	0.42
1:d:16:ILE:O	1:d:20:PHE:N	2.52	0.42
1:e:12:CYS:HB2	4:e:602:GDP:C5	2.55	0.42
1:f:12:CYS:CB	4:f:602:GDP:C4	3.03	0.42
1:k:293:MET:HB3	1:k:367:PHE:HB2	2.01	0.42
2:N:109:THR:OG1	2:N:411:GLU:O	2.37	0.42
2:O:20:CYS:SG	2:O:138:PHE:HE2	2.42	0.42
2:O:224:TYR:CE2	6:O:502:GTP:C6	3.08	0.42
2:P:44:GLY:O	2:P:48:SER:N	2.52	0.42
2:Q:109:THR:OG1	2:Q:411:GLU:O	2.37	0.42
2:R:326:LYS:HE2	1:r:218:THR:O	2.20	0.42
2:T:109:THR:OG1	2:T:411:GLU:O	2.37	0.42
2:T:262:TYR:HE2	2:T:435:VAL:CG2	2.33	0.42
2:V:44:GLY:O	2:V:48:SER:N	2.52	0.42
2:W:122:ILE:O	2:W:126:ALA:N	2.53	0.42
2:Y:44:GLY:O	2:Y:48:SER:N	2.52	0.42
2:Z:49:PHE:CE2	2:Z:55:GLU:HB2	2.54	0.42
2:Z:109:THR:OG1	2:Z:411:GLU:O	2.37	0.42
2:A:44:GLY:O	2:A:48:SER:N	2.52	0.42
2:A:109:THR:OG1	2:A:411:GLU:O	2.37	0.42
2:B:280:LYS:HB3	2:B:280:LYS:HE2	1.80	0.42
2:C:21:TRP:CZ3	2:C:63:PRO:HB3	2.54	0.42
2:F:262:TYR:HE2	2:F:435:VAL:CG2	2.30	0.42
2:I:44:GLY:O	2:I:48:SER:N	2.52	0.42
2:J:122:ILE:O	2:J:126:ALA:N	2.53	0.42
2:K:194:THR:O	2:K:198:SER:OG	2.30	0.42
2:M:109:THR:OG1	2:M:411:GLU:O	2.37	0.42
1:n:232:THR:O	1:n:236:VAL:HG23	2.19	0.42
1:q:232:THR:O	1:q:236:VAL:HG23	2.19	0.42
1:r:16:ILE:O	1:r:20:PHE:N	2.52	0.42
1:u:293:MET:HB3	1:u:367:PHE:HB2	2.01	0.42
1:x:155:ILE:CG2	1:x:164:MET:HE1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:y:207:LEU:HB3	1:y:225:LEU:HD22	2.02	0.42
1:a:232:THR:O	1:a:236:VAL:HG23	2.19	0.42
1:c:218:THR:O	2:C:326:LYS:NZ	2.47	0.42
1:c:246:LEU:HD11	1:c:323:MET:HE1	2.02	0.42
1:c:322:SER:HG	1:c:325:GLU:HB2	1.83	0.42
1:d:214:THR:HG22	1:d:273:LEU:O	2.20	0.42
1:d:232:THR:O	1:d:236:VAL:HG23	2.19	0.42
1:e:16:ILE:O	1:e:20:PHE:N	2.53	0.42
1:f:16:ILE:O	1:f:20:PHE:N	2.53	0.42
1:i:46:ARG:HA	1:i:46:ARG:HD3	1.87	0.42
1:i:214:THR:HG22	1:i:273:LEU:O	2.20	0.42
1:i:232:THR:O	1:i:236:VAL:HG23	2.19	0.42
1:j:214:THR:HG22	1:j:273:LEU:O	2.20	0.42
1:m:256:ASN:HD21	1:m:350:LYS:HD2	1.84	0.42
3:m:601:TA1:H091	3:m:601:TA1:H141	2.01	0.42
2:N:44:GLY:O	2:N:48:SER:N	2.52	0.42
2:Q:62:VAL:O	2:Q:62:VAL:HG13	2.18	0.42
2:R:122:ILE:O	2:R:126:ALA:N	2.53	0.42
2:S:306:ASP:C	2:S:308:ARG:N	2.75	0.42
2:S:324:VAL:HA	2:S:325:PRO:HD3	1.93	0.42
2:T:238:ILE:HG23	2:T:255:PHE:CE2	2.54	0.42
2:T:262:TYR:CB	2:T:263:PRO:HD2	2.25	0.42
2:U:368:LEU:HD12	2:U:368:LEU:N	2.35	0.42
2:V:171:ILE:CD1	6:V:502:GTP:N3	2.82	0.42
2:W:171:ILE:HD11	6:W:502:GTP:C2	2.55	0.42
2:Y:49:PHE:CE2	2:Y:55:GLU:HB2	2.54	0.42
2:Y:122:ILE:O	2:Y:126:ALA:N	2.53	0.42
2:Z:324:VAL:HA	2:Z:325:PRO:HD3	1.93	0.42
2:B:122:ILE:O	2:B:126:ALA:N	2.53	0.42
2:D:285:GLN:O	2:D:287:SER:N	2.47	0.42
2:F:79:ARG:NH2	2:F:94:THR:HG21	2.35	0.42
2:G:109:THR:OG1	2:G:411:GLU:O	2.37	0.42
2:K:79:ARG:NH2	2:K:94:THR:HG21	2.35	0.42
2:L:122:ILE:O	2:L:126:ALA:N	2.53	0.42
1:q:16:ILE:O	1:q:20:PHE:N	2.52	0.42
1:v:232:THR:O	1:v:236:VAL:HG23	2.19	0.42
1:z:395:LEU:HD12	1:z:395:LEU:HA	1.82	0.42
1:a:138:SER:OG	4:a:602:GDP:N2	2.53	0.41
1:c:214:THR:HG22	1:c:273:LEU:O	2.20	0.41
1:d:23:VAL:HG11	3:d:601:TA1:C41	2.49	0.41
1:f:214:THR:HG22	1:f:273:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:12:CYS:SG	4:g:602:GDP:N1	2.93	0.41
1:g:215:LEU:HD21	3:g:601:TA1:O06	2.20	0.41
1:g:274:THR:O	3:g:601:TA1:H192	2.20	0.41
1:g:322:SER:HG	1:g:325:GLU:HB2	1.85	0.41
1:g:415:MET:HE3	1:g:415:MET:HB2	1.90	0.41
1:h:23:VAL:CG1	3:h:601:TA1:H411	2.49	0.41
1:j:11:GLN:CB	4:j:602:GDP:O2B	2.67	0.41
3:k:601:TA1:C26	3:k:601:TA1:C46	2.98	0.41
1:l:16:ILE:O	1:l:20:PHE:N	2.53	0.41
2:O:44:GLY:O	2:O:48:SER:N	2.52	0.41
2:U:224:TYR:OH	6:U:502:GTP:C2'	2.67	0.41
2:V:140:SER:OG	6:V:502:GTP:H4'	2.20	0.41
2:W:16:ILE:HD11	2:W:171:ILE:HD11	2.02	0.41
2:Y:16:ILE:HD11	2:Y:171:ILE:HD11	2.02	0.41
2:B:285:GLN:O	2:B:287:SER:N	2.48	0.41
2:F:202:PHE:HE2	2:F:238:ILE:HD13	1.84	0.41
2:G:79:ARG:NH2	2:G:94:THR:HG21	2.35	0.41
2:I:79:ARG:NH2	2:I:94:THR:HG21	2.35	0.41
2:K:304:LYS:HA	2:K:304:LYS:HD2	1.89	0.41
2:M:324:VAL:HA	2:M:325:PRO:HD3	1.93	0.41
1:q:86:ARG:HG3	1:r:281:TYR:CD2	2.55	0.41
1:t:207:LEU:HB3	1:t:225:LEU:HD22	2.02	0.41
1:v:46:ARG:HA	1:v:46:ARG:HD3	1.88	0.41
1:x:16:ILE:O	1:x:20:PHE:N	2.52	0.41
1:x:207:LEU:HB3	1:x:225:LEU:HD22	2.01	0.41
1:a:214:THR:HG22	1:a:273:LEU:O	2.20	0.41
1:b:218:THR:O	2:B:326:LYS:CE	2.68	0.41
1:k:214:THR:HG22	1:k:273:LEU:O	2.20	0.41
1:m:164:MET:HE3	1:m:164:MET:HB2	1.71	0.41
2:P:21:TRP:CZ3	2:P:63:PRO:HB3	2.54	0.41
2:R:304:LYS:HD2	2:R:304:LYS:HA	1.90	0.41
2:X:44:GLY:O	2:X:48:SER:N	2.52	0.41
2:X:67:PHE:HB2	2:X:92:LEU:CD2	2.47	0.41
2:X:109:THR:OG1	2:X:411:GLU:O	2.37	0.41
2:X:194:THR:O	2:X:198:SER:OG	2.30	0.41
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.54	0.41
2:C:262:TYR:HE2	2:C:435:VAL:CG2	2.32	0.41
2:F:306:ASP:C	2:F:308:ARG:N	2.75	0.41
2:J:44:GLY:O	2:J:48:SER:N	2.52	0.41
2:J:89:PRO:HD3	2:K:283:HIS:CG	2.55	0.41
2:K:16:ILE:HD11	2:K:171:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:44:GLY:O	2:K:48:SER:N	2.52	0.41
2:L:49:PHE:CE2	2:L:55:GLU:HB2	2.54	0.41
2:L:79:ARG:NH2	2:L:94:THR:HG21	2.35	0.41
1:n:86:ARG:HG3	1:o:281:TYR:CD2	2.56	0.41
1:n:415:MET:HE3	1:n:415:MET:HB2	1.90	0.41
1:o:155:ILE:CG2	1:o:164:MET:HE1	2.50	0.41
1:o:214:THR:HG22	1:o:273:LEU:O	2.20	0.41
1:r:207:LEU:HB3	1:r:225:LEU:HD22	2.01	0.41
1:t:261:PRO:O	1:t:262:ARG:CB	2.65	0.41
1:a:358:PRO:HB3	3:a:601:TA1:C37	2.51	0.41
1:b:169:VAL:HG11	4:b:602:GDP:N1	2.34	0.41
1:c:1:MET:HE3	2:P:96:LYS:HG2	2.02	0.41
1:f:394:PHE:CE1	2:F:257:THR:O	2.74	0.41
1:h:214:THR:HG22	1:h:273:LEU:O	2.20	0.41
1:i:207:LEU:HB3	1:i:225:LEU:HD22	2.02	0.41
1:j:10:GLY:O	1:j:14:ASN:ND2	2.53	0.41
2:Q:306:ASP:C	2:Q:308:ARG:N	2.75	0.41
2:T:242:LEU:HD11	2:T:252:LEU:HG	2.02	0.41
2:U:44:GLY:O	2:U:48:SER:N	2.52	0.41
2:W:44:GLY:O	2:W:48:SER:N	2.53	0.41
2:W:109:THR:OG1	2:W:411:GLU:O	2.37	0.41
2:X:368:LEU:HD12	2:X:368:LEU:N	2.36	0.41
2:Y:256:GLN:H	2:Y:256:GLN:HG3	1.63	0.41
2:Y:285:GLN:O	2:Y:287:SER:N	2.46	0.41
2:A:280:LYS:HB3	2:A:280:LYS:HE2	1.79	0.41
2:C:368:LEU:HD12	2:C:368:LEU:N	2.36	0.41
2:D:67:PHE:HB2	2:D:92:LEU:CD2	2.47	0.41
2:I:109:THR:OG1	2:I:411:GLU:O	2.37	0.41
2:J:109:THR:OG1	2:J:411:GLU:O	2.37	0.41
2:K:109:THR:OG1	2:K:411:GLU:O	2.37	0.41
1:s:214:THR:HG22	1:s:273:LEU:O	2.21	0.41
1:v:207:LEU:HB3	1:v:225:LEU:HD22	2.02	0.41
1:w:214:THR:HG22	1:w:273:LEU:O	2.20	0.41
1:c:207:LEU:HB3	1:c:225:LEU:HD22	2.02	0.41
1:c:358:PRO:HB2	3:c:601:TA1:H281	2.03	0.41
1:e:155:ILE:CG2	1:e:164:MET:HE1	2.50	0.41
1:e:243:PRO:HB2	2:R:77:GLU:OE2	2.21	0.41
1:e:356:ILE:HA	1:e:357:PRO:HD2	1.92	0.41
1:f:222:TYR:CZ	4:f:602:GDP:C6	2.82	0.41
1:m:220:PRO:HD2	2:M:326:LYS:CG	2.27	0.41
2:O:282:TYR:O	2:O:283:HIS:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:368:LEU:HD12	2:S:368:LEU:N	2.36	0.41
2:T:262:TYR:CB	2:T:263:PRO:CD	2.97	0.41
2:V:109:THR:OG1	2:V:411:GLU:O	2.37	0.41
2:W:285:GLN:O	2:W:287:SER:N	2.46	0.41
2:W:368:LEU:N	2:W:368:LEU:HD12	2.35	0.41
2:A:89:PRO:HD3	2:B:283:HIS:HE1	1.50	0.41
2:F:368:LEU:HD12	2:F:368:LEU:N	2.36	0.41
2:G:368:LEU:N	2:G:368:LEU:HD12	2.36	0.41
2:H:44:GLY:O	2:H:48:SER:N	2.52	0.41
2:H:79:ARG:NH2	2:H:94:THR:HG21	2.35	0.41
2:K:221:ARG:HE	2:K:221:ARG:HB2	1.70	0.41
2:L:209:ILE:O	2:L:213:CYS:SG	2.68	0.41
1:p:207:LEU:HB3	1:p:225:LEU:HD22	2.02	0.41
1:p:322:SER:O	1:p:326:VAL:CG2	2.68	0.41
1:s:106:TYR:HE2	1:s:403:MET:HG2	1.85	0.41
1:t:172:SER:HA	1:t:173:PRO:HD3	1.89	0.41
1:w:207:LEU:HB3	1:w:225:LEU:HD22	2.02	0.41
1:w:293:MET:HB3	1:w:367:PHE:HB2	2.01	0.41
1:c:155:ILE:CG2	1:c:164:MET:HE1	2.50	0.41
1:f:222:TYR:CG	4:f:602:GDP:C6	3.04	0.41
1:g:214:THR:HG22	1:g:273:LEU:O	2.20	0.41
1:i:261:PRO:O	1:i:262:ARG:CB	2.65	0.41
1:j:87:PRO:HD3	1:k:281:TYR:CD2	2.55	0.41
1:k:256:ASN:HA	2:X:404:PHE:HE1	1.85	0.41
1:m:10:GLY:O	1:m:14:ASN:ND2	2.54	0.41
2:N:122:ILE:O	2:N:126:ALA:N	2.53	0.41
2:S:16:ILE:HD11	2:S:171:ILE:HD11	2.02	0.41
2:X:79:ARG:NH2	2:X:94:THR:HG21	2.36	0.41
2:X:282:TYR:O	2:X:283:HIS:C	2.62	0.41
2:C:20:CYS:SG	2:C:138:PHE:HE2	2.42	0.41
2:D:306:ASP:C	2:D:308:ARG:N	2.75	0.41
2:F:221:ARG:HE	2:F:221:ARG:HB2	1.70	0.41
2:I:304:LYS:HA	2:I:304:LYS:HD2	1.90	0.41
1:o:403:MET:HE2	1:o:403:MET:HB3	1.88	0.41
1:p:86:ARG:HA	1:q:281:TYR:CD2	2.55	0.41
1:q:86:ARG:CG	1:r:281:TYR:HB3	2.50	0.41
1:q:322:SER:O	1:q:326:VAL:CG2	2.68	0.41
1:r:293:MET:HB3	1:r:367:PHE:HB2	2.01	0.41
1:y:46:ARG:HA	1:y:46:ARG:HD3	1.88	0.41
1:a:354:CYS:HG	1:a:355:ASP:H	1.62	0.41
1:b:164:MET:HB2	1:b:164:MET:HE3	1.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:356:ILE:HA	1:f:357:PRO:HD2	1.90	0.41
1:h:261:PRO:O	1:h:262:ARG:CB	2.65	0.41
1:j:155:ILE:CG2	1:j:164:MET:HE1	2.50	0.41
1:j:321:MET:HE2	1:j:321:MET:HB3	1.96	0.41
1:l:231:ALA:HB1	3:l:601:TA1:H391	2.02	0.41
1:m:155:ILE:CG2	1:m:164:MET:HE1	2.51	0.41
2:O:79:ARG:NH2	2:O:94:THR:HG21	2.36	0.41
2:Q:122:ILE:O	2:Q:126:ALA:N	2.53	0.41
2:S:12:ALA:HB2	6:S:502:GTP:C4	2.56	0.41
2:U:79:ARG:NH2	2:U:94:THR:HG21	2.36	0.41
2:Z:44:GLY:O	2:Z:48:SER:N	2.52	0.41
2:Z:100:ALA:N	6:Z:502:GTP:O2G	2.45	0.41
2:Z:304:LYS:HD2	2:Z:304:LYS:HA	1.89	0.41
2:A:90:GLU:HG3	2:B:280:LYS:HE3	2.02	0.41
2:A:157:LEU:HD23	2:A:157:LEU:HA	1.86	0.41
2:B:16:ILE:HD11	2:B:171:ILE:HD11	2.02	0.41
2:C:79:ARG:NH2	2:C:94:THR:HG21	2.35	0.41
2:D:256:GLN:H	2:D:256:GLN:HG3	1.62	0.41
1:o:207:LEU:HB3	1:o:225:LEU:HD22	2.02	0.41
1:o:232:THR:O	1:o:236:VAL:HG23	2.19	0.41
1:q:403:MET:HE2	1:q:403:MET:HB3	1.87	0.41
1:t:86:ARG:HG3	1:u:281:TYR:CB	2.50	0.41
1:w:10:GLY:O	1:w:14:ASN:ND2	2.54	0.41
1:x:214:THR:HG22	1:x:273:LEU:O	2.20	0.41
1:z:10:GLY:O	1:z:14:ASN:ND2	2.54	0.41
1:z:207:LEU:HB3	1:z:225:LEU:HD22	2.02	0.41
1:a:175:VAL:HG13	2:A:329:ASN:CG	2.46	0.41
3:g:601:TA1:H141	3:g:601:TA1:H091	2.02	0.41
1:i:141:GLY:CA	4:i:602:GDP:O5'	2.69	0.41
1:k:16:ILE:O	1:k:20:PHE:N	2.53	0.41
1:l:155:ILE:CG2	1:l:164:MET:HE1	2.50	0.41
1:l:215:LEU:HD21	3:l:601:TA1:C14	2.50	0.41
1:m:214:THR:HG22	1:m:273:LEU:O	2.20	0.41
2:P:368:LEU:HD12	2:P:368:LEU:N	2.36	0.41
2:R:282:TYR:O	2:R:283:HIS:C	2.61	0.41
2:U:282:TYR:O	2:U:283:HIS:C	2.62	0.41
2:V:368:LEU:HD12	2:V:368:LEU:N	2.35	0.41
2:W:101:ASN:N	6:W:502:GTP:O3G	2.49	0.41
2:W:121:ARG:HA	2:W:121:ARG:HD2	1.96	0.41
2:B:262:TYR:HE2	2:B:435:VAL:CG2	2.32	0.41
2:D:304:LYS:HD2	2:D:304:LYS:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:262:TYR:CB	2:G:263:PRO:CD	2.97	0.41
2:J:304:LYS:HA	2:J:304:LYS:HD2	1.90	0.41
2:M:44:GLY:O	2:M:48:SER:N	2.52	0.41
1:q:207:LEU:HB3	1:q:225:LEU:HD22	2.02	0.41
1:s:69:GLU:HA	1:s:70:PRO:HD3	1.92	0.41
1:s:322:SER:O	1:s:326:VAL:CG2	2.68	0.41
1:v:261:PRO:O	1:v:262:ARG:CB	2.65	0.41
1:a:415:MET:HE3	1:a:415:MET:HB2	1.90	0.41
1:b:10:GLY:O	1:b:14:ASN:ND2	2.54	0.41
1:b:12:CYS:HB3	4:b:602:GDP:H1'	0.42	0.41
1:b:232:THR:O	1:b:236:VAL:HG23	2.19	0.41
1:d:243:PRO:HB2	2:Q:77:GLU:OE2	2.20	0.41
1:k:10:GLY:O	1:k:14:ASN:ND2	2.53	0.41
1:k:164:MET:HE3	1:k:164:MET:HB2	1.71	0.41
1:l:46:ARG:HA	1:l:46:ARG:HD3	1.88	0.41
1:l:207:LEU:HB3	1:l:225:LEU:HD22	2.02	0.41
1:l:214:THR:HG22	1:l:273:LEU:O	2.20	0.41
2:N:79:ARG:NH2	2:N:94:THR:HG21	2.36	0.41
2:N:121:ARG:HA	2:N:121:ARG:HD2	1.95	0.41
2:N:157:LEU:HD23	2:N:157:LEU:HA	1.86	0.41
2:P:282:TYR:O	2:P:283:HIS:C	2.62	0.41
2:T:122:ILE:O	2:T:126:ALA:N	2.53	0.41
2:V:304:LYS:HD2	2:V:304:LYS:HA	1.89	0.41
2:Y:88:HIS:CD2	2:Z:283:HIS:CB	3.04	0.41
2:A:16:ILE:HD11	2:A:171:ILE:HD11	2.03	0.41
2:A:79:ARG:NH2	2:A:94:THR:HG21	2.36	0.41
2:A:333:ALA:O	2:A:337:THR:OG1	2.34	0.41
2:B:79:ARG:NH2	2:B:94:THR:HG21	2.36	0.41
2:B:202:PHE:HE2	2:B:238:ILE:HD13	1.86	0.41
2:J:79:ARG:NH2	2:J:94:THR:HG21	2.35	0.41
2:M:16:ILE:HD11	2:M:171:ILE:HD11	2.03	0.41
2:M:221:ARG:HE	2:M:221:ARG:HB2	1.70	0.41
1:o:10:GLY:O	1:o:14:ASN:ND2	2.54	0.41
1:o:164:MET:HB2	1:o:164:MET:HE3	1.71	0.41
1:u:261:PRO:O	1:u:262:ARG:CB	2.65	0.41
1:z:214:THR:HG22	1:z:273:LEU:O	2.20	0.41
1:b:207:LEU:HB3	1:b:225:LEU:HD22	2.02	0.41
1:d:155:ILE:CG2	1:d:164:MET:HE1	2.51	0.41
1:h:172:SER:HA	1:h:173:PRO:HD3	1.89	0.41
1:h:215:LEU:HD21	3:h:601:TA1:O06	2.21	0.41
1:j:207:LEU:HB3	1:j:225:LEU:HD22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:222:TYR:CE2	4:j:602:GDP:N7	2.88	0.41
1:k:207:LEU:HB3	1:k:225:LEU:HD22	2.02	0.41
1:m:234:SER:HB3	3:m:601:TA1:H401	2.02	0.41
2:P:79:ARG:NH2	2:P:94:THR:HG21	2.36	0.41
2:Q:368:LEU:N	2:Q:368:LEU:HD12	2.36	0.41
2:U:304:LYS:HA	2:U:304:LYS:HD2	1.89	0.41
2:V:79:ARG:NH2	2:V:94:THR:HG21	2.36	0.41
2:W:79:ARG:NH2	2:W:94:THR:HG21	2.36	0.41
2:X:16:ILE:HD11	2:X:171:ILE:HD11	2.03	0.41
2:Z:79:ARG:NH2	2:Z:94:THR:HG21	2.36	0.41
2:C:157:LEU:HD23	2:C:157:LEU:HA	1.85	0.41
2:D:122:ILE:O	2:D:126:ALA:N	2.53	0.41
2:F:256:GLN:H	2:F:256:GLN:HG3	1.62	0.41
2:G:122:ILE:O	2:G:126:ALA:N	2.53	0.41
2:H:280:LYS:HB3	2:H:280:LYS:HE2	1.84	0.41
2:H:368:LEU:HD12	2:H:368:LEU:N	2.36	0.41
2:I:16:ILE:HD11	2:I:171:ILE:HD11	2.03	0.41
2:M:368:LEU:HD12	2:M:368:LEU:N	2.36	0.41
1:n:10:GLY:O	1:n:14:ASN:ND2	2.54	0.41
1:n:214:THR:HG22	1:n:273:LEU:O	2.20	0.41
1:s:207:LEU:HB3	1:s:225:LEU:HD22	2.02	0.41
1:s:356:ILE:HA	1:s:357:PRO:HD2	1.91	0.41
1:t:322:SER:O	1:t:326:VAL:CG2	2.68	0.41
1:t:415:MET:HE3	1:t:415:MET:HB2	1.90	0.41
1:u:207:LEU:HB3	1:u:225:LEU:HD22	2.02	0.41
1:w:16:ILE:O	1:w:20:PHE:N	2.52	0.41
1:w:183:TYR:HE2	1:w:388:MET:HE2	1.86	0.41
1:y:214:THR:HG22	1:y:273:LEU:O	2.20	0.41
1:z:164:MET:HE3	1:z:164:MET:HB2	1.71	0.41
1:e:46:ARG:HD3	1:e:46:ARG:HA	1.87	0.41
1:h:10:GLY:O	1:h:14:ASN:ND2	2.53	0.41
1:k:12:CYS:SG	4:k:602:GDP:C4	3.14	0.41
1:l:403:MET:HB3	1:l:403:MET:HE2	1.87	0.41
2:P:83:TYR:HD1	2:P:83:TYR:HA	1.74	0.41
2:Q:304:LYS:HD2	2:Q:304:LYS:HA	1.89	0.41
2:S:221:ARG:HE	2:S:221:ARG:HB2	1.72	0.41
2:T:224:TYR:CE1	6:T:502:GTP:N7	2.89	0.41
2:X:256:GLN:HB3	1:x:397:TRP:CH2	2.56	0.41
2:Y:79:ARG:NH2	2:Y:94:THR:HG21	2.36	0.41
2:Y:368:LEU:N	2:Y:368:LEU:HD12	2.36	0.41
2:A:122:ILE:O	2:A:126:ALA:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:304:LYS:HD2	2:M:304:LYS:HA	1.90	0.41
1:p:214:THR:HG22	1:p:273:LEU:O	2.21	0.41
1:t:214:THR:HG22	1:t:273:LEU:O	2.21	0.41
1:x:10:GLY:O	1:x:14:ASN:ND2	2.54	0.41
1:y:256:ASN:HD21	1:y:350:LYS:HD2	1.85	0.41
1:a:395:LEU:HD12	1:a:395:LEU:HA	1.82	0.40
1:d:268:PRO:HG2	1:d:300:MET:HB2	2.03	0.40
1:e:268:PRO:HG2	1:e:300:MET:HB2	2.03	0.40
1:j:54:ALA:C	1:k:283:ALA:HB2	2.46	0.40
1:k:87:PRO:HD3	1:l:281:TYR:CD2	2.56	0.40
1:k:155:ILE:CG2	1:k:164:MET:HE1	2.50	0.40
1:m:179:VAL:N	2:M:258:ASN:ND2	2.52	0.40
2:Q:285:GLN:O	2:Q:287:SER:N	2.46	0.40
2:S:143:GLY:HA3	6:S:502:GTP:O2B	2.21	0.40
2:S:262:TYR:CB	2:S:263:PRO:CD	2.97	0.40
2:T:181:VAL:O	2:T:181:VAL:CG1	2.70	0.40
2:Z:368:LEU:HD12	2:Z:368:LEU:N	2.36	0.40
2:A:283:HIS:CG	2:M:89:PRO:HD3	2.54	0.40
2:D:157:LEU:HD23	2:D:157:LEU:HA	1.85	0.40
2:L:368:LEU:N	2:L:368:LEU:HD12	2.37	0.40
2:M:79:ARG:NH2	2:M:94:THR:HG21	2.36	0.40
1:n:246:LEU:HB2	1:n:352:ALA:HA	2.02	0.40
1:q:214:THR:HG22	1:q:273:LEU:O	2.21	0.40
1:q:248:ALA:HA	1:q:252:LYS:HD2	2.04	0.40
1:r:256:ASN:HD21	1:r:350:LYS:HD2	1.86	0.40
1:t:268:PRO:HG2	1:t:300:MET:HB2	2.04	0.40
1:u:106:TYR:HE2	1:u:403:MET:HG2	1.86	0.40
1:u:322:SER:O	1:u:326:VAL:CG2	2.69	0.40
1:w:268:PRO:HG2	1:w:300:MET:HB2	2.04	0.40
1:a:361:LEU:CD2	3:a:601:TA1:H442	2.42	0.40
1:f:12:CYS:SG	4:f:602:GDP:C6	3.14	0.40
1:g:207:LEU:HB3	1:g:225:LEU:HD22	2.03	0.40
1:i:10:GLY:O	1:i:14:ASN:ND2	2.53	0.40
1:k:215:LEU:CD2	3:k:601:TA1:C14	2.98	0.40
1:k:345:ILE:CG2	2:X:181:VAL:HG11	2.51	0.40
2:N:304:LYS:HD2	2:N:304:LYS:HA	1.89	0.40
2:N:368:LEU:HD12	2:N:368:LEU:N	2.36	0.40
2:Q:79:ARG:NH2	2:Q:94:THR:HG21	2.36	0.40
2:T:324:VAL:HA	2:T:325:PRO:HD3	1.92	0.40
2:W:221:ARG:HE	2:W:221:ARG:HB2	1.70	0.40
2:Y:157:LEU:HD23	2:Y:157:LEU:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:265:ILE:HG22	2:B:265:ILE:O	2.22	0.40
2:C:89:PRO:HD3	2:D:283:HIS:CG	2.56	0.40
2:D:368:LEU:HD12	2:D:368:LEU:N	2.36	0.40
2:E:368:LEU:HD12	2:E:368:LEU:N	2.36	0.40
2:G:16:ILE:HD11	2:G:171:ILE:HD11	2.03	0.40
2:G:181:VAL:O	2:G:181:VAL:CG1	2.70	0.40
2:G:265:ILE:HG22	2:G:265:ILE:O	2.22	0.40
2:G:280:LYS:HB3	2:G:280:LYS:HE2	1.86	0.40
2:L:282:TYR:O	2:L:283:HIS:C	2.62	0.40
1:n:207:LEU:HB3	1:n:225:LEU:HD22	2.02	0.40
1:v:214:THR:HG22	1:v:273:LEU:O	2.21	0.40
1:y:403:MET:HB3	1:y:403:MET:HE2	1.88	0.40
1:e:256:ASN:HD21	1:e:350:LYS:HD2	1.87	0.40
1:h:322:SER:HG	1:h:325:GLU:HB2	1.85	0.40
1:i:321:MET:HE2	1:i:321:MET:HB3	1.96	0.40
1:k:273:LEU:HA	3:k:601:TA1:O06	2.22	0.40
1:k:415:MET:HE3	1:k:415:MET:HB2	1.90	0.40
2:N:16:ILE:HD11	6:N:502:GTP:N2	2.36	0.40
2:O:171:ILE:CD1	6:O:502:GTP:N2	2.79	0.40
2:Q:171:ILE:HD11	6:Q:502:GTP:C2	2.54	0.40
2:R:121:ARG:HA	2:R:121:ARG:HD2	1.97	0.40
2:W:326:LYS:CE	1:w:218:THR:O	2.69	0.40
2:X:262:TYR:HE2	2:X:435:VAL:CG2	2.32	0.40
2:D:79:ARG:NH2	2:D:94:THR:HG21	2.36	0.40
2:H:304:LYS:HA	2:H:304:LYS:HD2	1.89	0.40
2:I:368:LEU:HD12	2:I:368:LEU:N	2.36	0.40
2:J:368:LEU:N	2:J:368:LEU:HD12	2.37	0.40
2:L:157:LEU:HD23	2:L:157:LEU:HA	1.85	0.40
1:n:69:GLU:HA	1:n:70:PRO:HD3	1.92	0.40
1:p:403:MET:HE2	1:p:403:MET:HB3	1.88	0.40
1:q:268:PRO:HG2	1:q:300:MET:HB2	2.04	0.40
1:s:46:ARG:HD3	1:s:46:ARG:HA	1.88	0.40
1:u:10:GLY:O	1:u:14:ASN:ND2	2.54	0.40
1:b:256:ASN:ND2	2:O:180:ALA:HA	2.37	0.40
1:d:207:LEU:HB3	1:d:225:LEU:HD22	2.02	0.40
1:e:214:THR:HG22	1:e:273:LEU:O	2.21	0.40
1:g:10:GLY:O	1:g:14:ASN:ND2	2.53	0.40
1:g:87:PRO:HA	1:g:90:PHE:HD2	1.86	0.40
1:g:234:SER:HB3	3:g:601:TA1:H411	2.04	0.40
1:g:272:PRO:HD3	1:g:364:SER:HA	2.02	0.40
1:i:12:CYS:SG	4:i:602:GDP:C4	3.15	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:42:LEU:HD23	1:l:42:LEU:HA	1.94	0.40
1:l:87:PRO:HA	1:l:90:PHE:HD2	1.86	0.40
1:l:274:THR:H	3:l:601:TA1:H162	1.86	0.40
2:Q:67:PHE:HB2	2:Q:92:LEU:CD2	2.48	0.40
2:S:256:GLN:H	2:S:256:GLN:HG3	1.62	0.40
2:Y:109:THR:OG1	2:Y:411:GLU:O	2.37	0.40
2:Z:256:GLN:HB3	1:z:397:TRP:CH2	2.56	0.40
2:E:79:ARG:NH2	2:E:94:THR:HG21	2.36	0.40
2:L:109:THR:OG1	2:L:411:GLU:O	2.37	0.40
1:o:69:GLU:HA	1:o:70:PRO:HD3	1.92	0.40
1:t:10:GLY:O	1:t:14:ASN:ND2	2.54	0.40
1:u:268:PRO:HG2	1:u:300:MET:HB2	2.03	0.40
1:v:10:GLY:O	1:v:14:ASN:ND2	2.54	0.40
1:v:256:ASN:HD21	1:v:350:LYS:HD2	1.86	0.40
1:x:46:ARG:HD3	1:x:46:ARG:HA	1.89	0.40
1:y:321:MET:HE2	1:y:321:MET:HB3	1.97	0.40
1:c:164:MET:HE3	1:c:164:MET:HB2	1.71	0.40
1:c:281:TYR:CE2	1:o:87:PRO:CD	3.02	0.40
1:d:222:TYR:CE1	4:d:602:GDP:C4	2.99	0.40
1:d:231:ALA:HA	3:d:601:TA1:C39	2.51	0.40
1:f:87:PRO:HA	1:f:90:PHE:HD2	1.87	0.40
3:f:601:TA1:H101	3:f:601:TA1:C25	2.51	0.40
1:g:69:GLU:HA	1:g:70:PRO:HD3	1.92	0.40
1:h:140:GLY:C	4:h:602:GDP:H4'	2.46	0.40
1:j:16:ILE:O	1:j:20:PHE:N	2.53	0.40
1:k:360:GLY:HA3	3:k:601:TA1:H443	2.04	0.40
1:l:358:PRO:CB	3:l:601:TA1:H281	2.51	0.40
3:l:601:TA1:H441	3:l:601:TA1:C27	2.51	0.40
2:N:265:ILE:O	2:N:265:ILE:HG22	2.22	0.40
2:P:265:ILE:O	2:P:265:ILE:HG22	2.22	0.40
2:Q:256:GLN:H	2:Q:256:GLN:HG3	1.62	0.40
2:R:79:ARG:NH2	2:R:94:THR:HG21	2.36	0.40
2:A:265:ILE:O	2:A:265:ILE:HG22	2.22	0.40
2:A:304:LYS:HD2	2:A:304:LYS:HA	1.90	0.40
2:C:67:PHE:HB2	2:C:92:LEU:CD2	2.47	0.40
2:C:282:TYR:O	2:C:283:HIS:C	2.61	0.40
2:D:262:TYR:HE2	2:D:435:VAL:CG2	2.32	0.40
2:E:265:ILE:O	2:E:265:ILE:HG22	2.22	0.40
2:H:265:ILE:HG22	2:H:265:ILE:O	2.22	0.40
2:J:67:PHE:HB2	2:J:92:LEU:CD2	2.47	0.40
1:p:248:ALA:HA	1:p:252:LYS:HD2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:214:THR:HG22	1:r:273:LEU:O	2.21	0.40
1:r:248:ALA:HA	1:r:252:LYS:HD2	2.04	0.40
1:u:214:THR:HG22	1:u:273:LEU:O	2.21	0.40
1:x:42:LEU:HD23	1:x:42:LEU:HA	1.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	427/446 (96%)	389 (91%)	36 (8%)	2 (0%)	24	63
1	b	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	c	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	d	427/446 (96%)	389 (91%)	36 (8%)	2 (0%)	24	63
1	e	427/446 (96%)	388 (91%)	37 (9%)	2 (0%)	24	63
1	f	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
1	g	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
1	h	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	i	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	j	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	k	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	l	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	m	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	n	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	o	427/446 (96%)	392 (92%)	33 (8%)	2 (0%)	24	63
1	p	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	q	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	r	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
1	s	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
1	t	427/446 (96%)	392 (92%)	33 (8%)	2 (0%)	24	63
1	u	427/446 (96%)	392 (92%)	33 (8%)	2 (0%)	24	63
1	v	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
1	w	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
1	x	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	y	427/446 (96%)	390 (91%)	35 (8%)	2 (0%)	24	63
1	z	427/446 (96%)	391 (92%)	34 (8%)	2 (0%)	24	63
2	A	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	B	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	C	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	D	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	E	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	F	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	G	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	H	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	I	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	J	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	K	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	L	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	M	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	N	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	O	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	P	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	Q	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	R	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	S	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	T	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	U	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	V	439/451 (97%)	402 (92%)	36 (8%)	1 (0%)	43	77
2	W	439/451 (97%)	404 (92%)	34 (8%)	1 (0%)	43	77
2	X	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	Y	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
2	Z	439/451 (97%)	403 (92%)	35 (8%)	1 (0%)	43	77
All	All	22516/23322 (96%)	20640 (92%)	1798 (8%)	78 (0%)	37	71

All (78) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	304	LYS
2	F	304	LYS
2	G	304	LYS
2	H	304	LYS
2	J	304	LYS
2	L	304	LYS
2	N	304	LYS
2	O	304	LYS
2	P	304	LYS
2	Q	304	LYS
2	R	304	LYS
2	S	304	LYS
2	T	304	LYS
2	U	304	LYS
2	V	304	LYS
2	W	304	LYS
2	X	304	LYS
2	Y	304	LYS
2	Z	304	LYS
2	A	304	LYS
2	C	304	LYS
2	D	304	LYS
2	E	304	LYS
2	I	304	LYS
2	K	304	LYS
2	M	304	LYS
1	e	360	GLY
1	a	360	GLY
1	b	360	GLY
1	c	259	PRO

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Mol	Chain	Res	Type
1	c	360	GLY
1	d	360	GLY
1	f	259	PRO
1	f	360	GLY
1	g	360	GLY
1	h	259	PRO
1	h	360	GLY
1	i	259	PRO
1	i	360	GLY
1	j	259	PRO
1	j	360	GLY
1	k	259	PRO
1	k	360	GLY
1	l	259	PRO
1	l	360	GLY
1	m	259	PRO
1	m	360	GLY
1	n	259	PRO
1	o	259	PRO
1	q	259	PRO
1	r	259	PRO
1	u	360	GLY
1	y	259	PRO
1	y	360	GLY
1	z	259	PRO
1	a	259	PRO
1	b	259	PRO
1	d	259	PRO
1	e	259	PRO
1	g	259	PRO
1	n	360	GLY
1	o	360	GLY
1	p	259	PRO
1	p	360	GLY
1	r	360	GLY
1	s	259	PRO
1	s	360	GLY
1	t	259	PRO
1	t	360	GLY
1	u	259	PRO
1	v	259	PRO
1	v	360	GLY

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Mol	Chain	Res	Type
1	w	259	PRO
1	w	360	GLY
1	x	259	PRO
1	x	360	GLY
1	z	360	GLY
1	q	360	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	b	371/383 (97%)	366 (99%)	5 (1%)	61	72
1	c	371/383 (97%)	366 (99%)	5 (1%)	61	72
1	d	371/383 (97%)	364 (98%)	7 (2%)	50	66
1	e	371/383 (97%)	366 (99%)	5 (1%)	61	72
1	f	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	g	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	h	371/383 (97%)	366 (99%)	5 (1%)	61	72
1	i	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	j	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	k	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	l	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	m	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	n	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	o	371/383 (97%)	366 (99%)	5 (1%)	61	72
1	p	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	q	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	r	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	s	371/383 (97%)	367 (99%)	4 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	t	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	u	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	v	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	w	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	x	371/383 (97%)	367 (99%)	4 (1%)	65	74
1	y	371/383 (97%)	365 (98%)	6 (2%)	55	69
1	z	371/383 (97%)	367 (99%)	4 (1%)	65	74
2	A	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	B	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	C	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	D	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	E	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	F	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	G	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	H	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	I	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	J	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	K	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	L	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	M	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	N	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	O	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	P	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	Q	372/379 (98%)	370 (100%)	2 (0%)	81	82
2	R	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	S	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	T	372/379 (98%)	371 (100%)	1 (0%)	86	84
2	U	372/379 (98%)	368 (99%)	4 (1%)	65	74
2	V	372/379 (98%)	368 (99%)	4 (1%)	65	74
2	W	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	X	372/379 (98%)	368 (99%)	4 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Y	372/379 (98%)	369 (99%)	3 (1%)	73	78
2	Z	372/379 (98%)	369 (99%)	3 (1%)	73	78
All	All	19318/19812 (98%)	19146 (99%)	172 (1%)	68	77

All (172) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	222	TYR
1	a	276	ARG
1	a	406	MET
1	a	418	LEU
1	b	1	MET
1	b	222	TYR
1	b	276	ARG
1	b	406	MET
1	b	418	LEU
1	c	1	MET
1	c	222	TYR
1	c	276	ARG
1	c	406	MET
1	c	418	LEU
1	d	1	MET
1	d	47	ILE
1	d	222	TYR
1	d	276	ARG
1	d	300	MET
1	d	406	MET
1	d	418	LEU
1	e	1	MET
1	e	276	ARG
1	e	300	MET
1	e	406	MET
1	e	418	LEU
1	f	1	MET
1	f	276	ARG
1	f	406	MET
1	f	418	LEU
1	g	1	MET
1	g	276	ARG
1	g	406	MET
1	g	418	LEU

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Mol	Chain	Res	Type
1	h	1	MET
1	h	222	TYR
1	h	276	ARG
1	h	406	MET
1	h	418	LEU
1	i	1	MET
1	i	276	ARG
1	i	406	MET
1	i	418	LEU
1	j	222	TYR
1	j	276	ARG
1	j	406	MET
1	j	418	LEU
1	k	1	MET
1	k	276	ARG
1	k	406	MET
1	k	418	LEU
1	l	1	MET
1	l	276	ARG
1	l	406	MET
1	l	418	LEU
1	m	222	TYR
1	m	276	ARG
1	m	406	MET
1	m	418	LEU
2	N	5	ILE
2	N	89	PRO
2	N	283	HIS
2	O	89	PRO
2	O	283	HIS
2	P	89	PRO
2	P	171	ILE
2	P	283	HIS
2	Q	89	PRO
2	Q	283	HIS
2	R	89	PRO
2	R	283	HIS
2	R	368	LEU
2	S	283	HIS
2	T	283	HIS
2	U	5	ILE
2	U	60	LYS

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Mol	Chain	Res	Type
2	U	171	ILE
2	U	283	HIS
2	V	5	ILE
2	V	60	LYS
2	V	89	PRO
2	V	283	HIS
2	W	5	ILE
2	W	89	PRO
2	W	283	HIS
2	X	5	ILE
2	X	60	LYS
2	X	89	PRO
2	X	283	HIS
2	Y	5	ILE
2	Y	89	PRO
2	Y	283	HIS
2	Z	5	ILE
2	Z	89	PRO
2	Z	283	HIS
2	A	283	HIS
2	B	283	HIS
2	C	5	ILE
2	C	89	PRO
2	C	283	HIS
2	D	5	ILE
2	D	283	HIS
2	D	361	THR
2	E	5	ILE
2	E	283	HIS
2	F	42	ILE
2	F	283	HIS
2	G	42	ILE
2	G	283	HIS
2	H	283	HIS
2	I	283	HIS
2	J	283	HIS
2	K	89	PRO
2	K	283	HIS
2	L	283	HIS
2	L	361	THR
2	M	283	HIS
1	n	222	TYR

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Mol	Chain	Res	Type
1	n	276	ARG
1	n	406	MET
1	n	418	LEU
1	o	222	TYR
1	o	276	ARG
1	o	300	MET
1	o	406	MET
1	o	418	LEU
1	p	222	TYR
1	p	276	ARG
1	p	406	MET
1	p	418	LEU
1	q	222	TYR
1	q	276	ARG
1	q	406	MET
1	q	418	LEU
1	r	222	TYR
1	r	276	ARG
1	r	406	MET
1	r	418	LEU
1	s	222	TYR
1	s	276	ARG
1	s	406	MET
1	s	418	LEU
1	t	222	TYR
1	t	276	ARG
1	t	406	MET
1	t	418	LEU
1	u	222	TYR
1	u	276	ARG
1	u	406	MET
1	u	418	LEU
1	v	222	TYR
1	v	276	ARG
1	v	406	MET
1	v	418	LEU
1	w	222	TYR
1	w	276	ARG
1	w	406	MET
1	w	418	LEU
1	x	222	TYR
1	x	276	ARG

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Mol	Chain	Res	Type
1	x	406	MET
1	x	418	LEU
1	y	1	MET
1	y	222	TYR
1	y	276	ARG
1	y	300	MET
1	y	406	MET
1	y	418	LEU
1	z	222	TYR
1	z	276	ARG
1	z	406	MET
1	z	418	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (275) such sidechains are listed below:

Mol	Chain	Res	Type
1	a	43	GLN
1	a	57	ASN
1	a	329	GLN
1	a	414	ASN
1	a	416	ASN
1	b	43	GLN
1	b	57	ASN
1	b	247	ASN
1	b	329	GLN
1	b	414	ASN
1	b	416	ASN
1	c	43	GLN
1	c	57	ASN
1	c	226	ASN
1	c	247	ASN
1	c	329	GLN
1	c	414	ASN
1	c	416	ASN
1	d	43	GLN
1	d	57	ASN
1	d	329	GLN
1	d	347	ASN
1	d	414	ASN
1	d	416	ASN
1	e	43	GLN
1	e	57	ASN

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Mol	Chain	Res	Type
1	e	329	GLN
1	e	414	ASN
1	e	416	ASN
1	f	43	GLN
1	f	57	ASN
1	f	247	ASN
1	f	329	GLN
1	f	347	ASN
1	f	414	ASN
1	f	416	ASN
1	g	43	GLN
1	g	57	ASN
1	g	329	GLN
1	g	414	ASN
1	g	416	ASN
1	h	43	GLN
1	h	57	ASN
1	h	247	ASN
1	h	329	GLN
1	h	414	ASN
1	h	416	ASN
1	i	43	GLN
1	i	57	ASN
1	i	329	GLN
1	i	414	ASN
1	i	416	ASN
1	j	43	GLN
1	j	57	ASN
1	j	329	GLN
1	j	414	ASN
1	j	416	ASN
1	k	43	GLN
1	k	57	ASN
1	k	329	GLN
1	k	414	ASN
1	k	416	ASN
1	l	43	GLN
1	l	57	ASN
1	l	329	GLN
1	l	347	ASN
1	l	414	ASN
1	l	416	ASN

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Mol	Chain	Res	Type
1	m	43	GLN
1	m	57	ASN
1	m	329	GLN
1	m	414	ASN
1	m	416	ASN
2	N	256	GLN
2	N	258	ASN
2	N	329	ASN
2	O	256	GLN
2	O	258	ASN
2	O	329	ASN
2	P	256	GLN
2	P	258	ASN
2	P	309	HIS
2	P	329	ASN
2	Q	256	GLN
2	Q	258	ASN
2	Q	309	HIS
2	Q	329	ASN
2	R	256	GLN
2	R	258	ASN
2	R	309	HIS
2	R	329	ASN
2	S	256	GLN
2	S	258	ASN
2	S	283	HIS
2	S	309	HIS
2	S	406	HIS
2	T	256	GLN
2	T	258	ASN
2	T	309	HIS
2	T	329	ASN
2	T	406	HIS
2	U	101	ASN
2	U	102	ASN
2	U	256	GLN
2	U	258	ASN
2	U	329	ASN
2	U	406	HIS
2	V	256	GLN
2	V	258	ASN
2	V	309	HIS

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Mol	Chain	Res	Type
2	V	329	ASN
2	V	406	HIS
2	W	256	GLN
2	W	258	ASN
2	W	283	HIS
2	W	309	HIS
2	W	329	ASN
2	W	406	HIS
2	X	101	ASN
2	X	256	GLN
2	X	258	ASN
2	X	329	ASN
2	Y	101	ASN
2	Y	228	ASN
2	Y	256	GLN
2	Y	258	ASN
2	Y	283	HIS
2	Y	329	ASN
2	Z	256	GLN
2	Z	258	ASN
2	Z	329	ASN
2	Z	406	HIS
2	A	228	ASN
2	A	256	GLN
2	A	258	ASN
2	A	309	HIS
2	A	406	HIS
2	B	228	ASN
2	B	256	GLN
2	B	258	ASN
2	B	309	HIS
2	B	406	HIS
2	C	228	ASN
2	C	256	GLN
2	C	258	ASN
2	C	329	ASN
2	C	406	HIS
2	D	228	ASN
2	D	256	GLN
2	D	258	ASN
2	D	283	HIS
2	D	309	HIS

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Mol	Chain	Res	Type
2	D	329	ASN
2	D	406	HIS
2	E	228	ASN
2	E	256	GLN
2	E	258	ASN
2	E	309	HIS
2	E	329	ASN
2	E	406	HIS
2	F	228	ASN
2	F	256	GLN
2	F	258	ASN
2	F	283	HIS
2	F	309	HIS
2	F	342	GLN
2	F	406	HIS
2	G	228	ASN
2	G	256	GLN
2	G	258	ASN
2	G	309	HIS
2	G	406	HIS
2	H	228	ASN
2	H	256	GLN
2	H	258	ASN
2	H	309	HIS
2	H	342	GLN
2	H	406	HIS
2	I	228	ASN
2	I	256	GLN
2	I	258	ASN
2	I	309	HIS
2	I	406	HIS
2	J	228	ASN
2	J	256	GLN
2	J	258	ASN
2	J	309	HIS
2	J	406	HIS
2	K	228	ASN
2	K	256	GLN
2	K	258	ASN
2	K	309	HIS
2	K	406	HIS
2	L	228	ASN

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Mol	Chain	Res	Type
2	L	256	GLN
2	L	258	ASN
2	L	406	HIS
2	M	228	ASN
2	M	256	GLN
2	M	258	ASN
2	M	406	HIS
1	n	43	GLN
1	n	57	ASN
1	n	247	ASN
1	n	329	GLN
1	n	414	ASN
1	n	416	ASN
1	o	43	GLN
1	o	57	ASN
1	o	247	ASN
1	o	329	GLN
1	o	414	ASN
1	o	416	ASN
1	p	43	GLN
1	p	57	ASN
1	p	226	ASN
1	p	329	GLN
1	p	414	ASN
1	p	416	ASN
1	q	43	GLN
1	q	57	ASN
1	q	247	ASN
1	q	329	GLN
1	q	414	ASN
1	q	416	ASN
1	r	43	GLN
1	r	57	ASN
1	r	329	GLN
1	r	414	ASN
1	r	416	ASN
1	s	43	GLN
1	s	57	ASN
1	s	247	ASN
1	s	329	GLN
1	s	414	ASN
1	s	416	ASN

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Mol	Chain	Res	Type
1	t	43	GLN
1	t	57	ASN
1	t	329	GLN
1	t	414	ASN
1	t	416	ASN
1	u	43	GLN
1	u	57	ASN
1	u	247	ASN
1	u	329	GLN
1	u	414	ASN
1	u	416	ASN
1	v	43	GLN
1	v	57	ASN
1	v	247	ASN
1	v	329	GLN
1	v	414	ASN
1	v	416	ASN
1	w	43	GLN
1	w	57	ASN
1	w	329	GLN
1	w	414	ASN
1	w	416	ASN
1	x	43	GLN
1	x	57	ASN
1	x	329	GLN
1	x	414	ASN
1	x	416	ASN
1	y	43	GLN
1	y	57	ASN
1	y	329	GLN
1	y	414	ASN
1	y	416	ASN
1	z	43	GLN
1	z	57	ASN
1	z	226	ASN
1	z	247	ASN
1	z	329	GLN
1	z	414	ASN
1	z	416	ASN

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 ⓘ

Of 52 ligands modelled in this entry, 13 are monoatomic - leaving 39 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	GTP	Z	502	5	33,34,34	2.18	9 (27%)	50,54,54	2.26	13 (26%)
4	GDP	e	602	-	29,30,30	1.44	4 (13%)	45,47,47	2.22	15 (33%)
4	GDP	c	602	-	29,30,30	1.66	7 (24%)	45,47,47	2.15	18 (40%)
4	GDP	j	602	-	29,30,30	1.46	3 (10%)	45,47,47	2.19	17 (37%)
4	GDP	a	602	-	29,30,30	1.58	5 (17%)	45,47,47	2.45	14 (31%)
4	GDP	m	602	-	29,30,30	1.38	5 (17%)	45,47,47	2.28	14 (31%)
4	GDP	d	602	-	29,30,30	1.56	5 (17%)	45,47,47	2.49	17 (37%)
3	TA1	h	601	-	68,68,68	1.22	7 (10%)	105,105,105	1.69	17 (16%)
4	GDP	b	602	-	29,30,30	2.10	4 (13%)	45,47,47	2.06	15 (33%)
3	TA1	m	601	-	68,68,68	1.31	7 (10%)	105,105,105	1.52	18 (17%)
3	TA1	j	601	-	68,68,68	1.07	4 (5%)	105,105,105	1.37	15 (14%)
6	GTP	N	502	5	33,34,34	1.38	4 (12%)	50,54,54	1.51	11 (22%)
6	GTP	S	502	5	33,34,34	1.34	5 (15%)	50,54,54	2.01	15 (30%)
4	GDP	g	602	-	29,30,30	1.53	5 (17%)	45,47,47	2.29	17 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GTP	U	502	5	33,34,34	1.82	6 (18%)	50,54,54	2.09	15 (30%)
6	GTP	Q	502	5	33,34,34	2.08	11 (33%)	50,54,54	2.00	15 (30%)
6	GTP	Y	502	5	33,34,34	1.16	2 (6%)	50,54,54	1.62	9 (18%)
3	TA1	l	601	-	68,68,68	1.10	4 (5%)	105,105,105	1.24	15 (14%)
4	GDP	i	602	-	29,30,30	1.76	6 (20%)	45,47,47	2.21	18 (40%)
4	GDP	h	602	-	29,30,30	1.46	4 (13%)	45,47,47	2.33	20 (44%)
3	TA1	b	601	-	68,68,68	1.21	7 (10%)	105,105,105	1.40	14 (13%)
6	GTP	R	502	5	33,34,34	1.99	8 (24%)	50,54,54	2.19	15 (30%)
3	TA1	a	601	-	68,68,68	1.04	3 (4%)	105,105,105	1.23	10 (9%)
4	GDP	k	602	-	29,30,30	1.43	3 (10%)	45,47,47	2.22	15 (33%)
3	TA1	f	601	-	68,68,68	1.55	11 (16%)	105,105,105	1.63	21 (20%)
3	TA1	c	601	-	68,68,68	1.11	5 (7%)	105,105,105	1.48	18 (17%)
4	GDP	l	602	-	29,30,30	1.32	3 (10%)	45,47,47	2.23	15 (33%)
6	GTP	P	502	5	33,34,34	1.87	8 (24%)	50,54,54	2.48	17 (34%)
6	GTP	T	502	5	33,34,34	2.44	12 (36%)	50,54,54	2.94	24 (48%)
4	GDP	f	602	-	29,30,30	1.55	3 (10%)	45,47,47	2.35	18 (40%)
6	GTP	V	502	5	33,34,34	1.14	2 (6%)	50,54,54	1.75	14 (28%)
3	TA1	d	601	-	68,68,68	1.17	7 (10%)	105,105,105	1.29	14 (13%)
6	GTP	W	502	5	33,34,34	2.22	9 (27%)	50,54,54	2.30	17 (34%)
3	TA1	g	601	-	68,68,68	1.72	15 (22%)	105,105,105	3.29	39 (37%)
6	GTP	O	502	5	33,34,34	1.00	2 (6%)	50,54,54	1.46	9 (18%)
3	TA1	k	601	-	68,68,68	1.68	13 (19%)	105,105,105	2.00	23 (21%)
3	TA1	i	601	-	68,68,68	1.05	5 (7%)	105,105,105	1.28	11 (10%)
6	GTP	X	502	5	33,34,34	1.16	4 (12%)	50,54,54	1.22	5 (10%)
3	TA1	e	601	-	68,68,68	1.23	6 (8%)	105,105,105	1.48	19 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GTP	Z	502	5	-	7/22/38/38	0/3/3/3
4	GDP	e	602	-	-	5/16/32/32	0/3/3/3
4	GDP	c	602	-	-	4/16/32/32	0/3/3/3
4	GDP	j	602	-	-	5/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GDP	a	602	-	-	4/16/32/32	0/3/3/3
4	GDP	m	602	-	-	5/16/32/32	0/3/3/3
4	GDP	d	602	-	-	4/16/32/32	0/3/3/3
3	TA1	h	601	-	-	12/41/127/127	0/7/7/7
4	GDP	b	602	-	-	5/16/32/32	0/3/3/3
3	TA1	m	601	-	-	10/41/127/127	0/7/7/7
3	TA1	j	601	-	-	10/41/127/127	0/7/7/7
6	GTP	N	502	5	-	4/22/38/38	0/3/3/3
6	GTP	S	502	5	-	4/22/38/38	0/3/3/3
4	GDP	g	602	-	-	5/16/32/32	0/3/3/3
6	GTP	U	502	5	-	3/22/38/38	0/3/3/3
6	GTP	Q	502	5	-	5/22/38/38	0/3/3/3
6	GTP	Y	502	5	-	4/22/38/38	0/3/3/3
3	TA1	l	601	-	-	9/41/127/127	0/7/7/7
4	GDP	i	602	-	-	4/16/32/32	0/3/3/3
4	GDP	h	602	-	-	5/16/32/32	0/3/3/3
3	TA1	b	601	-	-	10/41/127/127	0/7/7/7
6	GTP	R	502	5	-	2/22/38/38	0/3/3/3
3	TA1	a	601	-	-	8/41/127/127	0/7/7/7
4	GDP	k	602	-	-	5/16/32/32	0/3/3/3
3	TA1	f	601	-	-	6/41/127/127	0/7/7/7
3	TA1	c	601	-	-	9/41/127/127	0/7/7/7
4	GDP	l	602	-	-	5/16/32/32	0/3/3/3
6	GTP	P	502	5	-	5/22/38/38	0/3/3/3
6	GTP	T	502	5	-	2/22/38/38	0/3/3/3
4	GDP	f	602	-	-	4/16/32/32	0/3/3/3
6	GTP	V	502	5	-	4/22/38/38	0/3/3/3
3	TA1	d	601	-	-	8/41/127/127	0/7/7/7
6	GTP	W	502	5	-	4/22/38/38	0/3/3/3
3	TA1	g	601	-	-	14/41/127/127	0/7/7/7
6	GTP	O	502	5	-	3/22/38/38	0/3/3/3
3	TA1	k	601	-	-	9/41/127/127	0/7/7/7
3	TA1	i	601	-	-	12/41/127/127	0/7/7/7
6	GTP	X	502	5	-	4/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TA1	e	601	-	-	8/41/127/127	0/7/7/7

All (233) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	b	602	GDP	PA-O3A	8.35	1.68	1.59
6	Z	502	GTP	C1'-N9	6.54	1.66	1.47
6	W	502	GTP	C4-N3	6.45	1.49	1.34
6	T	502	GTP	C1'-N9	6.40	1.65	1.47
6	W	502	GTP	C6-N1	6.06	1.50	1.38
6	T	502	GTP	C4-N9	6.06	1.53	1.38
3	f	601	TA1	C45-C24	6.01	1.64	1.54
4	i	602	GDP	PA-O3A	5.98	1.65	1.59
6	Z	502	GTP	C4-N9	5.59	1.52	1.38
3	k	601	TA1	C45-C24	5.34	1.62	1.54
4	f	602	GDP	PA-O3A	5.10	1.65	1.59
6	Q	502	GTP	C4-N9	5.01	1.50	1.38
3	k	601	TA1	C18-C10	5.00	1.68	1.57
6	U	502	GTP	PB-O3B	4.97	1.64	1.59
4	d	602	GDP	PA-O3A	4.85	1.64	1.59
6	U	502	GTP	C6-N1	4.83	1.47	1.38
6	T	502	GTP	PB-O3B	4.79	1.64	1.59
4	a	602	GDP	PA-O3A	4.74	1.64	1.59
6	R	502	GTP	C4-N9	4.65	1.49	1.38
4	k	602	GDP	PA-O3A	4.42	1.64	1.59
6	R	502	GTP	C4-N3	4.42	1.44	1.34
4	j	602	GDP	PA-O3A	4.37	1.64	1.59
3	f	601	TA1	C18-C10	4.37	1.66	1.57
3	g	601	TA1	C31-C30	4.33	1.59	1.50
3	m	601	TA1	C45-C24	4.33	1.61	1.54
3	k	601	TA1	C21-C24	4.28	1.60	1.51
3	b	601	TA1	C45-C24	4.27	1.61	1.54
4	l	602	GDP	PA-O3A	4.27	1.64	1.59
6	T	502	GTP	C4-N3	4.24	1.44	1.34
6	Z	502	GTP	C4-N3	4.21	1.43	1.34
4	e	602	GDP	PA-O3A	4.17	1.64	1.59
6	W	502	GTP	PB-O3B	4.15	1.64	1.59
3	g	601	TA1	C04-C03	-4.11	1.40	1.50
4	g	602	GDP	PA-O3A	4.10	1.63	1.59
6	P	502	GTP	PB-O3A	4.05	1.63	1.59
6	P	502	GTP	PA-O3A	4.00	1.63	1.59
3	m	601	TA1	C43-C26	3.94	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	h	601	TA1	O07-C17	-3.94	1.37	1.43
6	R	502	GTP	C6-N1	3.93	1.46	1.38
3	e	601	TA1	C45-C24	3.92	1.60	1.54
3	g	601	TA1	C42-C37	3.90	1.45	1.39
3	a	601	TA1	C45-C24	3.87	1.60	1.54
3	m	601	TA1	O11-C26	3.87	1.52	1.45
6	U	502	GTP	O6-C6	3.86	1.30	1.23
6	Q	502	GTP	C4-N3	3.85	1.43	1.34
6	P	502	GTP	O6-C6	3.85	1.30	1.23
6	Y	502	GTP	PB-O3B	3.85	1.63	1.59
6	Q	502	GTP	C1'-N9	3.84	1.58	1.47
4	c	602	GDP	PA-O3A	3.83	1.63	1.59
3	c	601	TA1	C45-C24	3.82	1.60	1.54
6	N	502	GTP	C4-N3	3.81	1.43	1.34
3	g	601	TA1	C30-N01	3.80	1.43	1.34
6	N	502	GTP	C6-N1	3.73	1.45	1.38
4	h	602	GDP	C5-C4	3.71	1.49	1.38
4	h	602	GDP	PA-O3A	3.71	1.63	1.59
4	b	602	GDP	C5-C4	3.69	1.48	1.38
6	Q	502	GTP	PA-O3A	3.67	1.63	1.59
3	g	601	TA1	C32-C31	3.66	1.45	1.39
3	g	601	TA1	C38-C37	-3.64	1.33	1.39
4	c	602	GDP	C4-N9	-3.64	1.28	1.38
3	l	601	TA1	C45-C24	3.63	1.60	1.54
4	g	602	GDP	C5-C4	3.62	1.48	1.38
3	k	601	TA1	C31-C30	3.61	1.58	1.50
6	V	502	GTP	PB-O3B	3.61	1.63	1.59
4	f	602	GDP	C5-C4	3.54	1.48	1.38
6	P	502	GTP	PB-O3B	3.52	1.63	1.59
6	Z	502	GTP	PB-O3B	3.52	1.63	1.59
3	g	601	TA1	C37-C29	3.52	1.56	1.52
6	R	502	GTP	C1'-N9	3.50	1.57	1.47
6	Q	502	GTP	O6-C6	3.48	1.30	1.23
3	g	601	TA1	C43-C26	3.47	1.59	1.52
4	c	602	GDP	C5-C4	3.45	1.48	1.38
3	k	601	TA1	C32-C31	3.45	1.44	1.39
3	c	601	TA1	C43-C26	3.43	1.59	1.52
6	S	502	GTP	PB-O3B	3.43	1.63	1.59
3	m	601	TA1	C25-C24	3.40	1.39	1.34
6	P	502	GTP	O5'-C5'	3.39	1.57	1.44
4	i	602	GDP	C5-C4	3.39	1.48	1.38
3	e	601	TA1	C18-C10	3.39	1.64	1.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	j	601	TA1	C45-C24	3.37	1.59	1.54
6	Q	502	GTP	PB-O3B	3.35	1.63	1.59
6	X	502	GTP	PB-O3A	3.32	1.63	1.59
3	l	601	TA1	C43-C26	3.30	1.59	1.52
3	j	601	TA1	O11-C26	3.30	1.51	1.45
4	j	602	GDP	C5-C4	3.29	1.47	1.38
3	h	601	TA1	C43-C26	3.28	1.59	1.52
6	W	502	GTP	C4-N9	3.28	1.46	1.38
4	e	602	GDP	C5-C4	3.26	1.47	1.38
4	g	602	GDP	C4-N9	-3.26	1.29	1.38
6	R	502	GTP	PB-O3B	3.24	1.63	1.59
4	k	602	GDP	C5-C4	3.23	1.47	1.38
6	W	502	GTP	PB-O3A	3.23	1.63	1.59
6	T	502	GTP	C5-N7	3.21	1.45	1.39
4	m	602	GDP	PA-O3A	3.20	1.63	1.59
3	i	601	TA1	C45-C24	3.19	1.59	1.54
4	a	602	GDP	C6-N1	-3.18	1.32	1.38
4	d	602	GDP	C5-C4	3.15	1.47	1.38
6	R	502	GTP	C5-N7	3.15	1.45	1.39
4	b	602	GDP	C4-N3	3.14	1.41	1.34
3	k	601	TA1	C43-C26	3.14	1.58	1.52
3	f	601	TA1	C43-C26	3.12	1.58	1.52
3	b	601	TA1	O11-C26	3.11	1.51	1.45
4	l	602	GDP	C5-C4	3.09	1.47	1.38
3	d	601	TA1	C18-C10	3.09	1.63	1.57
4	d	602	GDP	C2-N3	3.05	1.40	1.33
3	k	601	TA1	C30-N01	3.03	1.41	1.34
6	Q	502	GTP	C6-N1	2.98	1.44	1.38
3	b	601	TA1	C43-C26	2.94	1.58	1.52
4	k	602	GDP	C4-N9	-2.94	1.30	1.38
4	c	602	GDP	O4'-C1'	2.94	1.48	1.42
4	m	602	GDP	C5-C4	2.93	1.46	1.38
3	k	601	TA1	C10-C02	2.93	1.64	1.57
3	j	601	TA1	C43-C26	2.89	1.58	1.52
6	N	502	GTP	C4-N9	2.87	1.45	1.38
6	P	502	GTP	C4-N9	2.87	1.45	1.38
3	i	601	TA1	C43-C26	2.85	1.58	1.52
3	d	601	TA1	C43-C26	2.85	1.58	1.52
4	i	602	GDP	C4-N9	-2.84	1.30	1.38
3	f	601	TA1	C10-C02	2.83	1.64	1.57
3	g	601	TA1	C06-C05	-2.80	1.34	1.38
3	g	601	TA1	C45-C24	2.79	1.58	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	f	601	TA1	C30-N01	2.79	1.40	1.34
4	i	602	GDP	O4'-C4'	2.78	1.51	1.45
3	k	601	TA1	C26-C25	2.78	1.56	1.51
3	a	601	TA1	C43-C26	2.78	1.58	1.52
3	f	601	TA1	C18-C17	2.77	1.63	1.55
3	e	601	TA1	C43-C26	2.77	1.58	1.52
3	c	601	TA1	O11-C26	2.75	1.50	1.45
6	S	502	GTP	PB-O3A	2.73	1.62	1.59
3	d	601	TA1	C45-C24	2.72	1.58	1.54
3	f	601	TA1	C31-C30	2.71	1.56	1.50
6	U	502	GTP	O2'-C2'	2.71	1.49	1.43
4	e	602	GDP	C4-N9	-2.70	1.31	1.38
6	W	502	GTP	C5-N7	2.70	1.44	1.39
3	l	601	TA1	O11-C26	2.69	1.50	1.45
6	O	502	GTP	C6-N1	2.68	1.43	1.38
4	j	602	GDP	C4-N9	-2.68	1.31	1.38
6	U	502	GTP	C2'-C1'	2.65	1.61	1.53
6	Q	502	GTP	C5-C4	2.65	1.46	1.38
6	Y	502	GTP	PB-O3A	2.65	1.62	1.59
3	d	601	TA1	O09-C21	2.65	1.50	1.44
6	P	502	GTP	C1'-N9	2.63	1.55	1.47
3	k	601	TA1	O02-C02	2.62	1.49	1.45
4	h	602	GDP	C4-N9	-2.62	1.31	1.38
6	Z	502	GTP	C8-N9	2.62	1.43	1.37
3	e	601	TA1	O09-C21	2.61	1.50	1.44
6	Z	502	GTP	C5-N7	2.61	1.44	1.39
6	P	502	GTP	C5-C4	2.61	1.45	1.38
6	U	502	GTP	C2-N1	2.60	1.43	1.37
3	k	601	TA1	C11-C15	2.59	1.59	1.55
4	g	602	GDP	C2-N3	2.59	1.39	1.33
3	d	601	TA1	O11-C26	2.58	1.50	1.45
6	O	502	GTP	PB-O3B	2.58	1.62	1.59
3	m	601	TA1	C43-C01	2.57	1.59	1.54
3	j	601	TA1	C25-C24	2.57	1.38	1.34
6	Q	502	GTP	PB-O3A	2.57	1.62	1.59
4	f	602	GDP	C4-N9	-2.56	1.31	1.38
6	Q	502	GTP	C5-N7	2.54	1.44	1.39
3	f	601	TA1	C11-C15	2.53	1.59	1.55
6	R	502	GTP	PA-O3A	2.52	1.62	1.59
4	a	602	GDP	C5-C4	2.52	1.45	1.38
3	c	601	TA1	O09-C21	2.52	1.50	1.44
6	N	502	GTP	PB-O3B	2.49	1.62	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	e	602	GDP	C2-N3	2.49	1.39	1.33
6	Z	502	GTP	C2'-C1'	2.48	1.61	1.53
4	m	602	GDP	C4-N9	-2.48	1.31	1.38
3	a	601	TA1	O11-C26	2.47	1.50	1.45
6	T	502	GTP	C2'-C3'	2.46	1.60	1.53
3	k	601	TA1	C37-C29	2.45	1.55	1.52
6	T	502	GTP	O2'-C2'	2.44	1.49	1.43
6	X	502	GTP	PB-O3B	2.44	1.62	1.59
3	h	601	TA1	C31-C30	2.43	1.55	1.50
4	l	602	GDP	C4-N9	-2.43	1.31	1.38
3	f	601	TA1	O11-C26	2.41	1.50	1.45
6	T	502	GTP	O4'-C1'	2.41	1.47	1.42
6	T	502	GTP	C8-N9	2.39	1.42	1.37
4	g	602	GDP	C5-C6	2.36	1.53	1.44
3	b	601	TA1	C37-C29	2.35	1.55	1.52
3	c	601	TA1	C25-C24	2.35	1.38	1.34
6	Z	502	GTP	O2'-C2'	2.35	1.48	1.43
4	d	602	GDP	C4-N9	-2.35	1.32	1.38
6	R	502	GTP	O6-C6	2.35	1.28	1.23
6	W	502	GTP	C2-N1	2.34	1.43	1.37
6	W	502	GTP	C1'-N9	2.33	1.54	1.47
6	T	502	GTP	C2-N1	-2.32	1.32	1.37
6	T	502	GTP	C2'-C1'	2.32	1.60	1.53
3	m	601	TA1	C31-C30	2.32	1.55	1.50
3	i	601	TA1	C31-C30	2.31	1.55	1.50
4	i	602	GDP	C2-N3	2.30	1.38	1.33
3	i	601	TA1	O11-C26	2.29	1.50	1.45
4	h	602	GDP	C2-N3	2.28	1.38	1.33
4	m	602	GDP	C2-N3	2.28	1.38	1.33
3	h	601	TA1	C45-C24	2.28	1.57	1.54
3	e	601	TA1	C37-C29	2.28	1.55	1.52
6	Q	502	GTP	C5-C6	2.27	1.52	1.44
4	b	602	GDP	O6-C6	2.27	1.27	1.23
3	k	601	TA1	O09-C21	2.26	1.49	1.44
4	m	602	GDP	O2'-C2'	2.25	1.48	1.43
6	S	502	GTP	PA-O3A	2.24	1.61	1.59
4	c	602	GDP	C5-N7	-2.24	1.34	1.39
3	g	601	TA1	C11-C10	2.23	1.59	1.54
3	d	601	TA1	C11-C15	2.22	1.59	1.55
4	c	602	GDP	C3'-C4'	2.20	1.58	1.53
4	i	602	GDP	O2'-C2'	2.19	1.48	1.43
6	X	502	GTP	C4-N3	2.18	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	V	502	GTP	C5-C6	-2.18	1.36	1.44
3	h	601	TA1	O11-C26	2.17	1.49	1.45
3	f	601	TA1	C25-C24	2.17	1.37	1.34
6	S	502	GTP	C6-N1	2.17	1.42	1.38
3	g	601	TA1	C01-C02	2.15	1.64	1.57
3	b	601	TA1	O09-C21	2.14	1.49	1.44
4	a	602	GDP	C4-N3	2.12	1.39	1.34
3	h	601	TA1	C25-C24	2.11	1.37	1.34
3	g	601	TA1	O13-C28	-2.10	1.38	1.42
3	b	601	TA1	C25-C24	2.10	1.37	1.34
3	e	601	TA1	C10-C02	2.10	1.62	1.57
3	b	601	TA1	C18-C20	2.10	1.61	1.55
6	X	502	GTP	C4-N9	2.10	1.43	1.38
3	l	601	TA1	C25-C24	2.10	1.37	1.34
6	T	502	GTP	C5-C6	2.10	1.52	1.44
6	W	502	GTP	C2-N2	2.08	1.39	1.34
3	m	601	TA1	C30-N01	2.08	1.39	1.34
3	f	601	TA1	C11-C10	2.08	1.59	1.54
6	Z	502	GTP	O4'-C1'	2.07	1.46	1.42
4	d	602	GDP	C4-N3	2.07	1.39	1.34
3	g	601	TA1	C36-C31	2.05	1.42	1.39
4	c	602	GDP	O2'-C2'	2.04	1.48	1.43
4	a	602	GDP	C4-N9	-2.03	1.32	1.38
6	S	502	GTP	C5-C6	-2.03	1.37	1.44
3	i	601	TA1	C25-C24	2.03	1.37	1.34
3	d	601	TA1	C10-C02	2.02	1.62	1.57
3	h	601	TA1	C43-C01	2.01	1.58	1.54
3	g	601	TA1	O14-C30	2.00	1.28	1.23

All (626) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	g	601	TA1	C42-C37-C29	15.02	144.64	120.78
3	g	601	TA1	C38-C37-C29	-14.25	98.14	120.78
3	g	601	TA1	C05-C04-C03	-8.57	101.51	120.40
6	T	502	GTP	C5-C4-N3	-8.14	115.44	128.39
3	g	601	TA1	C09-C04-C05	7.91	128.63	118.57
3	k	601	TA1	C45-C24-C25	-7.52	109.48	119.60
6	Z	502	GTP	O2'-C2'-C1'	7.50	135.93	110.10
6	T	502	GTP	O6-C6-N1	-7.28	106.42	120.11
3	g	601	TA1	C08-C09-C04	-6.57	113.90	120.36
6	P	502	GTP	O5'-C5'-C4'	6.55	131.31	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	U	502	GTP	O2'-C2'-C1'	6.47	132.37	110.10
3	g	601	TA1	C11-O04-C12	6.36	135.29	119.17
3	h	601	TA1	O07-C17-C16	-6.27	96.37	109.12
4	d	602	GDP	N9-C8-N7	-6.20	101.90	113.40
6	T	502	GTP	O2'-C2'-C1'	6.14	131.23	110.10
3	g	601	TA1	O02-C03-O03	6.11	133.47	123.55
4	d	602	GDP	C8-N9-C4	6.11	117.47	106.03
4	a	602	GDP	C6-C5-N7	5.98	141.18	130.29
4	g	602	GDP	C8-N9-C4	5.88	117.04	106.03
4	a	602	GDP	N9-C8-N7	-5.86	102.54	113.40
6	W	502	GTP	O2'-C2'-C1'	5.73	129.84	110.10
4	e	602	GDP	C8-N9-C4	5.63	116.59	106.03
3	g	601	TA1	C02-O02-C03	5.56	127.96	117.80
4	m	602	GDP	N9-C8-N7	-5.54	103.13	113.40
4	f	602	GDP	C8-N9-C4	5.33	116.01	106.03
4	l	602	GDP	N9-C8-N7	-5.33	103.52	113.40
3	c	601	TA1	C02-O02-C03	5.32	127.52	117.80
3	f	601	TA1	C01-C02-C10	5.31	126.15	118.19
3	k	601	TA1	C18-C10-C02	5.31	127.35	115.62
4	e	602	GDP	N9-C8-N7	-5.31	103.56	113.40
3	f	601	TA1	C17-C18-C20	5.30	114.48	102.58
4	m	602	GDP	C6-C5-N7	5.30	139.93	130.29
4	f	602	GDP	N9-C8-N7	-5.24	103.68	113.40
4	l	602	GDP	C6-C5-N7	5.24	139.82	130.29
4	a	602	GDP	C8-N7-C5	5.21	113.54	104.26
6	T	502	GTP	C2'-C1'-N9	5.21	127.74	113.25
4	l	602	GDP	C8-N9-C4	5.17	115.72	106.03
4	d	602	GDP	C6-C5-N7	5.15	139.67	130.29
4	m	602	GDP	C8-N9-C4	5.14	115.66	106.03
4	k	602	GDP	N9-C8-N7	-5.11	103.93	113.40
3	h	601	TA1	C11-O04-C12	5.10	132.09	119.17
6	P	502	GTP	C6-C5-C4	5.09	126.49	118.83
4	e	602	GDP	C6-C5-N7	5.06	139.49	130.29
4	a	602	GDP	C5-C4-N3	-5.03	120.38	128.39
6	W	502	GTP	C2'-C1'-N9	5.03	127.26	113.25
4	j	602	GDP	N9-C8-N7	-5.03	104.08	113.40
4	d	602	GDP	C8-N7-C5	5.00	113.17	104.26
3	g	601	TA1	O13-C28-C29	-4.99	95.65	109.69
6	U	502	GTP	C2'-C1'-N9	4.96	127.06	113.25
6	Q	502	GTP	C5-C4-N3	-4.96	120.49	128.39
3	b	601	TA1	C17-C18-C20	4.95	113.69	102.58
6	Z	502	GTP	C5-C4-N3	-4.94	120.52	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Z	502	GTP	C2'-C1'-N9	4.94	127.00	113.25
6	T	502	GTP	C2-N3-C4	4.94	120.80	112.30
3	k	601	TA1	C01-C02-C10	4.93	125.57	118.19
6	R	502	GTP	O2'-C2'-C1'	4.91	127.00	110.10
4	h	602	GDP	C8-N9-C4	4.90	115.22	106.03
4	k	602	GDP	C8-N9-C4	4.90	115.21	106.03
3	g	601	TA1	C37-C29-N01	4.89	121.48	112.07
4	h	602	GDP	N9-C8-N7	-4.87	104.36	113.40
6	W	502	GTP	C5-C4-N9	-4.87	96.93	105.66
4	c	602	GDP	C8-N9-C4	4.85	115.12	106.03
6	S	502	GTP	C4-C5-N7	4.84	118.33	110.67
6	S	502	GTP	C8-N7-C5	-4.83	95.66	104.26
6	P	502	GTP	C5'-C4'-C3'	-4.82	97.84	115.21
6	R	502	GTP	C1'-N9-C8	-4.82	113.03	126.73
6	R	502	GTP	C2'-C1'-N9	4.82	126.66	113.25
3	g	601	TA1	C36-C31-C32	-4.81	112.45	118.57
6	R	502	GTP	C1'-N9-C4	4.81	140.68	126.49
6	W	502	GTP	C1'-N9-C8	-4.79	113.11	126.73
4	m	602	GDP	C8-N7-C5	4.77	112.76	104.26
4	j	602	GDP	C8-N9-C4	4.77	114.97	106.03
6	P	502	GTP	C8-N9-C4	-4.76	97.11	106.03
4	f	602	GDP	C6-C5-N7	4.72	138.89	130.29
6	Q	502	GTP	C1'-N9-C4	4.71	140.40	126.49
3	m	601	TA1	C11-O04-C12	4.70	131.08	119.17
3	c	601	TA1	C11-O04-C12	4.70	131.07	119.17
4	k	602	GDP	C6-C5-N7	4.69	138.82	130.29
3	k	601	TA1	C19-C18-C20	-4.68	94.44	106.56
4	i	602	GDP	N9-C8-N7	-4.68	104.73	113.40
4	g	602	GDP	N9-C8-N7	-4.66	104.76	113.40
4	a	602	GDP	C4-C5-N7	-4.65	103.30	110.67
6	Z	502	GTP	O4'-C1'-N9	4.65	118.90	108.36
4	i	602	GDP	C8-N9-C4	4.65	114.74	106.03
4	k	602	GDP	C2'-C3'-C4'	4.64	111.58	102.61
4	a	602	GDP	C8-N9-C4	4.60	114.65	106.03
6	W	502	GTP	N1-C2-N3	-4.60	114.91	123.32
6	Y	502	GTP	O2'-C2'-C1'	4.60	125.94	110.10
3	j	601	TA1	C11-O04-C12	4.59	130.81	119.17
6	P	502	GTP	O4'-C4'-C5'	4.56	123.94	109.33
4	h	602	GDP	C6-C5-N7	4.56	138.59	130.29
6	W	502	GTP	N9-C4-N3	4.52	134.99	125.95
6	R	502	GTP	PA-O5'-C5'	-4.48	95.67	121.35
6	P	502	GTP	O4'-C4'-C3'	-4.47	96.29	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	a	602	GDP	C2-N3-C4	4.45	119.96	112.30
4	g	602	GDP	N9-C4-N3	4.44	134.84	125.95
4	j	602	GDP	C6-C5-N7	4.43	138.35	130.29
3	f	601	TA1	C19-C18-C20	-4.42	95.12	106.56
4	f	602	GDP	O3B-PB-O3A	4.42	119.44	104.64
4	d	602	GDP	N9-C4-N3	4.39	134.72	125.95
4	h	602	GDP	C8-N7-C5	4.38	112.06	104.26
3	g	601	TA1	C06-C05-C04	-4.36	116.08	120.36
3	h	601	TA1	C10-C18-C17	-4.35	98.28	106.55
3	g	601	TA1	C45-C01-C02	4.35	116.71	111.93
3	k	601	TA1	C10-C18-C20	4.33	123.44	116.30
3	k	601	TA1	C29-N01-C30	4.32	130.62	121.94
6	S	502	GTP	O6-C6-N1	4.29	128.18	120.11
4	b	602	GDP	C6-C5-N7	4.29	138.10	130.29
4	b	602	GDP	N9-C4-N3	4.27	134.50	125.95
3	h	601	TA1	C02-O02-C03	4.27	125.60	117.80
6	T	502	GTP	O4'-C1'-N9	4.27	118.03	108.36
6	T	502	GTP	N2-C2-N1	-4.26	107.76	116.76
6	Z	502	GTP	C1'-N9-C4	4.26	139.06	126.49
6	Q	502	GTP	O2'-C2'-C1'	4.25	124.75	110.10
4	c	602	GDP	C6-C5-N7	4.20	137.94	130.29
3	g	601	TA1	C09-C04-C03	4.20	129.66	120.40
6	P	502	GTP	C4-C5-N7	-4.19	104.03	110.67
3	i	601	TA1	C45-C01-C02	4.18	116.52	111.93
6	P	502	GTP	C5-C4-N9	4.11	113.02	105.66
4	i	602	GDP	N9-C4-N3	4.11	134.17	125.95
4	b	602	GDP	C5-C4-N3	-4.08	121.89	128.39
6	Q	502	GTP	C2-N3-C4	4.08	119.33	112.30
4	c	602	GDP	C2'-C3'-C4'	4.08	110.49	102.61
3	g	601	TA1	C37-C29-C28	4.06	121.55	111.46
4	g	602	GDP	N2-C2-N3	4.04	127.57	119.67
3	a	601	TA1	C11-O04-C12	4.03	129.40	119.17
4	e	602	GDP	C8-N7-C5	4.02	111.42	104.26
3	k	601	TA1	C44-C25-C24	-4.01	120.54	125.32
4	c	602	GDP	N9-C8-N7	-4.01	105.96	113.40
4	f	602	GDP	C8-N7-C5	4.01	111.40	104.26
6	R	502	GTP	C2-N3-C4	4.00	119.20	112.30
3	m	601	TA1	C42-C37-C29	4.00	127.13	120.78
4	f	602	GDP	N9-C4-N3	3.99	133.94	125.95
6	V	502	GTP	C5-C4-N9	-3.98	98.53	105.66
3	m	601	TA1	C21-C24-C25	3.97	125.93	120.29
3	a	601	TA1	C45-C01-C02	3.97	116.29	111.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	k	601	TA1	C45-C24-C21	3.96	131.53	119.08
3	i	601	TA1	C11-O04-C12	3.96	129.20	119.17
6	S	502	GTP	C2-N1-C6	3.95	132.28	125.11
6	U	502	GTP	C2-N1-C6	3.93	132.25	125.11
3	e	601	TA1	C29-N01-C30	3.93	129.84	121.94
3	g	601	TA1	C33-C32-C31	3.91	124.21	120.36
4	f	602	GDP	C2'-C3'-C4'	3.91	110.16	102.61
6	W	502	GTP	C4-C5-N7	3.89	116.83	110.67
6	T	502	GTP	O3'-C3'-C2'	3.89	124.28	111.82
6	P	502	GTP	C5-C6-N1	-3.87	103.40	113.25
3	d	601	TA1	C45-C01-C02	3.87	116.18	111.93
6	T	502	GTP	C1'-N9-C4	3.85	137.87	126.49
3	j	601	TA1	C02-O02-C03	3.84	124.81	117.80
3	g	601	TA1	C17-C18-C20	3.83	111.18	102.58
4	j	602	GDP	C8-N7-C5	3.83	111.08	104.26
4	h	602	GDP	C2'-C3'-C4'	3.83	110.00	102.61
3	b	601	TA1	C11-O04-C12	3.83	128.87	119.17
4	a	602	GDP	N9-C4-N3	3.82	133.60	125.95
3	k	601	TA1	C21-O09-C22	3.82	123.83	115.95
3	h	601	TA1	C45-C01-C02	3.81	116.11	111.93
6	V	502	GTP	C4-C5-N7	3.81	116.70	110.67
6	T	502	GTP	N9-C4-N3	3.80	133.54	125.95
6	Z	502	GTP	O2B-PB-O3A	-3.79	97.02	107.27
6	R	502	GTP	O2B-PB-O3B	3.78	117.49	107.27
6	T	502	GTP	C8-N9-C4	-3.76	98.98	106.03
3	m	601	TA1	C38-C37-C29	-3.76	114.81	120.78
3	l	601	TA1	C11-O04-C12	3.75	128.69	119.17
6	U	502	GTP	C5-C6-N1	-3.73	103.76	113.25
4	j	602	GDP	O3B-PB-O3A	3.72	117.13	104.64
3	l	601	TA1	C45-C01-C02	3.72	116.02	111.93
3	h	601	TA1	C17-C18-C20	3.72	110.93	102.58
6	P	502	GTP	O3'-C3'-C2'	3.72	123.73	111.82
4	i	602	GDP	O3B-PB-O3A	3.70	117.05	104.64
4	l	602	GDP	C2'-C3'-C4'	3.70	109.76	102.61
3	k	601	TA1	C32-C31-C30	3.69	132.57	120.60
4	g	602	GDP	C6-C5-N7	3.69	137.00	130.29
6	Q	502	GTP	C4-C5-N7	-3.68	104.83	110.67
4	i	602	GDP	C6-C5-N7	3.68	137.00	130.29
3	k	601	TA1	C36-C31-C32	-3.68	113.88	118.57
4	l	602	GDP	C8-N7-C5	3.68	110.82	104.26
4	c	602	GDP	N9-C4-N3	3.68	133.31	125.95
3	e	601	TA1	C45-C01-C02	3.67	115.97	111.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	d	601	TA1	C17-C18-C20	3.67	110.83	102.58
3	f	601	TA1	C29-N01-C30	3.67	129.32	121.94
4	h	602	GDP	N9-C4-N3	3.67	133.29	125.95
3	g	601	TA1	C32-C31-C30	3.67	132.49	120.60
4	i	602	GDP	C8-N7-C5	3.67	110.79	104.26
6	V	502	GTP	O2'-C2'-C1'	3.67	122.73	110.10
4	b	602	GDP	O2B-PB-O3A	-3.65	92.41	104.64
4	d	602	GDP	O6-C6-C5	-3.65	116.91	126.53
4	b	602	GDP	O6-C6-C5	-3.64	116.92	126.53
3	j	601	TA1	C42-C37-C29	3.63	126.55	120.78
6	S	502	GTP	C5'-C4'-C3'	-3.63	102.16	115.21
3	f	601	TA1	O04-C11-C14	-3.62	100.46	108.13
3	g	601	TA1	C29-N01-C30	3.62	129.22	121.94
4	l	602	GDP	C6-C5-C4	-3.61	113.39	118.83
6	U	502	GTP	O3'-C3'-C2'	3.60	123.36	111.82
3	e	601	TA1	C02-O02-C03	3.60	124.37	117.80
3	f	601	TA1	O01-C01-C02	3.60	113.34	105.54
3	c	601	TA1	C17-C18-C20	3.59	110.65	102.58
4	g	602	GDP	N2-C2-N1	-3.59	109.19	116.76
3	a	601	TA1	C17-C18-C20	3.57	110.59	102.58
3	j	601	TA1	C45-C01-C02	3.57	115.85	111.93
3	g	601	TA1	O04-C11-C15	-3.56	104.05	112.26
4	j	602	GDP	N9-C4-N3	3.54	133.04	125.95
6	S	502	GTP	C6-C5-N7	-3.54	123.85	130.29
6	R	502	GTP	C5-C4-N3	-3.53	122.77	128.39
6	T	502	GTP	C4-C5-N7	-3.52	105.09	110.67
3	e	601	TA1	C17-C18-C20	3.52	110.48	102.58
4	m	602	GDP	N9-C4-N3	3.52	132.99	125.95
3	h	601	TA1	C21-C24-C25	3.52	125.28	120.29
4	h	602	GDP	O2'-C2'-C3'	3.51	123.08	111.82
3	j	601	TA1	C17-C18-C20	3.51	110.47	102.58
3	g	601	TA1	O02-C02-C10	-3.51	101.80	108.17
4	l	602	GDP	C2-N3-C4	3.51	118.34	112.30
3	b	601	TA1	C02-O02-C03	3.49	124.17	117.80
3	f	601	TA1	C36-C31-C32	-3.48	114.14	118.57
4	d	602	GDP	C4-C5-N7	-3.48	105.16	110.67
4	k	602	GDP	C8-N7-C5	3.47	110.45	104.26
6	O	502	GTP	O2B-PB-O3B	3.47	116.65	107.27
4	g	602	GDP	C2'-C3'-C4'	3.46	109.29	102.61
3	g	601	TA1	O02-C02-C01	3.46	111.91	104.74
3	h	601	TA1	C29-N01-C30	3.46	128.90	121.94
6	S	502	GTP	N9-C8-N7	3.46	119.81	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	c	602	GDP	C8-N7-C5	3.45	110.41	104.26
6	Z	502	GTP	N9-C4-N3	3.44	132.83	125.95
6	U	502	GTP	PA-O5'-C5'	-3.43	101.72	121.35
3	e	601	TA1	C31-C30-N01	-3.41	110.71	117.04
3	k	601	TA1	C33-C32-C31	3.41	123.72	120.36
3	g	601	TA1	C08-C07-C06	3.41	124.54	119.87
3	b	601	TA1	C45-C01-C02	3.41	115.68	111.93
4	k	602	GDP	C6-C5-C4	-3.41	113.71	118.83
4	m	602	GDP	C4-C5-N7	-3.40	105.28	110.67
6	Q	502	GTP	C2'-C1'-N9	3.39	122.68	113.25
4	d	602	GDP	C5-C4-N3	-3.38	123.01	128.39
3	m	601	TA1	C47-C45-C24	3.37	126.25	112.78
4	k	602	GDP	N9-C4-N3	3.36	132.68	125.95
3	i	601	TA1	C02-O02-C03	3.34	123.89	117.80
4	b	602	GDP	C2-N3-C4	3.33	118.03	112.30
6	W	502	GTP	C2-N3-C4	3.33	118.03	112.30
6	R	502	GTP	O3'-C3'-C4'	3.32	120.62	111.08
4	h	602	GDP	O3B-PB-O3A	3.32	115.77	104.64
6	V	502	GTP	O5'-C5'-C4'	3.32	120.29	108.99
4	h	602	GDP	O6-C6-N1	3.31	126.34	120.11
3	b	601	TA1	C19-C18-C20	-3.31	98.00	106.56
6	Z	502	GTP	O5'-C5'-C4'	3.30	120.22	108.99
6	T	502	GTP	C2-N1-C6	-3.30	119.13	125.11
4	g	602	GDP	C6-C5-C4	-3.29	113.89	118.83
4	j	602	GDP	C2'-C3'-C4'	3.28	108.95	102.61
6	Z	502	GTP	O2B-PB-O3B	3.28	116.15	107.27
6	N	502	GTP	C1'-N9-C8	-3.28	117.41	126.73
3	k	601	TA1	C02-O02-C03	3.28	123.79	117.80
3	l	601	TA1	C17-C18-C20	3.28	109.94	102.58
6	Y	502	GTP	C2'-C1'-N9	3.27	122.36	113.25
3	d	601	TA1	C19-C18-C20	-3.27	98.09	106.56
6	N	502	GTP	O2B-PB-O3B	3.27	116.12	107.27
4	m	602	GDP	O2'-C2'-C3'	3.27	122.30	111.82
4	b	602	GDP	C8-N9-C4	3.27	112.15	106.03
4	b	602	GDP	N9-C8-N7	-3.27	107.34	113.40
4	f	602	GDP	O6-C6-C5	-3.26	117.93	126.53
4	e	602	GDP	N9-C4-N3	3.25	132.46	125.95
3	g	601	TA1	C10-C18-C17	-3.25	100.38	106.55
4	b	602	GDP	C8-N7-C5	3.24	110.03	104.26
4	k	602	GDP	C2-N3-C4	3.22	117.85	112.30
6	Y	502	GTP	C4-C5-N7	-3.22	105.57	110.67
3	c	601	TA1	C45-C01-C02	3.22	115.47	111.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	602	GDP	C2-N3-C4	3.20	117.80	112.30
4	e	602	GDP	C2'-C3'-C4'	3.19	108.78	102.61
6	P	502	GTP	C5-C4-N3	-3.19	123.31	128.39
3	m	601	TA1	C02-O02-C03	3.19	123.63	117.80
3	k	601	TA1	C43-C01-C45	-3.19	105.72	111.48
4	e	602	GDP	O6-C6-C5	-3.18	118.13	126.53
4	d	602	GDP	N2-C2-N3	3.18	125.87	119.67
6	Y	502	GTP	O2B-PB-O3B	3.17	115.85	107.27
6	T	502	GTP	N2-C2-N3	3.17	125.87	119.67
6	U	502	GTP	C5-C4-N3	3.17	133.44	128.39
4	c	602	GDP	O3B-PB-O3A	3.17	115.27	104.64
6	P	502	GTP	C2'-C1'-N9	3.16	122.06	113.25
6	S	502	GTP	C5-C4-N3	3.16	133.42	128.39
3	e	601	TA1	C19-C18-C20	-3.16	98.38	106.56
6	N	502	GTP	C1'-N9-C4	3.16	135.82	126.49
3	k	601	TA1	C01-C45-C24	3.15	108.22	105.26
4	j	602	GDP	O2'-C2'-C3'	3.15	121.91	111.82
4	e	602	GDP	C6-C5-C4	-3.14	114.10	118.83
4	h	602	GDP	O6-C6-C5	-3.14	118.24	126.53
3	k	601	TA1	O11-C27-C28	-3.14	106.16	111.13
6	Q	502	GTP	C1'-N9-C8	-3.13	117.83	126.73
4	c	602	GDP	O2'-C2'-C3'	3.13	121.84	111.82
3	b	601	TA1	C29-N01-C30	3.13	128.23	121.94
6	W	502	GTP	C1'-N9-C4	3.13	135.72	126.49
4	i	602	GDP	O6-C6-N1	3.11	125.96	120.11
6	T	502	GTP	C6-C5-N7	3.11	135.95	130.29
4	g	602	GDP	C5-C4-N9	-3.10	100.10	105.66
4	i	602	GDP	O6-C6-C5	-3.10	118.34	126.53
4	b	602	GDP	O6-C6-N1	3.10	125.94	120.11
6	V	502	GTP	O3'-C3'-C4'	3.10	119.98	111.08
3	f	601	TA1	C35-C36-C31	3.10	123.41	120.36
4	d	602	GDP	O3B-PB-O3A	3.07	114.92	104.64
4	m	602	GDP	C2'-C3'-C4'	3.06	108.52	102.61
3	e	601	TA1	C26-O11-C27	3.05	122.07	116.58
3	g	601	TA1	C35-C36-C31	3.05	123.37	120.36
4	e	602	GDP	O3B-PB-O3A	3.05	114.85	104.64
3	m	601	TA1	C05-C04-C03	-3.04	113.69	120.40
4	m	602	GDP	O6-C6-C5	-3.04	118.50	126.53
6	Y	502	GTP	PA-O5'-C5'	-3.04	103.94	121.35
3	c	601	TA1	C26-O11-C27	3.04	122.05	116.58
6	R	502	GTP	N9-C4-N3	3.03	132.02	125.95
3	m	601	TA1	C17-C18-C20	3.03	109.39	102.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	602	GDP	C6-C5-C4	-3.03	114.27	118.83
3	m	601	TA1	O04-C11-C10	3.03	113.93	109.24
3	g	601	TA1	O04-C11-C10	3.02	113.92	109.24
4	i	602	GDP	C2-N3-C4	3.02	117.50	112.30
4	l	602	GDP	N9-C4-N3	3.02	131.99	125.95
3	k	601	TA1	C45-C01-C02	3.02	115.25	111.93
3	i	601	TA1	C21-C24-C25	3.01	124.56	120.29
3	m	601	TA1	C26-O11-C27	3.01	121.99	116.58
6	N	502	GTP	C2-N3-C4	2.99	117.44	112.30
6	T	502	GTP	C5-C4-N9	2.98	110.98	105.66
4	j	602	GDP	C6-C5-C4	-2.97	114.36	118.83
6	U	502	GTP	O2B-PB-O3A	-2.96	99.27	107.27
3	i	601	TA1	C17-C18-C20	2.95	109.21	102.58
4	g	602	GDP	O3B-PB-O3A	2.95	114.53	104.64
3	e	601	TA1	O04-C11-C14	-2.95	101.88	108.13
6	W	502	GTP	N2-C2-N1	2.95	122.98	116.76
4	d	602	GDP	C2-N3-C4	2.94	117.37	112.30
4	i	602	GDP	C5-C4-N3	-2.94	123.71	128.39
6	S	502	GTP	N1-C2-N3	-2.93	117.95	123.32
4	d	602	GDP	C2'-C3'-C4'	2.93	108.28	102.61
6	O	502	GTP	C2-N1-C6	2.93	130.43	125.11
6	P	502	GTP	N9-C8-N7	2.93	118.83	113.40
6	T	502	GTP	O6-C6-C5	2.93	134.26	126.53
4	k	602	GDP	O2'-C2'-C3'	2.92	121.18	111.82
6	N	502	GTP	N9-C4-N3	2.92	131.79	125.95
3	c	601	TA1	C21-C24-C25	2.91	124.42	120.29
4	i	602	GDP	C2'-C3'-C4'	2.90	108.20	102.61
3	j	601	TA1	O04-C11-C10	2.90	113.72	109.24
3	g	601	TA1	O11-C27-C28	-2.89	106.55	111.13
4	i	602	GDP	O3'-C3'-C4'	-2.88	102.80	111.08
6	R	502	GTP	C8-N7-C5	2.87	109.37	104.26
6	R	502	GTP	O5'-C5'-C4'	2.87	118.75	108.99
6	Z	502	GTP	C1'-N9-C8	-2.87	118.59	126.73
4	f	602	GDP	O3A-PB-O1B	-2.86	96.01	111.04
6	R	502	GTP	O2B-PB-O3A	-2.85	99.56	107.27
3	j	601	TA1	C21-C24-C25	2.84	124.31	120.29
3	c	601	TA1	O02-C02-C01	2.81	110.57	104.74
6	X	502	GTP	O2'-C2'-C1'	2.81	119.78	110.10
6	V	502	GTP	C8-N9-C4	2.81	111.29	106.03
3	h	601	TA1	C36-C31-C32	-2.81	114.99	118.57
4	k	602	GDP	O6-C6-C5	-2.80	119.13	126.53
4	l	602	GDP	O6-C6-C5	-2.80	119.14	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	a	602	GDP	C3'-C2'-C1'	2.80	106.76	101.46
3	e	601	TA1	O04-C11-C10	2.80	113.57	109.24
6	Y	502	GTP	C5-C4-N9	2.80	110.66	105.66
6	P	502	GTP	O6-C6-C5	2.79	133.91	126.53
6	T	502	GTP	PA-O5'-C5'	-2.79	105.34	121.35
4	b	602	GDP	O3B-PB-O3A	2.79	114.00	104.64
4	m	602	GDP	C5-C4-N3	-2.79	123.95	128.39
3	a	601	TA1	C19-C18-C20	-2.78	99.37	106.56
4	k	602	GDP	O3B-PB-O3A	2.78	113.95	104.64
4	j	602	GDP	C2-N3-C4	2.78	117.08	112.30
4	l	602	GDP	O3B-PB-O3A	2.77	113.94	104.64
4	i	602	GDP	O3A-PB-O1B	-2.77	96.47	111.04
4	m	602	GDP	C2-N3-C4	2.77	117.07	112.30
3	a	601	TA1	C02-O02-C03	2.77	122.85	117.80
4	i	602	GDP	O2'-C2'-C3'	2.76	120.67	111.82
6	V	502	GTP	C6-C5-N7	-2.74	125.30	130.29
3	c	601	TA1	C10-C18-C20	2.74	120.81	116.30
3	b	601	TA1	C47-C45-C24	2.73	123.69	112.78
6	W	502	GTP	C8-N9-C4	2.73	111.14	106.03
6	S	502	GTP	C2'-C3'-C4'	2.73	107.88	102.61
3	k	601	TA1	O09-C21-C24	2.73	114.54	110.02
6	N	502	GTP	O2'-C2'-C1'	2.72	119.47	110.10
4	c	602	GDP	O2A-PA-O1A	2.71	125.06	112.44
3	m	601	TA1	C45-C01-C02	2.71	114.91	111.93
3	e	601	TA1	C39-C38-C37	2.70	123.88	120.65
4	g	602	GDP	C2-N3-C4	2.70	116.94	112.30
4	e	602	GDP	C4-C5-N7	-2.69	106.40	110.67
4	l	602	GDP	O2'-C2'-C3'	2.69	120.43	111.82
4	m	602	GDP	C6-C5-C4	-2.69	114.79	118.83
4	h	602	GDP	C4-C5-N7	-2.69	106.41	110.67
4	h	602	GDP	C2-N3-C4	2.68	116.92	112.30
4	j	602	GDP	O6-C6-C5	-2.68	119.45	126.53
4	c	602	GDP	O4'-C1'-C2'	2.68	112.35	106.62
3	l	601	TA1	O04-C11-C14	-2.67	102.46	108.13
3	e	601	TA1	C11-O04-C12	2.66	125.92	119.17
6	Y	502	GTP	C6-C5-C4	2.66	122.83	118.83
3	d	601	TA1	C21-O09-C22	2.66	121.44	115.95
4	f	602	GDP	C5-C4-N3	-2.66	124.16	128.39
3	g	601	TA1	C43-C01-C02	2.66	116.37	111.67
4	m	602	GDP	O3B-PB-O3A	2.66	113.54	104.64
3	e	601	TA1	C37-C29-C28	2.65	118.04	111.46
3	l	601	TA1	C02-O02-C03	2.64	122.63	117.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	g	602	GDP	O6-C6-C5	-2.64	119.56	126.53
3	d	601	TA1	O04-C11-C14	-2.63	102.54	108.13
6	W	502	GTP	C2'-C3'-C4'	2.63	107.69	102.61
6	Z	502	GTP	O3A-PB-O1B	-2.63	102.80	110.70
3	a	601	TA1	C10-C18-C20	2.63	120.63	116.30
4	g	602	GDP	C8-N7-C5	2.62	108.94	104.26
3	h	601	TA1	C26-O11-C27	2.62	121.30	116.58
3	b	601	TA1	O08-C20-C21	-2.62	116.14	119.28
6	S	502	GTP	C5-C4-N9	-2.62	100.97	105.66
3	c	601	TA1	O04-C11-C10	2.62	113.29	109.24
4	f	602	GDP	O6-C6-N1	2.61	125.03	120.11
6	O	502	GTP	O2B-PB-O3A	-2.60	100.25	107.27
6	U	502	GTP	C2'-C3'-C4'	2.60	107.62	102.61
3	j	601	TA1	C26-O11-C27	2.59	121.25	116.58
4	l	602	GDP	O3'-C3'-C4'	-2.59	103.63	111.08
3	g	601	TA1	O06-C15-C16	2.59	117.95	113.17
3	k	601	TA1	C11-O04-C12	2.59	125.74	119.17
6	V	502	GTP	O2B-PB-O3B	2.59	114.27	107.27
3	f	601	TA1	C37-C29-N01	2.59	117.05	112.07
3	d	601	TA1	C11-O04-C12	2.58	125.71	119.17
3	e	601	TA1	O14-C30-C31	2.56	125.97	120.90
6	T	502	GTP	O2'-C2'-C3'	2.56	120.01	111.82
4	h	602	GDP	C6-C5-C4	-2.55	114.99	118.83
3	j	601	TA1	C38-C37-C29	-2.55	116.73	120.78
4	c	602	GDP	C4-C5-N7	-2.55	106.63	110.67
6	Q	502	GTP	O2B-PB-O3B	2.55	114.16	107.27
4	b	602	GDP	C6-C5-C4	-2.55	115.00	118.83
6	U	502	GTP	O6-C6-N1	2.54	124.90	120.11
3	c	601	TA1	C29-N01-C30	2.54	127.06	121.94
4	d	602	GDP	O6-C6-N1	2.53	124.88	120.11
6	O	502	GTP	O6-C6-N1	2.53	124.88	120.11
3	d	601	TA1	C21-C24-C25	2.53	123.88	120.29
3	i	601	TA1	C10-C18-C20	2.53	120.46	116.30
4	f	602	GDP	O2'-C2'-C3'	2.52	119.91	111.82
3	m	601	TA1	C01-C45-C24	-2.52	102.89	105.26
6	V	502	GTP	PA-O5'-C5'	-2.51	106.96	121.35
3	b	601	TA1	C26-O11-C27	2.51	121.10	116.58
6	N	502	GTP	O2B-PB-O3A	-2.50	100.51	107.27
3	j	601	TA1	C47-C45-C24	2.50	122.76	112.78
6	V	502	GTP	O2'-C2'-C3'	2.50	119.83	111.82
3	f	601	TA1	C45-C01-C02	2.50	114.68	111.93
4	e	602	GDP	O6-C6-N1	2.49	124.80	120.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Z	502	GTP	O2A-PA-O3A	2.49	114.00	107.27
3	f	601	TA1	C43-C01-C02	-2.46	107.31	111.67
4	e	602	GDP	C2-N3-C4	2.46	116.53	112.30
3	b	601	TA1	C47-C45-C46	-2.46	99.32	106.29
6	Q	502	GTP	O6-C6-C5	2.46	133.02	126.53
4	l	602	GDP	C4-C5-N7	-2.45	106.78	110.67
3	f	601	TA1	C18-C10-C02	2.45	121.02	115.62
3	e	601	TA1	C10-C18-C20	2.45	120.33	116.30
6	Q	502	GTP	C8-N7-C5	2.45	108.62	104.26
3	g	601	TA1	O06-C15-C11	2.44	93.25	90.58
4	k	602	GDP	C5-C4-N3	-2.44	124.50	128.39
6	Y	502	GTP	C8-N9-C4	-2.44	101.44	106.03
3	i	601	TA1	C29-N01-C30	2.44	126.85	121.94
4	g	602	GDP	O3A-PB-O1B	-2.44	98.20	111.04
6	Q	502	GTP	C8-N9-C4	-2.44	101.45	106.03
3	f	601	TA1	C11-C10-C02	2.44	116.39	111.70
4	d	602	GDP	C6-C5-C4	-2.43	115.17	118.83
3	m	601	TA1	C47-C45-C46	-2.43	99.40	106.29
3	h	601	TA1	C16-C17-C18	2.43	117.78	112.25
4	i	602	GDP	O2A-PA-O3A	2.42	113.83	107.27
4	j	602	GDP	O3A-PB-O1B	-2.42	98.29	111.04
3	b	601	TA1	C11-C10-C02	2.42	116.37	111.70
4	f	602	GDP	C4-C5-N7	-2.42	106.84	110.67
4	j	602	GDP	C5-C4-N3	-2.42	124.54	128.39
3	l	601	TA1	C21-C24-C25	2.41	123.72	120.29
3	g	601	TA1	C47-C45-C24	2.40	122.35	112.78
6	N	502	GTP	PA-O5'-C5'	-2.39	107.63	121.35
4	b	602	GDP	C4-C5-N7	-2.39	106.88	110.67
3	f	601	TA1	C33-C32-C31	2.39	122.71	120.36
3	f	601	TA1	O04-C11-C10	2.39	112.94	109.24
4	k	602	GDP	O3'-C3'-C4'	-2.38	104.24	111.08
4	h	602	GDP	O3A-PB-O1B	-2.38	98.53	111.04
3	i	601	TA1	C47-C45-C46	-2.37	99.56	106.29
6	O	502	GTP	C5-C6-N1	-2.37	107.22	113.25
3	a	601	TA1	C39-C38-C37	2.37	123.48	120.65
3	g	601	TA1	O14-C30-N01	-2.37	117.96	122.47
3	l	601	TA1	C10-C18-C20	2.37	120.20	116.30
6	P	502	GTP	O4'-C1'-N9	2.37	113.73	108.36
6	T	502	GTP	O5'-C5'-C4'	2.37	117.06	108.99
6	T	502	GTP	C5-C6-N1	2.37	119.28	113.25
6	U	502	GTP	N9-C4-N3	-2.36	121.23	125.95
4	a	602	GDP	O3B-PB-O3A	2.36	112.56	104.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	f	601	TA1	C47-C45-C46	-2.36	99.60	106.29
3	e	601	TA1	C47-C45-C46	-2.36	99.60	106.29
4	c	602	GDP	C2-N3-C4	2.34	116.33	112.30
6	R	502	GTP	C4-C5-N7	-2.33	106.97	110.67
4	h	602	GDP	O3'-C3'-C4'	-2.33	104.38	111.08
6	Q	502	GTP	N9-C4-N3	2.33	130.62	125.95
3	m	601	TA1	C09-C04-C03	2.33	125.52	120.40
6	U	502	GTP	O3G-PG-O3B	2.32	112.42	104.64
6	Q	502	GTP	O3'-C3'-C2'	2.32	119.25	111.82
3	g	601	TA1	C21-C24-C25	2.32	123.58	120.29
6	N	502	GTP	C5-C4-N3	-2.32	124.70	128.39
4	d	602	GDP	N2-C2-N1	-2.32	111.87	116.76
3	d	601	TA1	C02-O02-C03	2.31	122.02	117.80
3	l	601	TA1	C47-C45-C46	-2.31	99.74	106.29
6	Q	502	GTP	O2'-C2'-C3'	2.31	119.22	111.82
6	X	502	GTP	C2'-C1'-N9	2.31	119.67	113.25
6	X	502	GTP	O2A-PA-O3A	2.31	113.51	107.27
3	f	601	TA1	C02-O02-C03	2.30	122.01	117.80
6	N	502	GTP	C2'-C1'-N9	2.30	119.65	113.25
3	d	601	TA1	C47-C45-C46	-2.29	99.78	106.29
6	S	502	GTP	O2B-PB-O3B	2.29	113.45	107.27
4	g	602	GDP	O3'-C3'-C4'	-2.29	104.52	111.08
3	d	601	TA1	C10-C18-C20	2.28	120.06	116.30
3	l	601	TA1	C47-C45-C24	2.28	121.88	112.78
3	m	601	TA1	O11-C26-C25	2.28	115.26	109.85
6	W	502	GTP	O2B-PB-O3B	2.27	113.41	107.27
3	e	601	TA1	C21-O09-C22	2.27	120.63	115.95
3	h	601	TA1	C47-C45-C46	-2.27	99.85	106.29
3	a	601	TA1	C01-C02-C10	2.27	121.59	118.19
3	k	601	TA1	C37-C29-C28	2.26	117.09	111.46
4	c	602	GDP	O6-C6-N1	2.26	124.37	120.11
3	c	601	TA1	O01-C01-C02	-2.26	100.64	105.54
4	c	602	GDP	C6-C5-C4	-2.26	115.43	118.83
4	h	602	GDP	C5-C4-N3	-2.26	124.79	128.39
6	T	502	GTP	C8-N7-C5	2.26	108.29	104.26
4	c	602	GDP	C5-C4-N3	-2.25	124.80	128.39
4	h	602	GDP	C5'-C4'-C3'	2.25	123.31	115.21
3	i	601	TA1	C36-C31-C32	-2.25	115.71	118.57
4	c	602	GDP	O5'-PA-O1A	-2.25	100.03	108.94
3	f	601	TA1	O08-C20-C21	-2.25	116.58	119.28
3	a	601	TA1	O04-C11-C10	2.25	112.72	109.24
3	j	601	TA1	C47-C45-C46	-2.24	99.92	106.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	W	502	GTP	O5'-C5'-C4'	2.24	116.62	108.99
3	d	601	TA1	O04-C11-C10	2.24	112.71	109.24
4	f	602	GDP	C5'-C4'-C3'	2.23	123.25	115.21
3	m	601	TA1	C45-C24-C21	-2.23	112.07	119.08
3	l	601	TA1	C29-N01-C30	2.23	126.43	121.94
6	O	502	GTP	O3G-PG-O3B	2.23	112.11	104.64
6	W	502	GTP	C2-N1-C6	2.23	129.15	125.11
3	k	601	TA1	C36-C31-C30	-2.23	113.39	120.60
6	O	502	GTP	O2A-PA-O3A	2.22	113.28	107.27
4	b	602	GDP	O3B-PB-O2B	2.22	116.14	107.80
3	l	601	TA1	C19-C18-C20	-2.22	100.81	106.56
3	c	601	TA1	C21-O09-C22	2.22	120.53	115.95
3	e	601	TA1	C42-C37-C38	-2.22	115.56	118.30
4	d	602	GDP	O2A-PA-O1A	2.22	122.76	112.44
6	S	502	GTP	O3'-C3'-C4'	-2.21	104.72	111.08
3	m	601	TA1	C10-C18-C20	2.21	119.95	116.30
4	h	602	GDP	O2A-PA-O3A	2.21	113.25	107.27
4	a	602	GDP	O2'-C2'-C1'	2.21	117.72	110.10
3	h	601	TA1	C33-C32-C31	2.21	122.54	120.36
3	a	601	TA1	C26-O11-C27	2.21	120.56	116.58
4	c	602	GDP	O6-C6-C5	-2.20	120.72	126.53
4	a	602	GDP	C6-C5-C4	-2.20	115.52	118.83
4	e	602	GDP	O2A-PA-O1A	2.20	122.67	112.44
6	P	502	GTP	O2B-PB-O3B	2.20	113.21	107.27
6	U	502	GTP	C1'-N9-C8	-2.20	120.49	126.73
4	e	602	GDP	O3A-PB-O1B	-2.20	99.48	111.04
3	b	601	TA1	O08-C20-C18	2.20	124.06	119.22
4	j	602	GDP	O3'-C3'-C4'	-2.19	104.79	111.08
6	Z	502	GTP	C8-N9-C4	-2.19	101.92	106.03
6	O	502	GTP	C5-C4-N3	2.18	131.86	128.39
3	h	601	TA1	C35-C36-C31	2.18	122.51	120.36
4	a	602	GDP	O4'-C1'-C2'	-2.18	101.94	106.62
6	W	502	GTP	C6-C5-C4	-2.18	115.55	118.83
6	X	502	GTP	O5'-C5'-C4'	2.17	116.40	108.99
3	k	601	TA1	O11-C27-O12	2.17	127.87	123.95
4	i	602	GDP	C6-C5-C4	-2.17	115.57	118.83
3	h	601	TA1	C46-C45-C24	-2.15	104.19	112.78
3	g	601	TA1	C47-C45-C46	-2.15	100.19	106.29
4	h	602	GDP	N2-C2-N3	2.15	123.86	119.67
3	l	601	TA1	O04-C11-C10	2.14	112.56	109.24
3	g	601	TA1	O01-C01-C43	-2.14	101.58	107.04
4	l	602	GDP	C5-C4-N3	-2.14	124.99	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	j	602	GDP	C4-C5-N7	-2.14	107.28	110.67
3	j	601	TA1	C29-N01-C30	2.13	126.23	121.94
4	j	602	GDP	O2A-PA-O3A	2.13	113.03	107.27
3	c	601	TA1	O11-C26-C25	2.13	114.91	109.85
6	O	502	GTP	C3'-C2'-C1'	2.12	105.48	101.46
6	W	502	GTP	O2B-PB-O3A	-2.12	101.54	107.27
3	h	601	TA1	C16-C15-C11	-2.12	116.75	119.63
4	a	602	GDP	O4'-C1'-N9	2.12	113.16	108.36
3	g	601	TA1	C11-C10-C02	2.12	115.77	111.70
3	b	601	TA1	C01-C02-C10	2.11	121.36	118.19
4	c	602	GDP	C5-C4-N9	-2.11	101.88	105.66
4	h	602	GDP	C5-C4-N9	-2.11	101.88	105.66
4	k	602	GDP	O6-C6-N1	2.11	124.08	120.11
4	g	602	GDP	C5-C4-N3	-2.11	125.03	128.39
6	V	502	GTP	O3G-PG-O3B	2.11	111.70	104.64
4	f	602	GDP	C5-C4-N9	-2.11	101.89	105.66
6	V	502	GTP	C2-N3-C4	-2.10	108.67	112.30
4	g	602	GDP	O6-C6-N1	2.10	124.06	120.11
4	m	602	GDP	O6-C6-N1	2.10	124.06	120.11
3	c	601	TA1	O06-C15-C16	2.10	117.03	113.17
3	f	601	TA1	C45-C24-C25	-2.10	116.78	119.60
6	R	502	GTP	N2-C2-N1	2.10	121.19	116.76
6	T	502	GTP	C2'-C3'-C4'	2.08	106.64	102.61
3	c	601	TA1	C47-C45-C46	-2.08	100.38	106.29
4	j	602	GDP	O6-C6-N1	2.08	124.03	120.11
6	U	502	GTP	N2-C2-N1	2.08	121.15	116.76
3	f	601	TA1	C21-O09-C22	2.08	120.24	115.95
4	l	602	GDP	O6-C6-N1	2.08	124.02	120.11
3	j	601	TA1	O11-C26-C25	2.08	114.78	109.85
3	g	601	TA1	O11-C27-O12	2.08	127.70	123.95
3	l	601	TA1	C01-C02-C10	2.07	121.29	118.19
3	i	601	TA1	C33-C32-C31	2.07	122.40	120.36
6	T	502	GTP	O2B-PB-O3B	2.06	112.85	107.27
3	e	601	TA1	O11-C27-C28	-2.06	107.86	111.13
3	b	601	TA1	C16-C17-C18	2.06	116.95	112.25
3	g	601	TA1	O14-C30-C31	2.06	124.98	120.90
3	j	601	TA1	C19-C18-C20	-2.06	101.23	106.56
3	e	601	TA1	O11-C26-C25	2.06	114.73	109.85
3	i	601	TA1	C47-C45-C24	2.05	120.98	112.78
3	c	601	TA1	C19-C18-C20	-2.05	101.25	106.56
6	Q	502	GTP	PA-O5'-C5'	-2.05	109.62	121.35
3	c	601	TA1	C10-C18-C17	-2.05	102.67	106.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	i	602	GDP	C4-C5-N7	-2.04	107.43	110.67
4	e	602	GDP	C5-C4-N9	-2.04	102.00	105.66
6	N	502	GTP	O2A-PA-O3A	2.04	112.79	107.27
6	X	502	GTP	O3G-PG-O3B	2.04	111.47	104.64
3	h	601	TA1	O06-C15-C16	2.04	116.92	113.17
6	S	502	GTP	C4'-O4'-C1'	2.04	113.96	109.47
4	b	602	GDP	O2A-PA-O1A	2.03	121.89	112.44
4	d	602	GDP	O4'-C1'-C2'	2.03	110.96	106.62
6	V	502	GTP	C5-C4-N3	2.03	131.62	128.39
6	U	502	GTP	O4'-C1'-N9	-2.03	103.77	108.36
3	c	601	TA1	O02-C03-O03	2.02	126.83	123.55
3	d	601	TA1	C26-O11-C27	2.02	120.22	116.58
3	m	601	TA1	C01-C43-C26	2.02	118.71	114.98
3	l	601	TA1	C26-O11-C27	2.02	120.22	116.58
4	k	602	GDP	C4-C5-N7	-2.02	107.47	110.67
3	f	601	TA1	O08-C20-C18	2.02	123.68	119.22
6	V	502	GTP	C2'-C1'-N9	2.02	118.87	113.25
3	l	601	TA1	C36-C31-C32	-2.02	116.00	118.57
3	j	601	TA1	C46-C45-C24	-2.02	104.72	112.78
3	k	601	TA1	O09-C22-O10	2.02	126.89	122.99
4	f	602	GDP	C1'-N9-C4	-2.01	120.54	126.49
6	S	502	GTP	N2-C2-N1	2.01	121.01	116.76
4	i	602	GDP	N2-C2-N3	2.01	123.59	119.67
6	Y	502	GTP	C1'-N9-C4	2.01	132.42	126.49
3	d	601	TA1	C29-N01-C30	2.01	125.98	121.94
6	P	502	GTP	N1-C2-N3	2.01	126.99	123.32
3	d	601	TA1	C18-C10-C02	2.01	120.05	115.62
3	g	601	TA1	O02-C03-C04	-2.00	108.68	111.90

There are no chirality outliers.

All (236) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	c	601	TA1	O02-C03-C04-C05
3	g	601	TA1	C27-C28-C29-N01
4	a	602	GDP	PA-O3A-PB-O2B
4	a	602	GDP	C5'-O5'-PA-O3A
4	a	602	GDP	C5'-O5'-PA-O1A
4	b	602	GDP	PA-O3A-PB-O2B
4	b	602	GDP	C5'-O5'-PA-O1A
4	c	602	GDP	PA-O3A-PB-O2B
4	c	602	GDP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
4	d	602	GDP	PA-O3A-PB-O2B
4	d	602	GDP	C5'-O5'-PA-O3A
4	e	602	GDP	PA-O3A-PB-O2B
4	e	602	GDP	C5'-O5'-PA-O3A
4	f	602	GDP	PA-O3A-PB-O2B
4	f	602	GDP	C5'-O5'-PA-O3A
4	g	602	GDP	PA-O3A-PB-O2B
4	g	602	GDP	C5'-O5'-PA-O3A
4	h	602	GDP	PA-O3A-PB-O2B
4	h	602	GDP	C5'-O5'-PA-O3A
4	i	602	GDP	PA-O3A-PB-O2B
4	i	602	GDP	C5'-O5'-PA-O3A
4	j	602	GDP	PA-O3A-PB-O2B
4	j	602	GDP	C5'-O5'-PA-O3A
4	k	602	GDP	PA-O3A-PB-O2B
4	k	602	GDP	C5'-O5'-PA-O3A
4	l	602	GDP	PA-O3A-PB-O2B
4	l	602	GDP	C5'-O5'-PA-O3A
4	m	602	GDP	PA-O3A-PB-O2B
4	m	602	GDP	C5'-O5'-PA-O3A
6	N	502	GTP	C5'-O5'-PA-O3A
6	N	502	GTP	C5'-O5'-PA-O2A
6	O	502	GTP	C5'-O5'-PA-O3A
6	O	502	GTP	C5'-O5'-PA-O2A
6	P	502	GTP	C5'-O5'-PA-O3A
6	P	502	GTP	C5'-O5'-PA-O1A
6	P	502	GTP	C5'-O5'-PA-O2A
6	Q	502	GTP	C5'-O5'-PA-O3A
6	Q	502	GTP	C5'-O5'-PA-O1A
6	Q	502	GTP	C5'-O5'-PA-O2A
6	R	502	GTP	C5'-O5'-PA-O3A
6	R	502	GTP	C5'-O5'-PA-O2A
6	S	502	GTP	C5'-O5'-PA-O3A
6	S	502	GTP	C5'-O5'-PA-O1A
6	S	502	GTP	C5'-O5'-PA-O2A
6	T	502	GTP	C5'-O5'-PA-O3A
6	T	502	GTP	C5'-O5'-PA-O2A
6	U	502	GTP	C5'-O5'-PA-O3A
6	U	502	GTP	C5'-O5'-PA-O2A
6	V	502	GTP	C5'-O5'-PA-O3A
6	V	502	GTP	C5'-O5'-PA-O1A
6	V	502	GTP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
6	W	502	GTP	C5'-O5'-PA-O3A
6	W	502	GTP	C5'-O5'-PA-O2A
6	X	502	GTP	C5'-O5'-PA-O3A
6	X	502	GTP	C5'-O5'-PA-O2A
6	Y	502	GTP	C5'-O5'-PA-O3A
6	Y	502	GTP	C5'-O5'-PA-O1A
6	Y	502	GTP	C5'-O5'-PA-O2A
6	Z	502	GTP	C5'-O5'-PA-O3A
6	Z	502	GTP	C5'-O5'-PA-O1A
6	Z	502	GTP	C5'-O5'-PA-O2A
3	c	601	TA1	O02-C03-C04-C09
3	g	601	TA1	O02-C03-C04-C09
3	h	601	TA1	O02-C03-C04-C09
3	j	601	TA1	O02-C03-C04-C09
3	k	601	TA1	O02-C03-C04-C09
3	a	601	TA1	O02-C03-C04-C09
3	b	601	TA1	O02-C03-C04-C05
3	b	601	TA1	O02-C03-C04-C09
3	e	601	TA1	O02-C03-C04-C05
3	h	601	TA1	O02-C03-C04-C05
3	j	601	TA1	O02-C03-C04-C05
3	k	601	TA1	O02-C03-C04-C05
3	m	601	TA1	O02-C03-C04-C05
3	m	601	TA1	O02-C03-C04-C09
3	e	601	TA1	O02-C03-C04-C09
3	c	601	TA1	O03-C03-C04-C05
3	c	601	TA1	O03-C03-C04-C09
3	c	601	TA1	O14-C30-C31-C36
3	g	601	TA1	O14-C30-C31-C36
3	a	601	TA1	O02-C03-C04-C05
3	c	601	TA1	O14-C30-C31-C32
3	g	601	TA1	O02-C03-C04-C05
3	c	601	TA1	N01-C30-C31-C36
3	d	601	TA1	N01-C30-C31-C36
3	f	601	TA1	N01-C30-C31-C36
3	g	601	TA1	N01-C30-C31-C36
3	m	601	TA1	N01-C30-C31-C36
3	b	601	TA1	O14-C30-C31-C36
3	f	601	TA1	O14-C30-C31-C32
3	f	601	TA1	O14-C30-C31-C36
3	g	601	TA1	O14-C30-C31-C32
3	i	601	TA1	O02-C03-C04-C09

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Mol	Chain	Res	Type	Atoms
3	b	601	TA1	N01-C30-C31-C36
3	c	601	TA1	N01-C30-C31-C32
3	e	601	TA1	N01-C30-C31-C36
3	g	601	TA1	N01-C30-C31-C32
3	h	601	TA1	N01-C30-C31-C36
3	a	601	TA1	C31-C30-N01-C29
3	l	601	TA1	C31-C30-N01-C29
3	m	601	TA1	C31-C30-N01-C29
3	i	601	TA1	O02-C03-C04-C05
3	f	601	TA1	N01-C30-C31-C32
3	e	601	TA1	O14-C30-C31-C36
3	b	601	TA1	N01-C30-C31-C32
3	j	601	TA1	N01-C30-C31-C36
3	m	601	TA1	N01-C30-C31-C32
3	d	601	TA1	O02-C03-C04-C05
3	d	601	TA1	N01-C30-C31-C32
3	b	601	TA1	O14-C30-C31-C32
3	m	601	TA1	O14-C30-C31-C36
3	i	601	TA1	N01-C30-C31-C36
3	d	601	TA1	O02-C03-C04-C09
3	k	601	TA1	C31-C30-N01-C29
3	a	601	TA1	O03-C03-C04-C09
3	h	601	TA1	O03-C03-C04-C09
3	h	601	TA1	N01-C30-C31-C32
3	h	601	TA1	O03-C03-C04-C05
3	j	601	TA1	O03-C03-C04-C05
3	h	601	TA1	O14-C30-C31-C36
3	l	601	TA1	O02-C03-C04-C05
3	k	601	TA1	O03-C03-C04-C09
3	k	601	TA1	O03-C03-C04-C05
3	j	601	TA1	O03-C03-C04-C09
3	a	601	TA1	O03-C03-C04-C05
3	b	601	TA1	O03-C03-C04-C05
3	m	601	TA1	O03-C03-C04-C05
3	e	601	TA1	O03-C03-C04-C05
3	e	601	TA1	N01-C30-C31-C32
3	j	601	TA1	N01-C30-C31-C32
3	d	601	TA1	O14-C30-C31-C36
3	i	601	TA1	O14-C30-C31-C36
3	m	601	TA1	O14-C30-C31-C32
3	m	601	TA1	O03-C03-C04-C09
3	h	601	TA1	C31-C30-N01-C29

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Mol	Chain	Res	Type	Atoms
3	i	601	TA1	C31-C30-N01-C29
3	j	601	TA1	C31-C30-N01-C29
3	j	601	TA1	O14-C30-C31-C36
3	b	601	TA1	O03-C03-C04-C09
3	i	601	TA1	N01-C30-C31-C32
3	l	601	TA1	O14-C30-N01-C29
3	l	601	TA1	O02-C03-C04-C09
3	a	601	TA1	O14-C30-N01-C29
3	b	601	TA1	C31-C30-N01-C29
3	e	601	TA1	O03-C03-C04-C09
3	g	601	TA1	O03-C03-C04-C09
3	d	601	TA1	O14-C30-C31-C32
3	i	601	TA1	O03-C03-C04-C09
3	h	601	TA1	O14-C30-C31-C32
3	d	601	TA1	O03-C03-C04-C05
3	i	601	TA1	O03-C03-C04-C05
3	i	601	TA1	C23-C22-O09-C21
3	m	601	TA1	O14-C30-N01-C29
3	d	601	TA1	O03-C03-C04-C09
3	i	601	TA1	O14-C30-C31-C32
3	j	601	TA1	O14-C30-C31-C32
3	e	601	TA1	O14-C30-C31-C32
3	g	601	TA1	O03-C03-C04-C05
3	b	601	TA1	O14-C30-N01-C29
3	l	601	TA1	N01-C30-C31-C36
3	k	601	TA1	O14-C30-N01-C29
3	k	601	TA1	N01-C30-C31-C36
3	i	601	TA1	O14-C30-N01-C29
3	j	601	TA1	O14-C30-N01-C29
3	l	601	TA1	O03-C03-C04-C05
3	f	601	TA1	C31-C30-N01-C29
6	Z	502	GTP	PB-O3A-PA-O1A
3	f	601	TA1	O14-C30-N01-C29
3	l	601	TA1	O14-C30-C31-C36
3	h	601	TA1	O14-C30-N01-C29
3	l	601	TA1	O03-C03-C04-C09
3	i	601	TA1	O10-C22-O09-C21
6	Z	502	GTP	PB-O3A-PA-O2A
3	g	601	TA1	C14-C11-O04-C12
3	l	601	TA1	N01-C30-C31-C32
4	c	602	GDP	C5'-O5'-PA-O1A
4	d	602	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
4	e	602	GDP	C5'-O5'-PA-O1A
4	f	602	GDP	C5'-O5'-PA-O1A
4	g	602	GDP	C5'-O5'-PA-O1A
4	h	602	GDP	C5'-O5'-PA-O1A
4	i	602	GDP	C5'-O5'-PA-O1A
4	j	602	GDP	C5'-O5'-PA-O1A
4	k	602	GDP	C5'-O5'-PA-O1A
4	l	602	GDP	C5'-O5'-PA-O1A
4	m	602	GDP	C5'-O5'-PA-O1A
3	a	601	TA1	N01-C30-C31-C36
3	k	601	TA1	N01-C30-C31-C32
3	g	601	TA1	C37-C29-N01-C30
3	a	601	TA1	C23-C22-O09-C21
3	g	601	TA1	C15-C11-O04-C12
3	g	601	TA1	O13-C28-C29-N01
3	h	601	TA1	C14-C11-O04-C12
3	k	601	TA1	O14-C30-C31-C36
4	b	602	GDP	PA-O3A-PB-O1B
4	e	602	GDP	PA-O3A-PB-O1B
4	g	602	GDP	PA-O3A-PB-O1B
4	h	602	GDP	PA-O3A-PB-O1B
4	j	602	GDP	PA-O3A-PB-O1B
4	k	602	GDP	PA-O3A-PB-O1B
4	l	602	GDP	PA-O3A-PB-O1B
4	m	602	GDP	PA-O3A-PB-O1B
6	X	502	GTP	PG-O3B-PB-O3A
4	a	602	GDP	PA-O3A-PB-O3B
4	b	602	GDP	PA-O3A-PB-O3B
4	c	602	GDP	PA-O3A-PB-O3B
4	d	602	GDP	PA-O3A-PB-O3B
4	e	602	GDP	PA-O3A-PB-O3B
4	g	602	GDP	PA-O3A-PB-O3B
4	h	602	GDP	PA-O3A-PB-O3B
4	j	602	GDP	PA-O3A-PB-O3B
4	k	602	GDP	PA-O3A-PB-O3B
4	l	602	GDP	PA-O3A-PB-O3B
4	m	602	GDP	PA-O3A-PB-O3B
3	g	601	TA1	C10-C11-O04-C12
6	Y	502	GTP	PG-O3B-PB-O3A
3	c	601	TA1	C15-C11-O04-C12
3	h	601	TA1	C15-C11-O04-C12
6	P	502	GTP	PG-O3B-PB-O2B

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Mol	Chain	Res	Type	Atoms
6	S	502	GTP	PG-O3B-PB-O2B
4	b	602	GDP	C4'-C5'-O5'-PA
6	N	502	GTP	PG-O3B-PB-O3A
6	Q	502	GTP	PG-O3B-PB-O3A
6	W	502	GTP	PG-O3B-PB-O3A
4	f	602	GDP	PA-O3A-PB-O1B
4	i	602	GDP	PA-O3A-PB-O1B
6	N	502	GTP	PG-O3B-PB-O2B
6	O	502	GTP	PG-O3B-PB-O2B
6	Q	502	GTP	PG-O3B-PB-O2B
6	U	502	GTP	PG-O3B-PB-O2B
6	V	502	GTP	PG-O3B-PB-O2B
6	W	502	GTP	PG-O3B-PB-O2B
6	X	502	GTP	PG-O3B-PB-O2B
6	Z	502	GTP	PG-O3B-PB-O2B
6	P	502	GTP	PG-O3B-PB-O3A
6	Z	502	GTP	PG-O3B-PB-O3A

There are no ring outliers.

39 monomers are involved in 933 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	Z	502	GTP	30	0
4	e	602	GDP	33	0
4	c	602	GDP	40	0
4	j	602	GDP	15	0
4	a	602	GDP	19	0
4	m	602	GDP	30	0
4	d	602	GDP	35	0
3	h	601	TA1	18	0
4	b	602	GDP	61	0
3	m	601	TA1	15	0
3	j	601	TA1	14	0
6	N	502	GTP	30	0
6	S	502	GTP	31	0
4	g	602	GDP	15	0
6	U	502	GTP	38	0
6	Q	502	GTP	23	0
6	Y	502	GTP	31	0
3	l	601	TA1	17	0
4	i	602	GDP	12	0
4	h	602	GDP	29	0

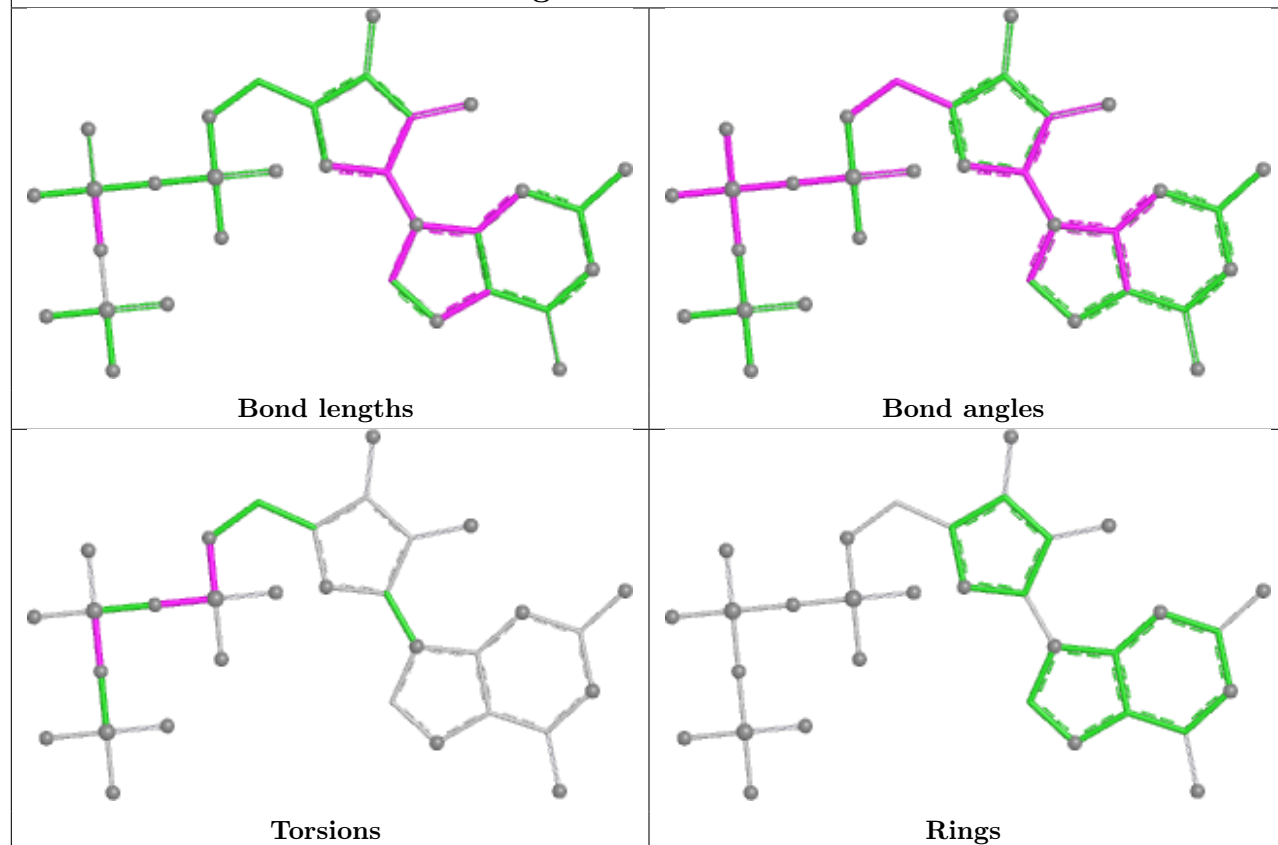
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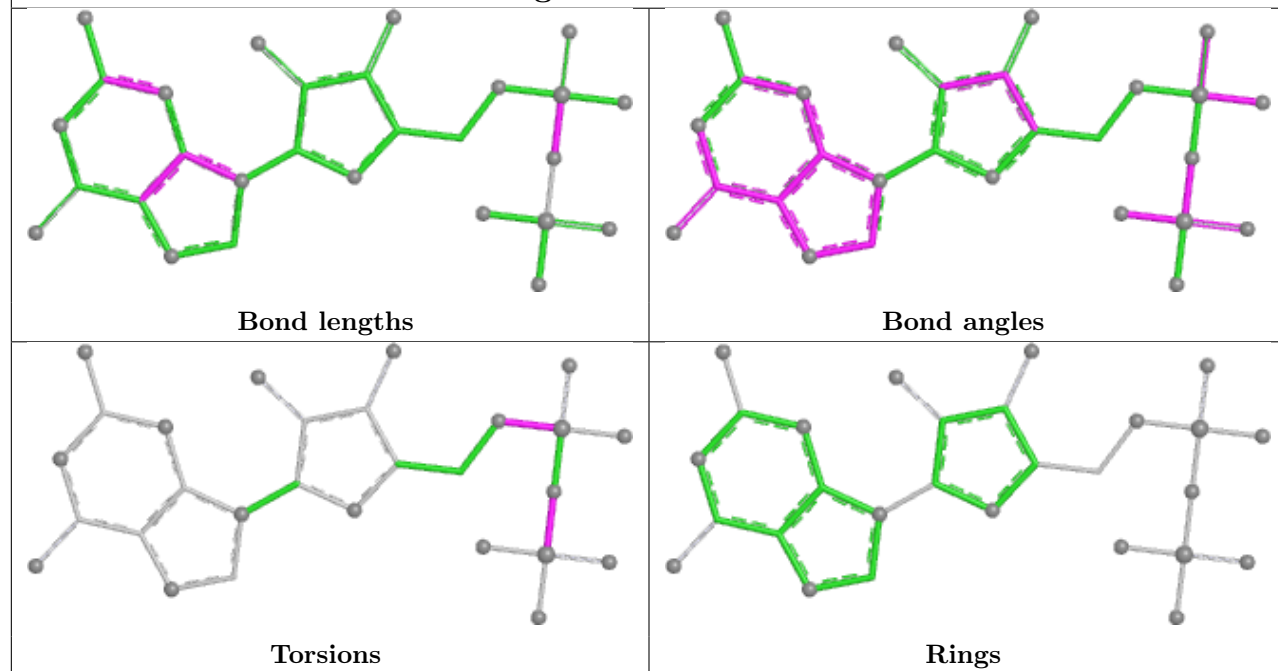
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	b	601	TA1	11	0
6	R	502	GTP	19	0
3	a	601	TA1	18	0
4	k	602	GDP	13	0
3	f	601	TA1	10	0
3	c	601	TA1	23	0
4	l	602	GDP	16	0
6	P	502	GTP	17	0
6	T	502	GTP	31	0
4	f	602	GDP	31	0
6	V	502	GTP	28	0
3	d	601	TA1	19	0
6	W	502	GTP	28	0
3	g	601	TA1	18	0
6	O	502	GTP	27	0
3	k	601	TA1	16	0
3	i	601	TA1	24	0
6	X	502	GTP	29	0
3	e	601	TA1	19	0

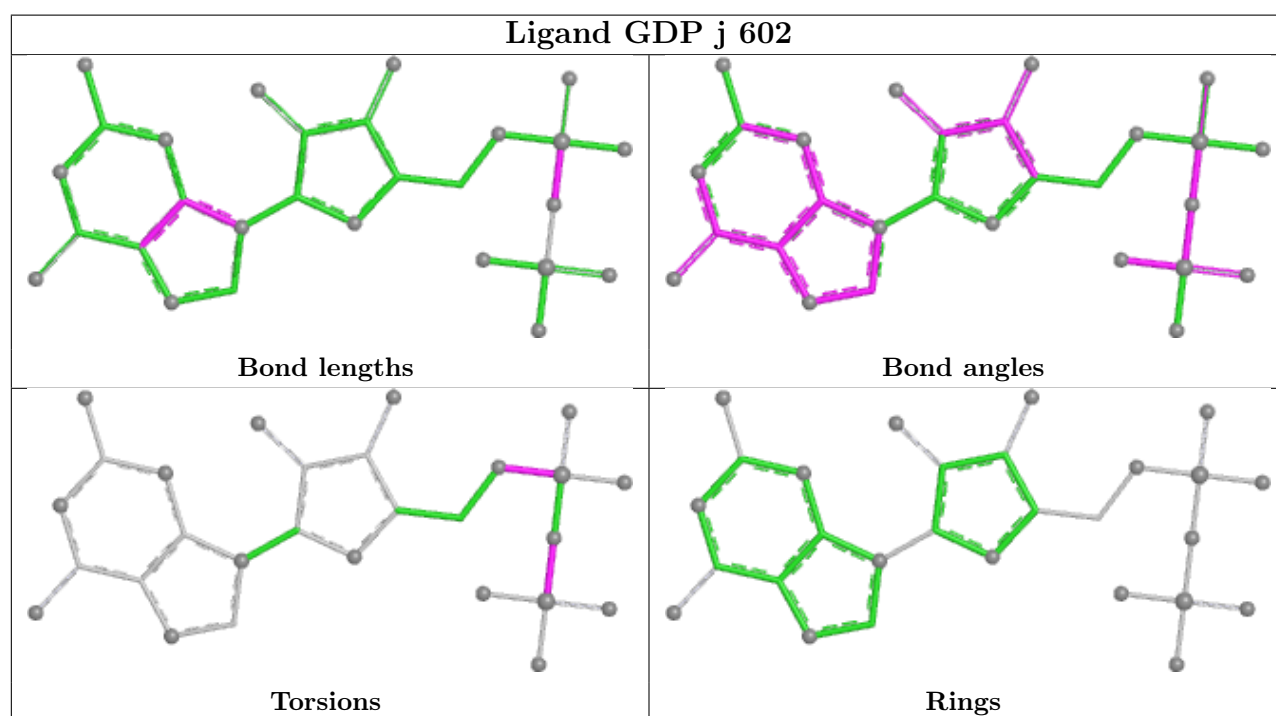
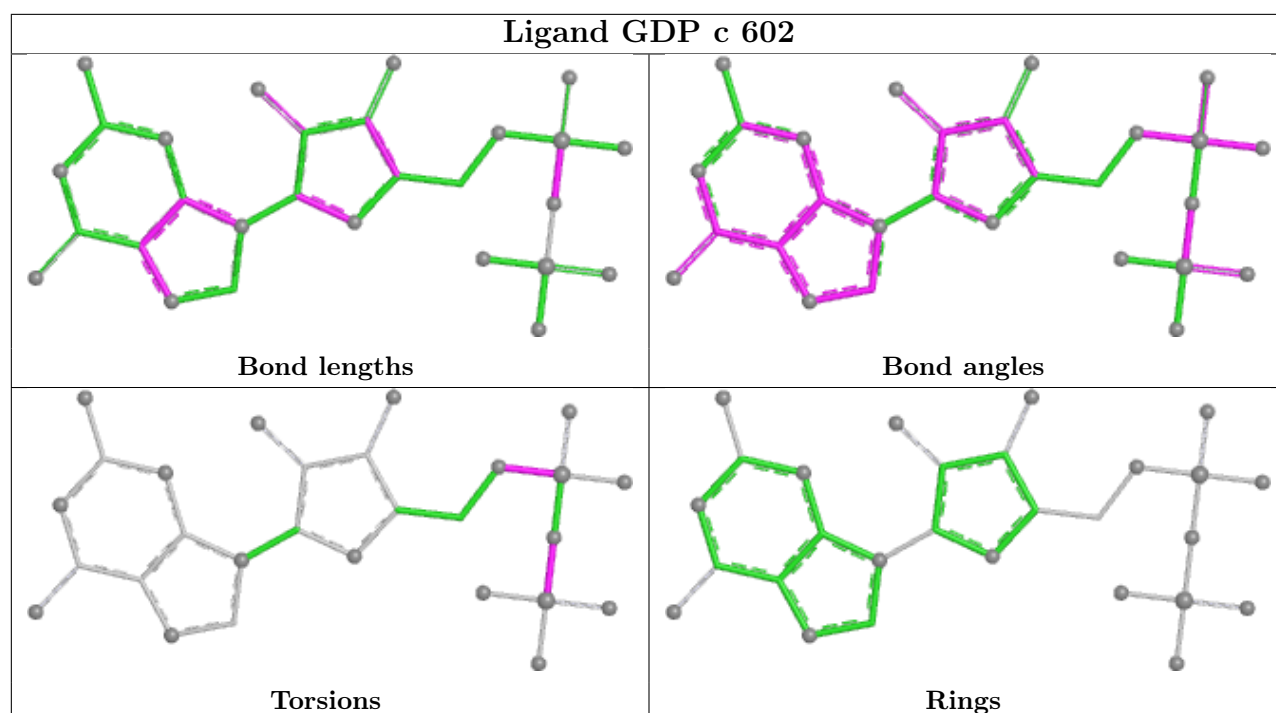
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

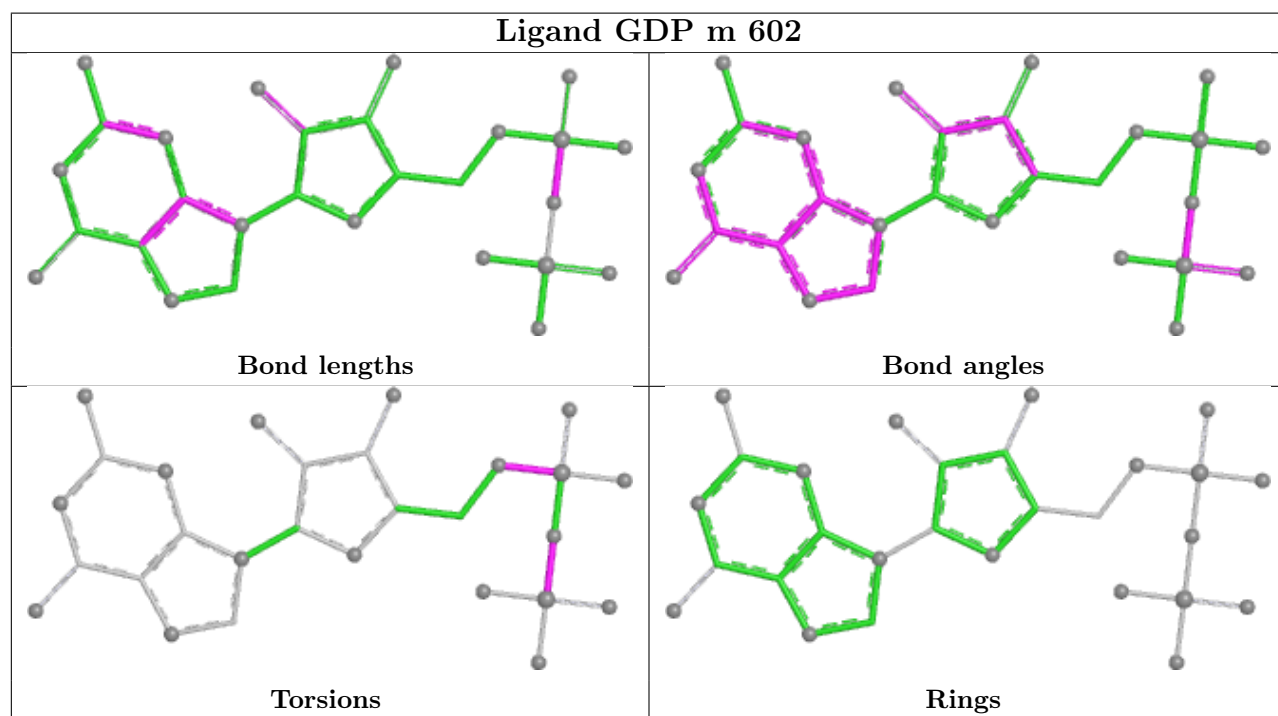
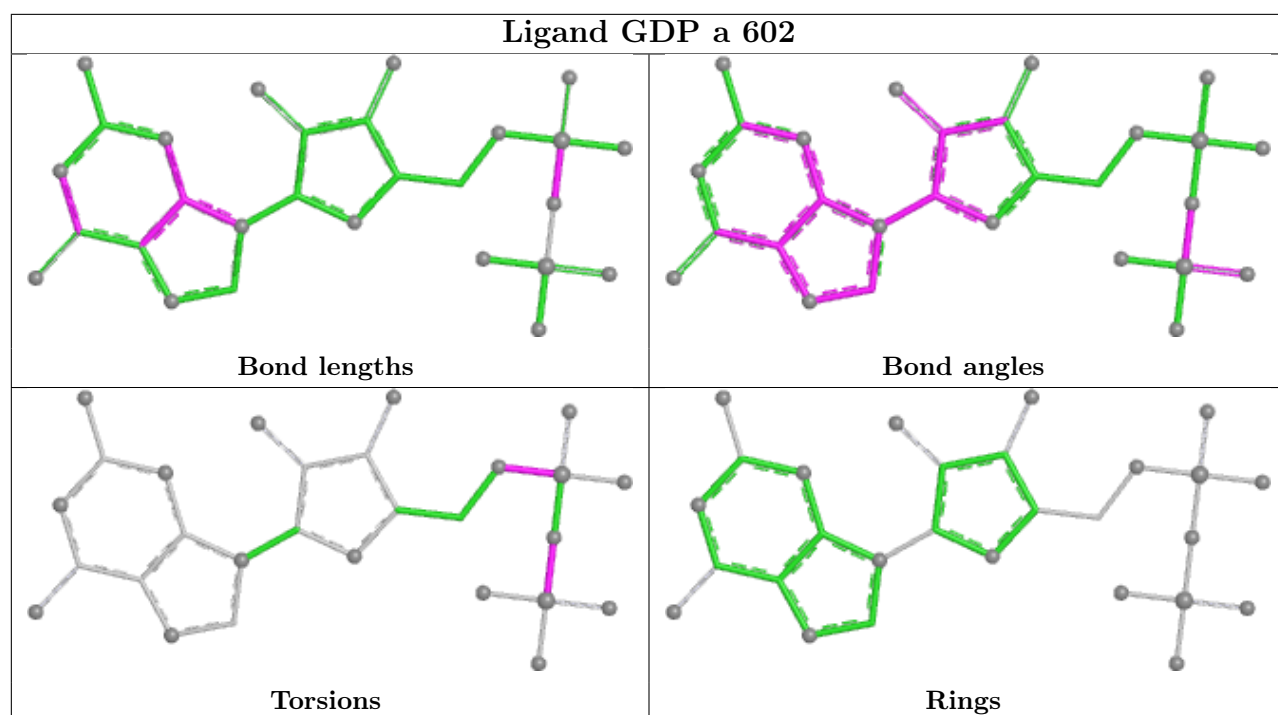
Ligand GTP Z 502

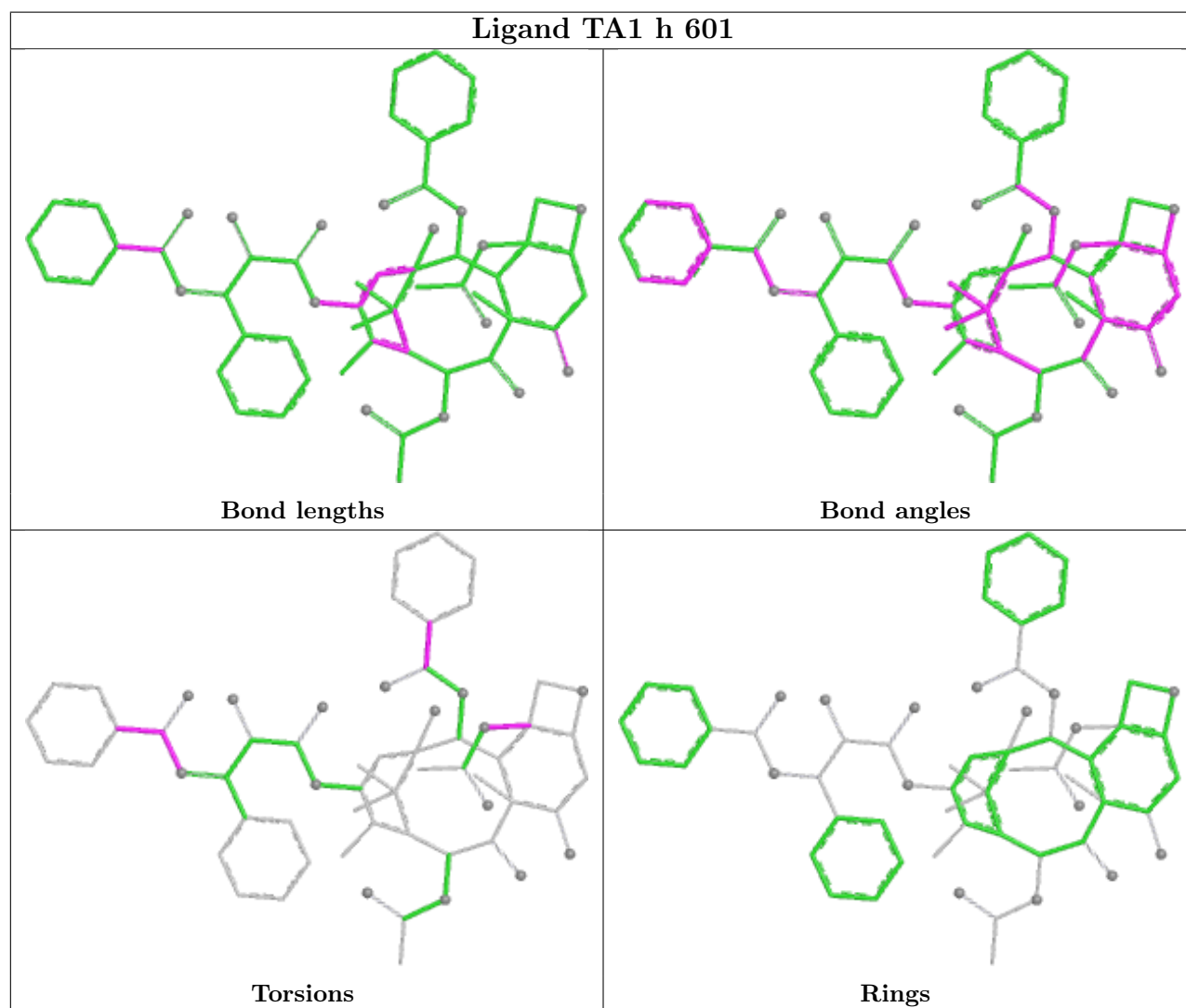
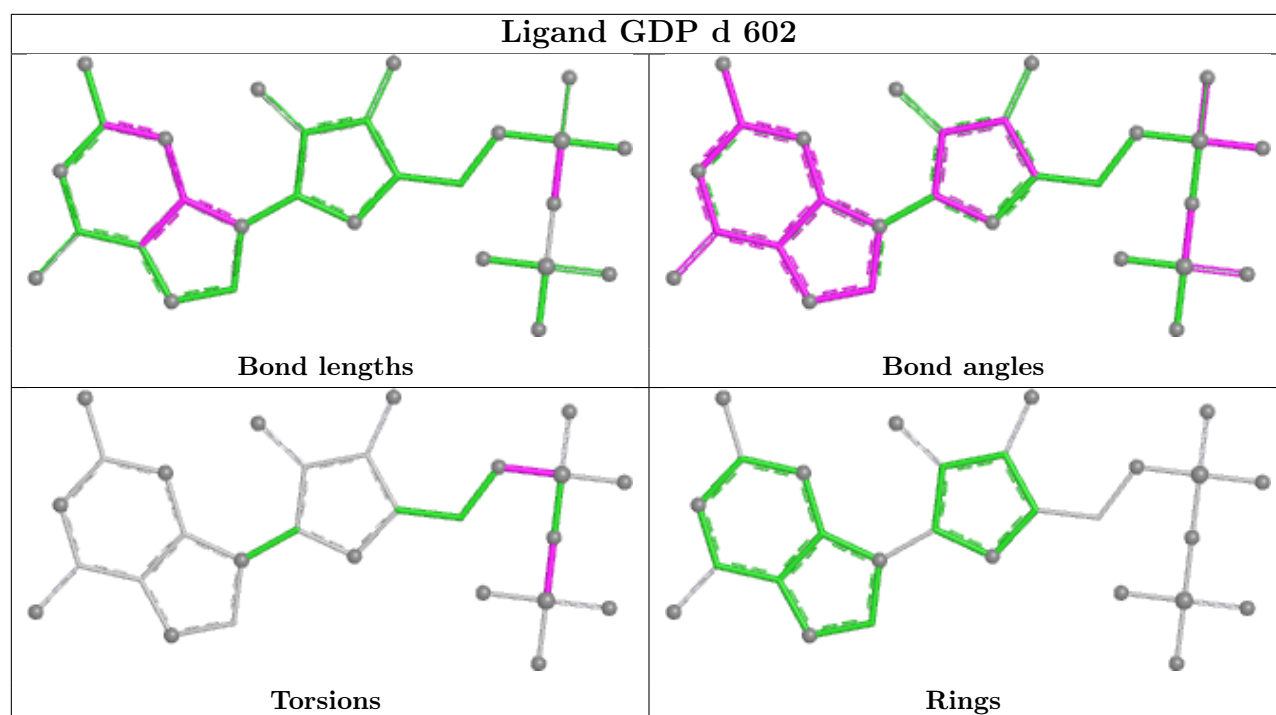


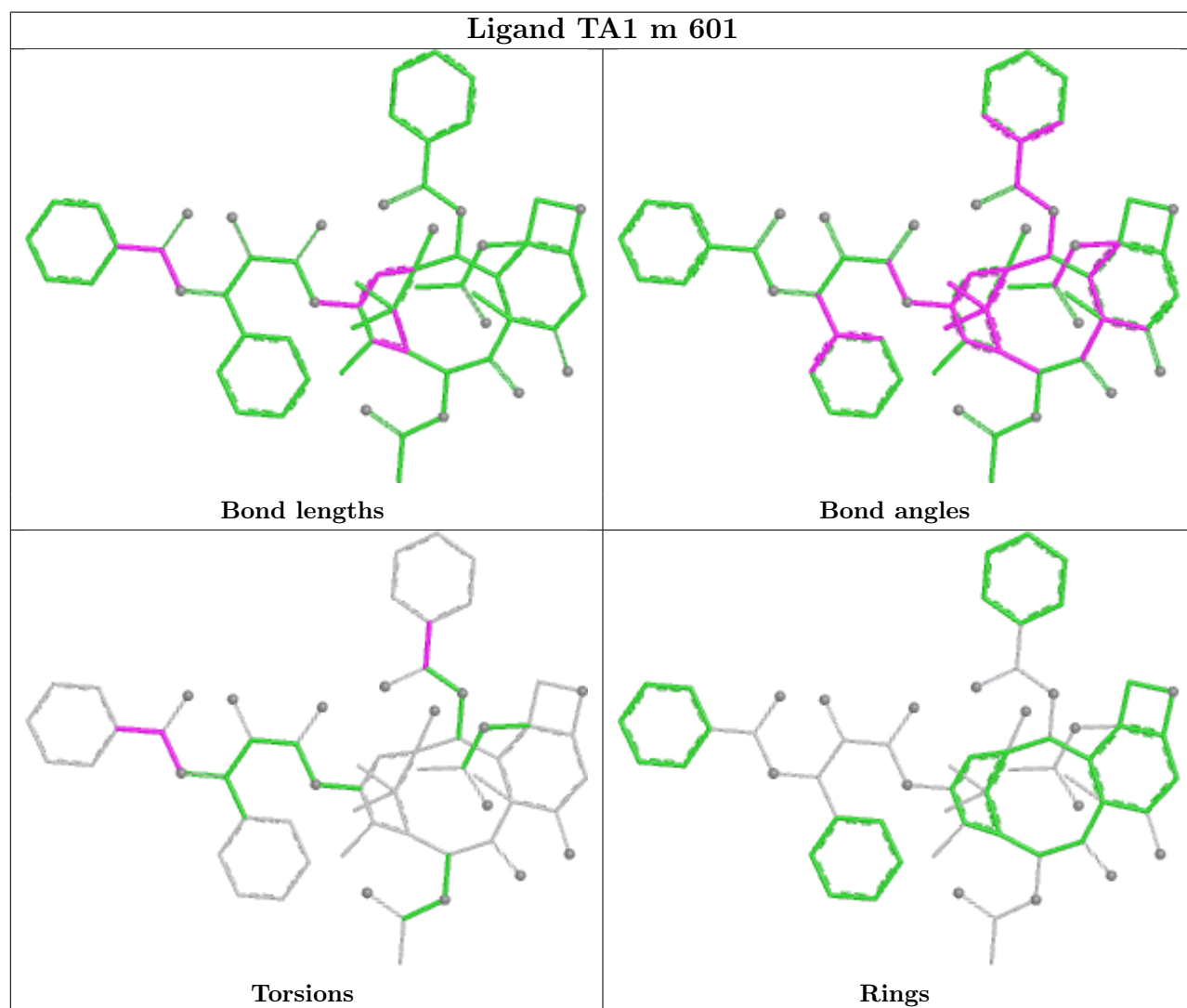
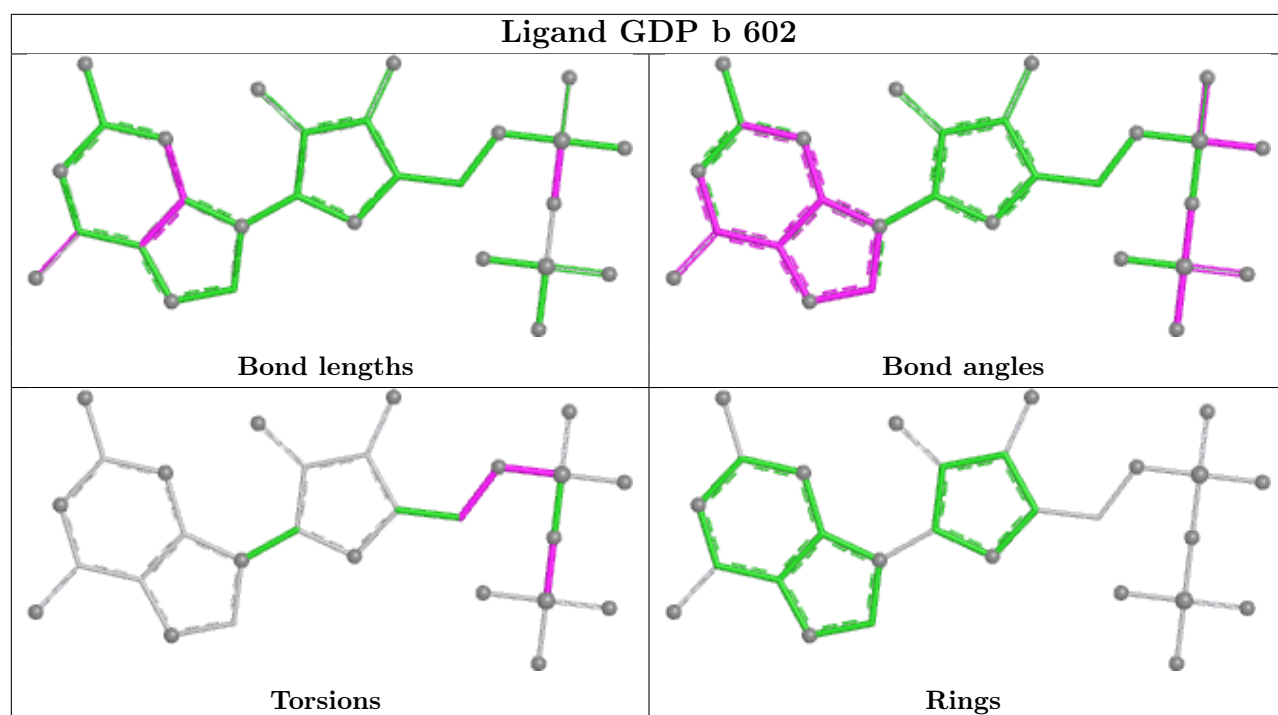
Ligand GDP e 602



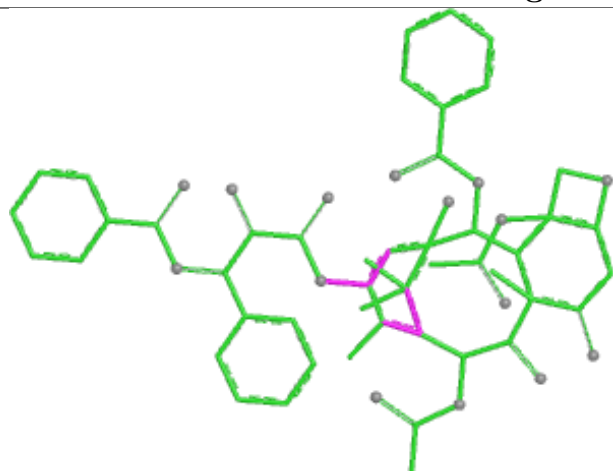




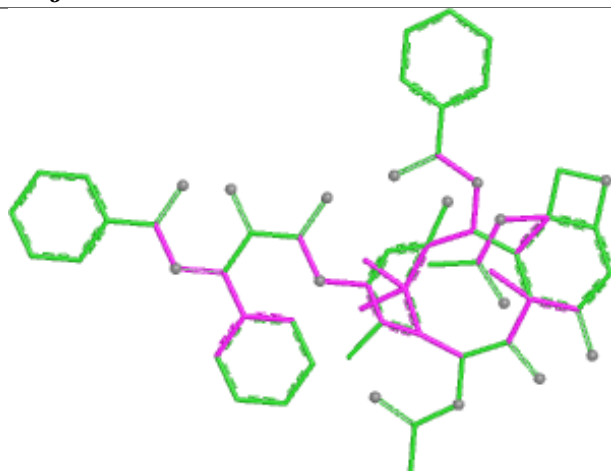




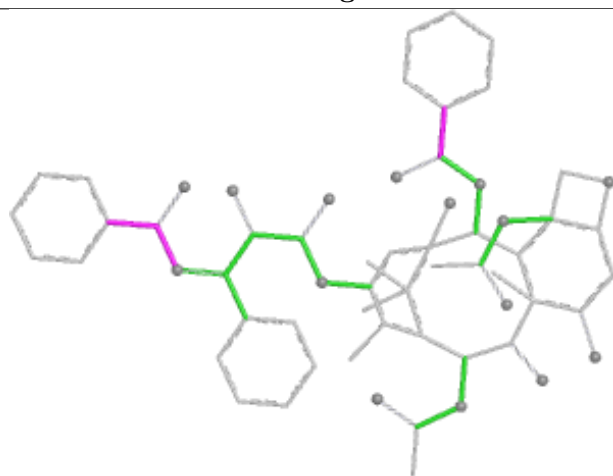
Ligand TA1 j 601



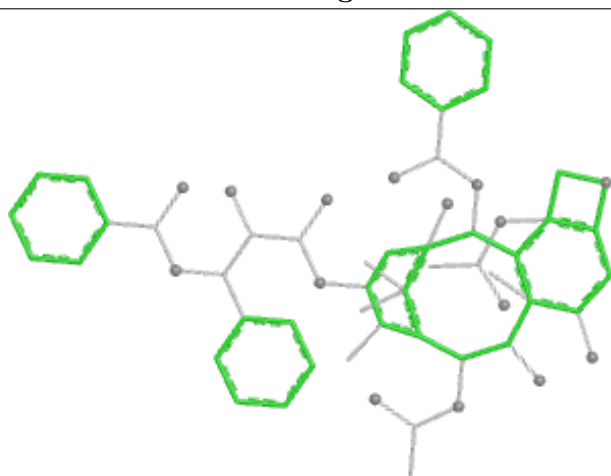
Bond lengths



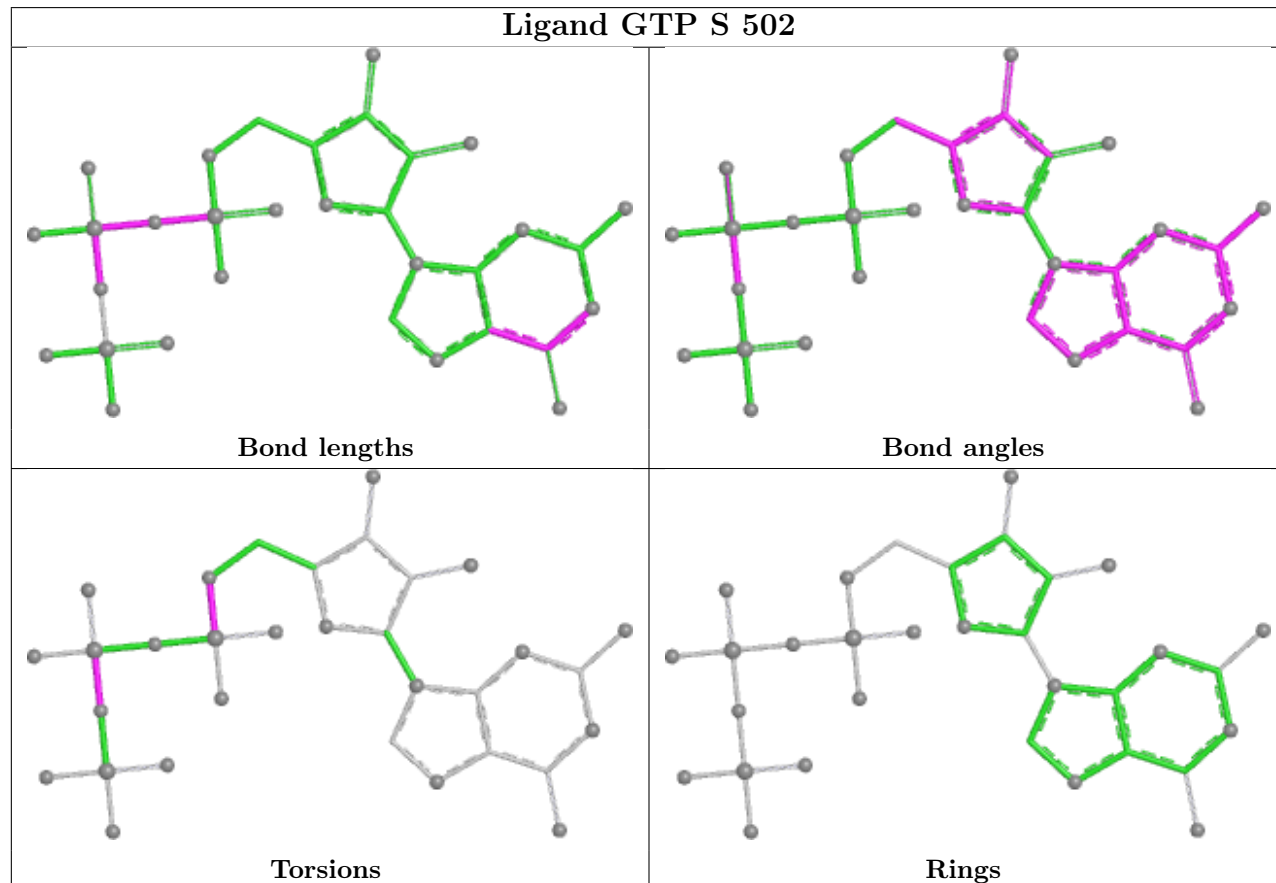
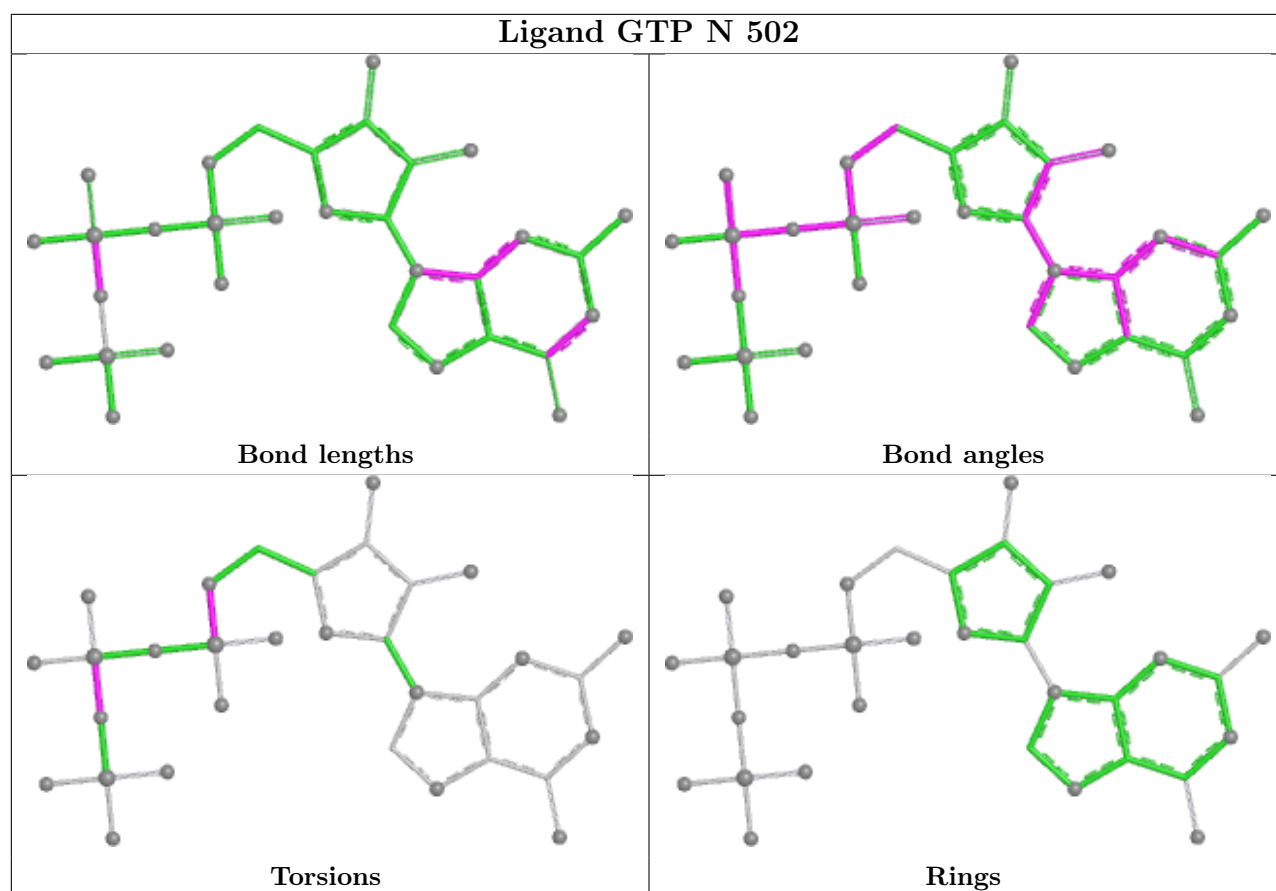
Bond angles

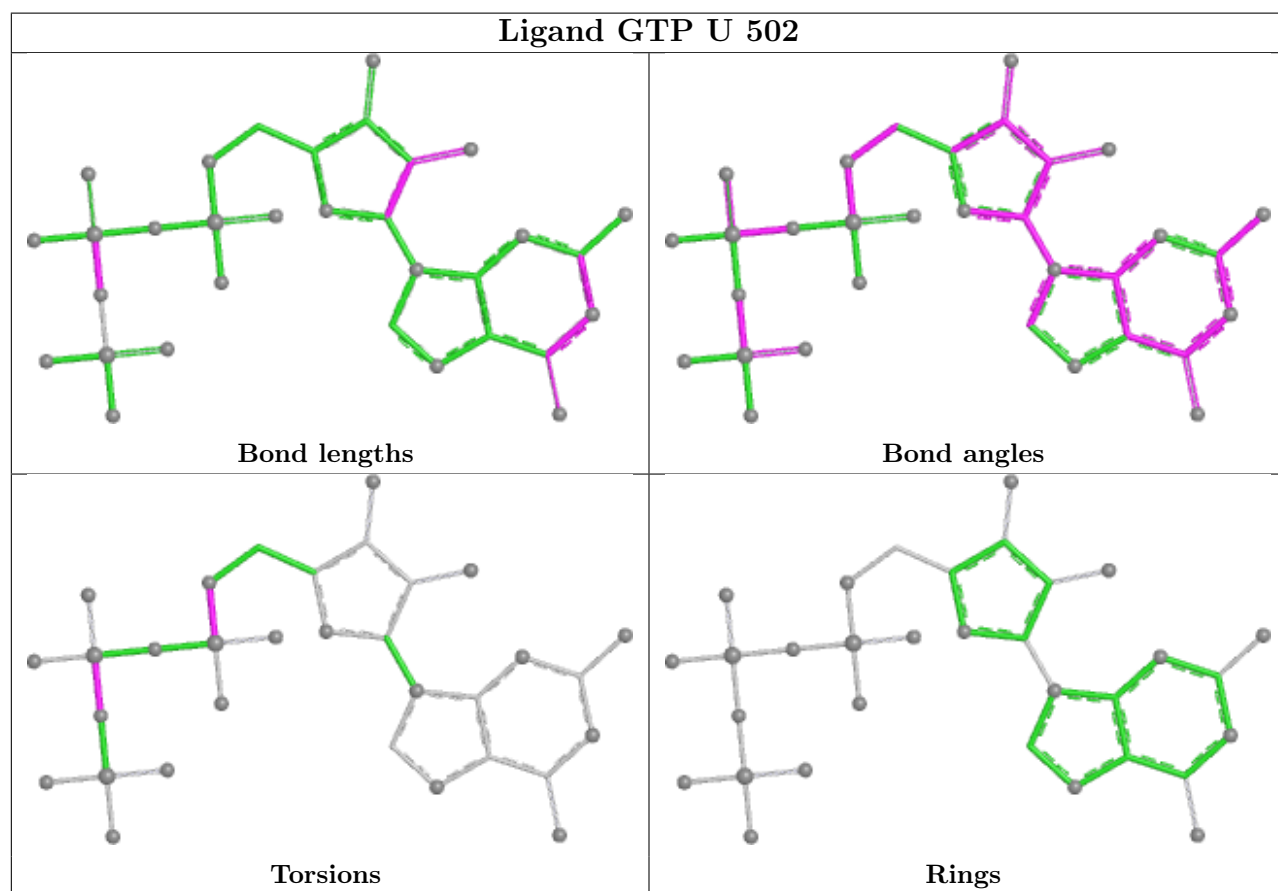
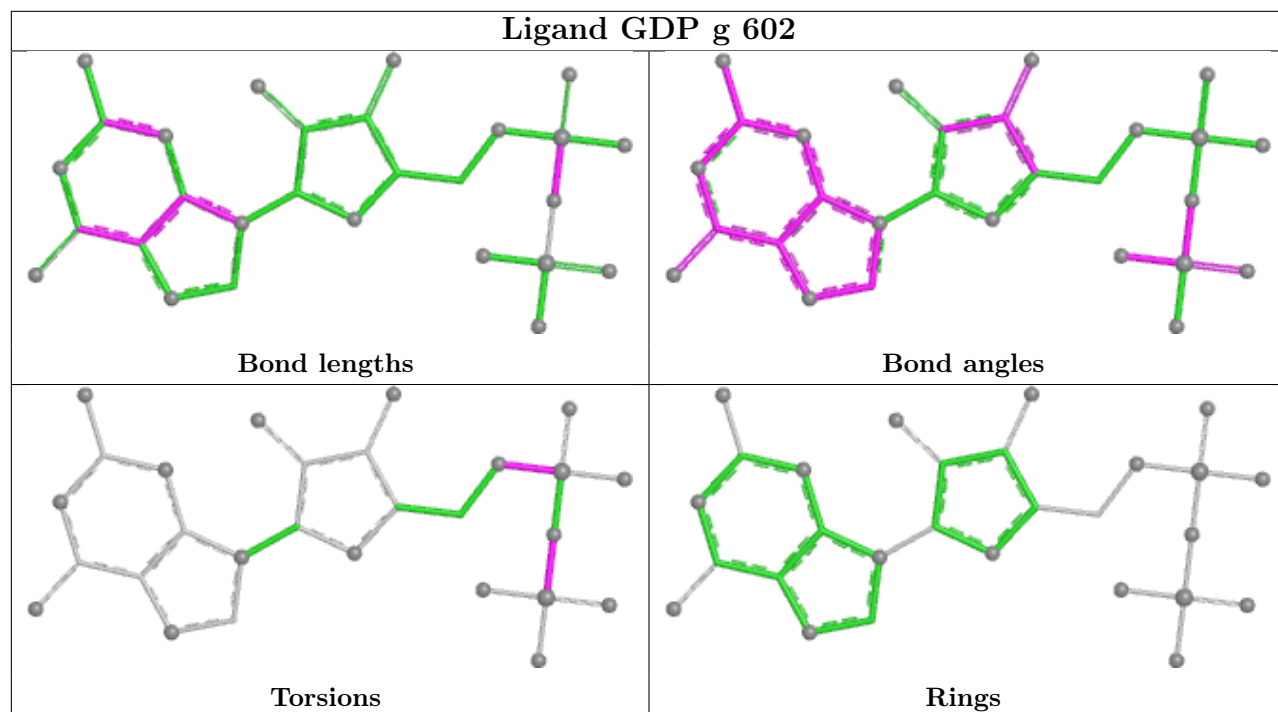


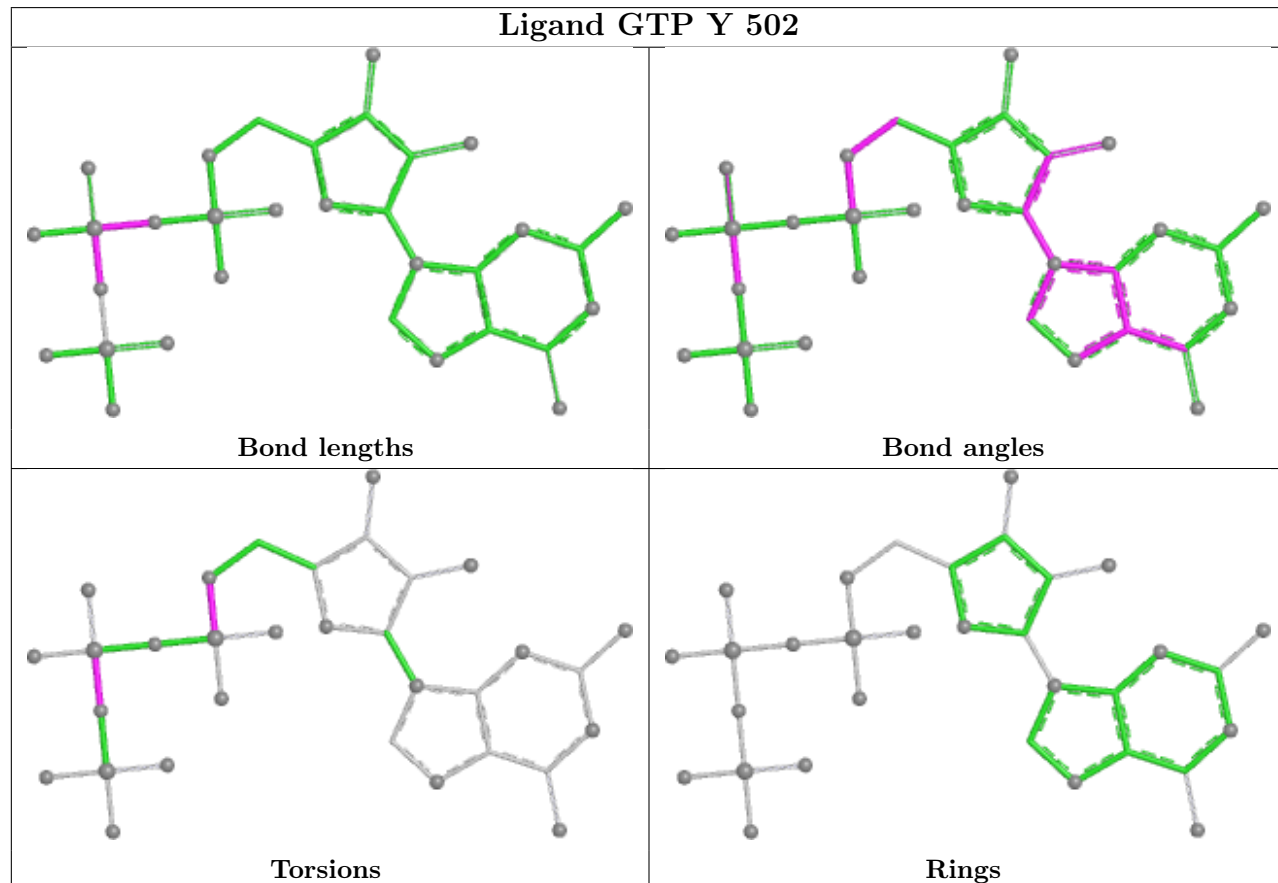
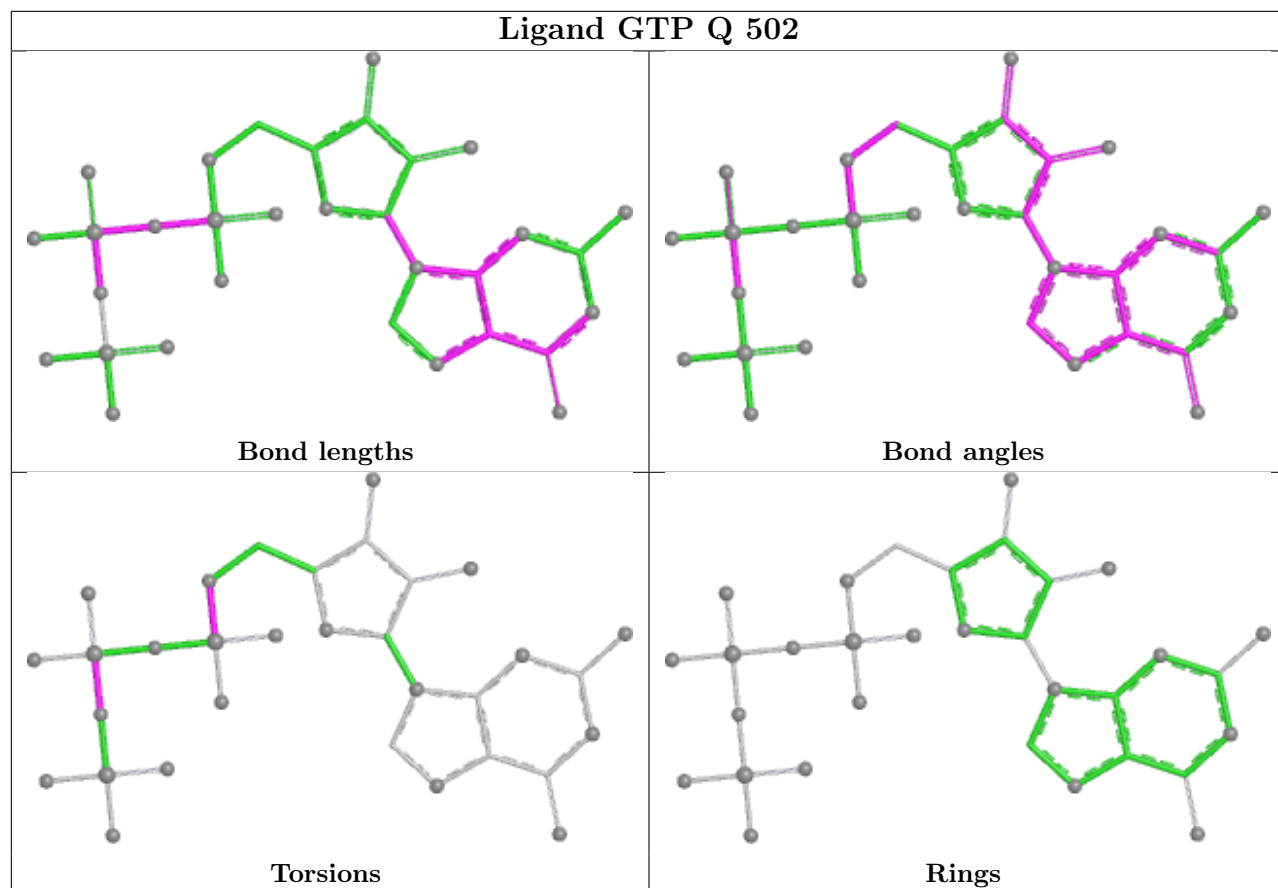
Torsions



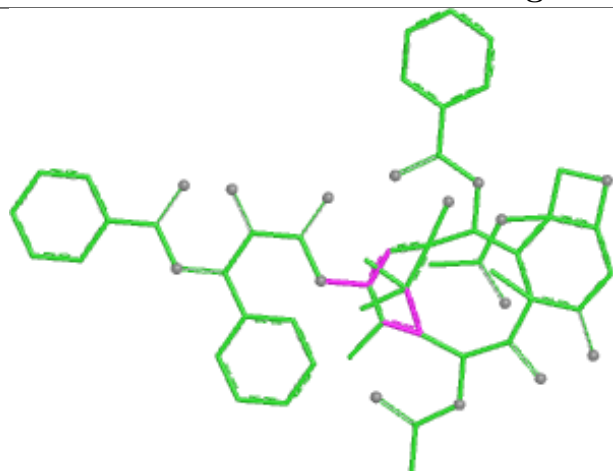
Rings



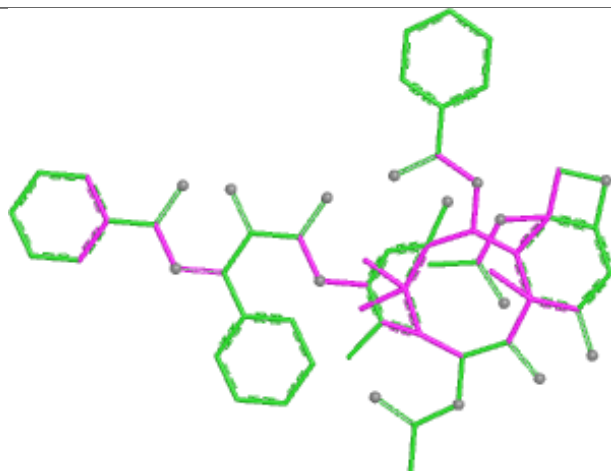




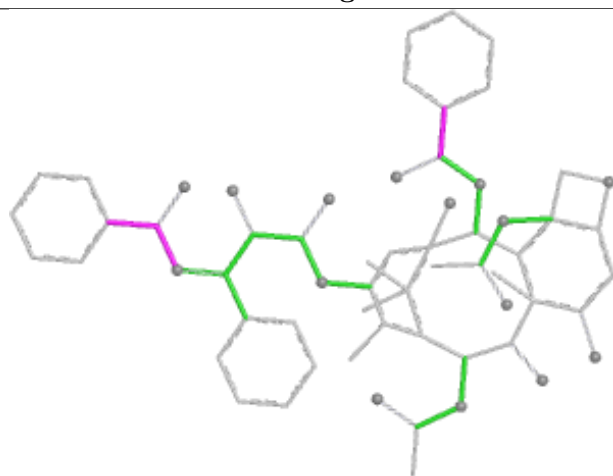
Ligand TA1 i 601



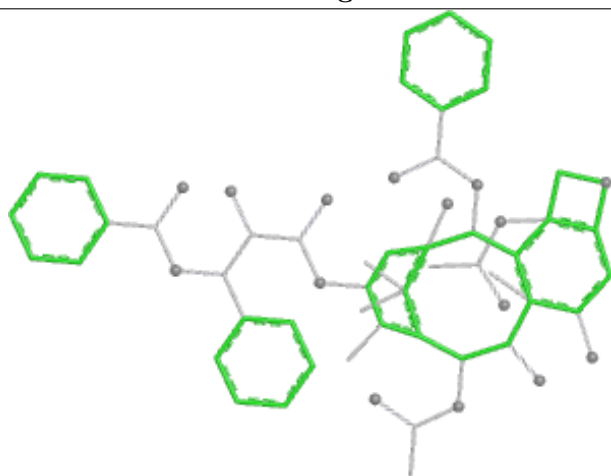
Bond lengths



Bond angles

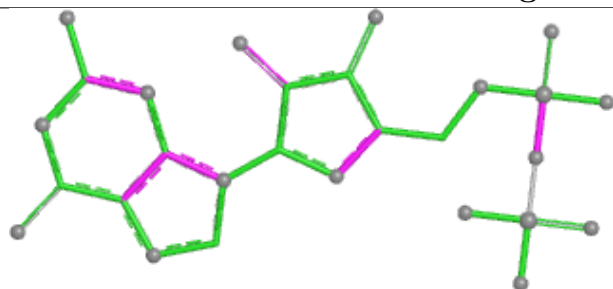


Torsions

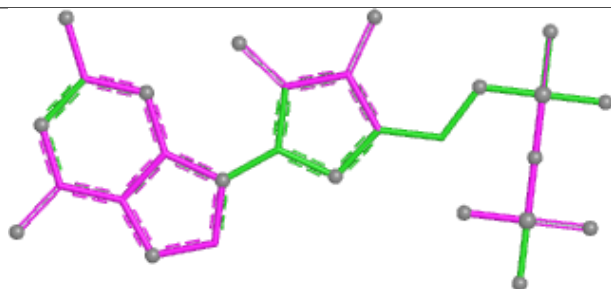


Rings

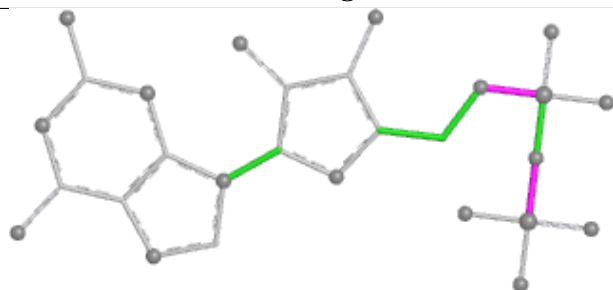
Ligand GDP i 602



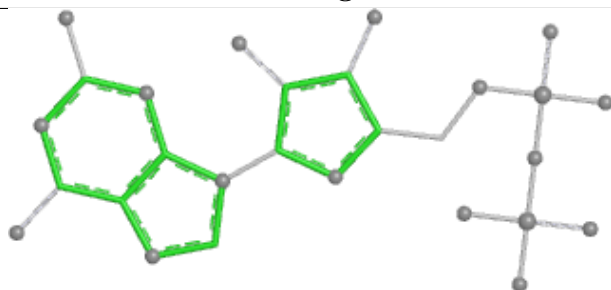
Bond lengths



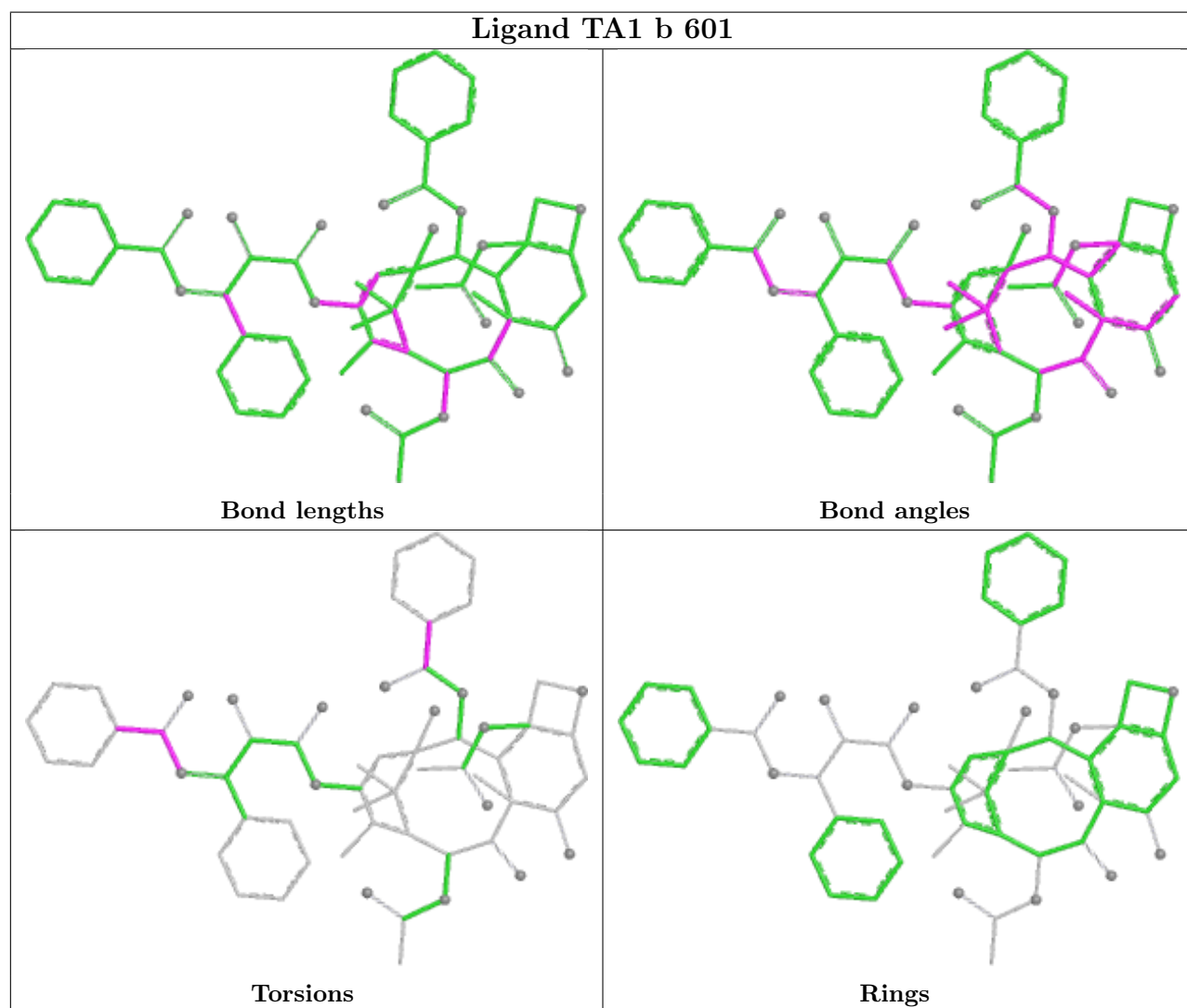
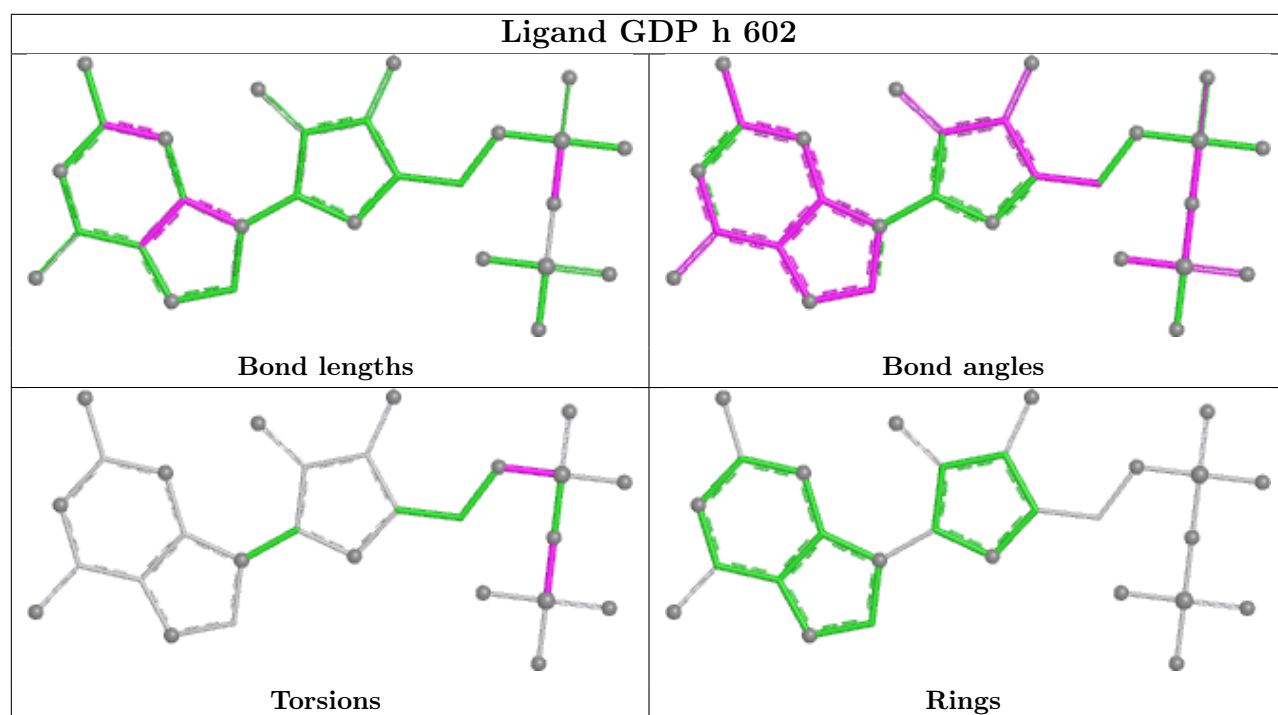
Bond angles

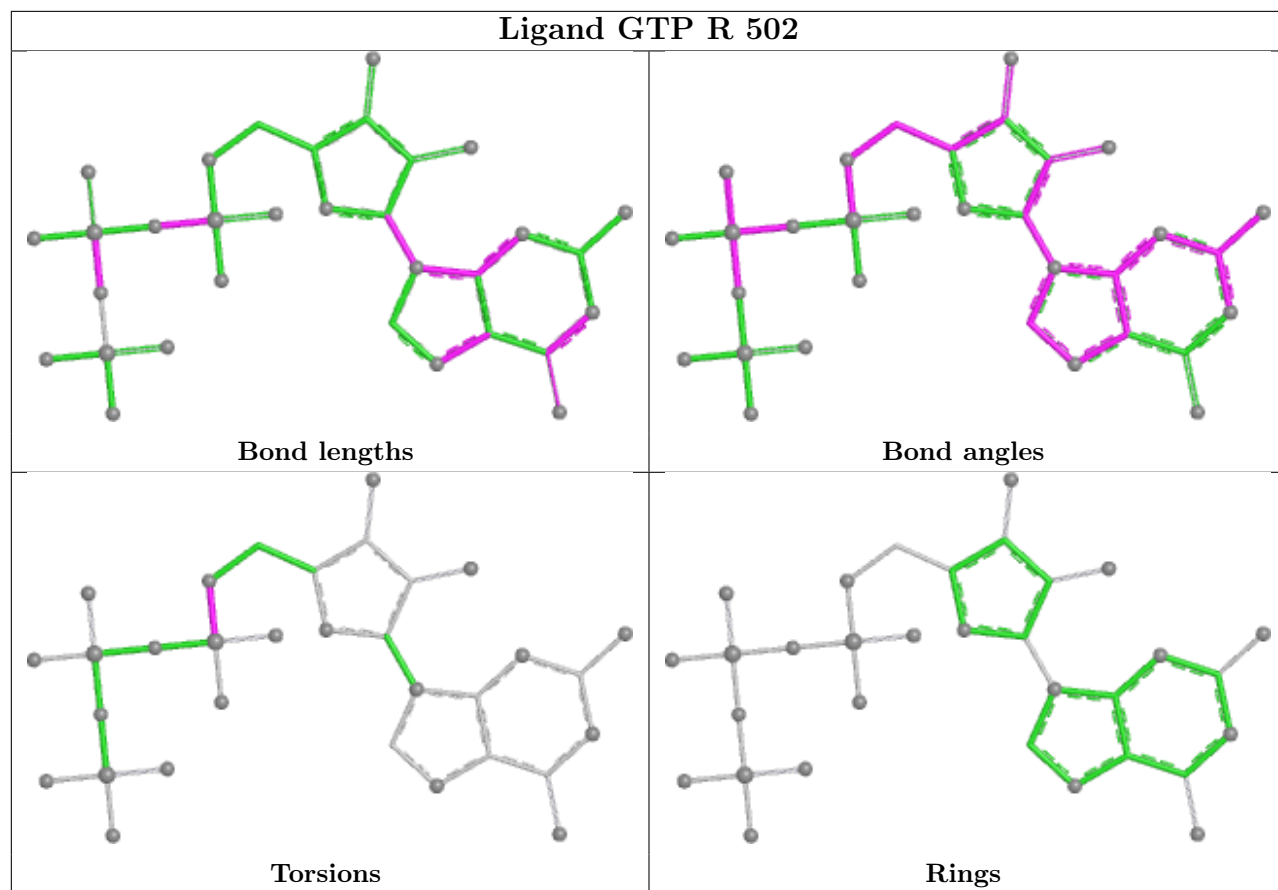


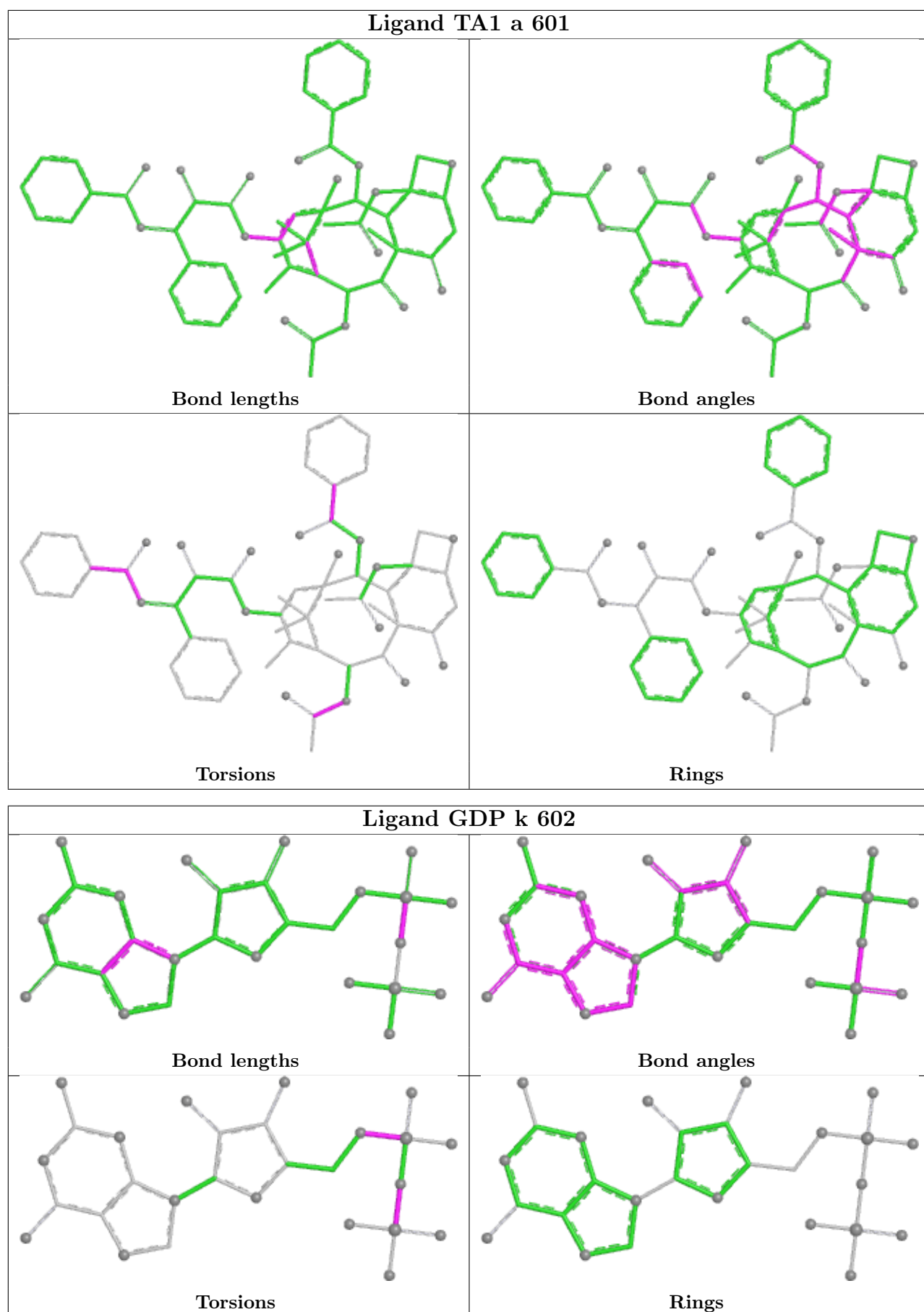
Torsions

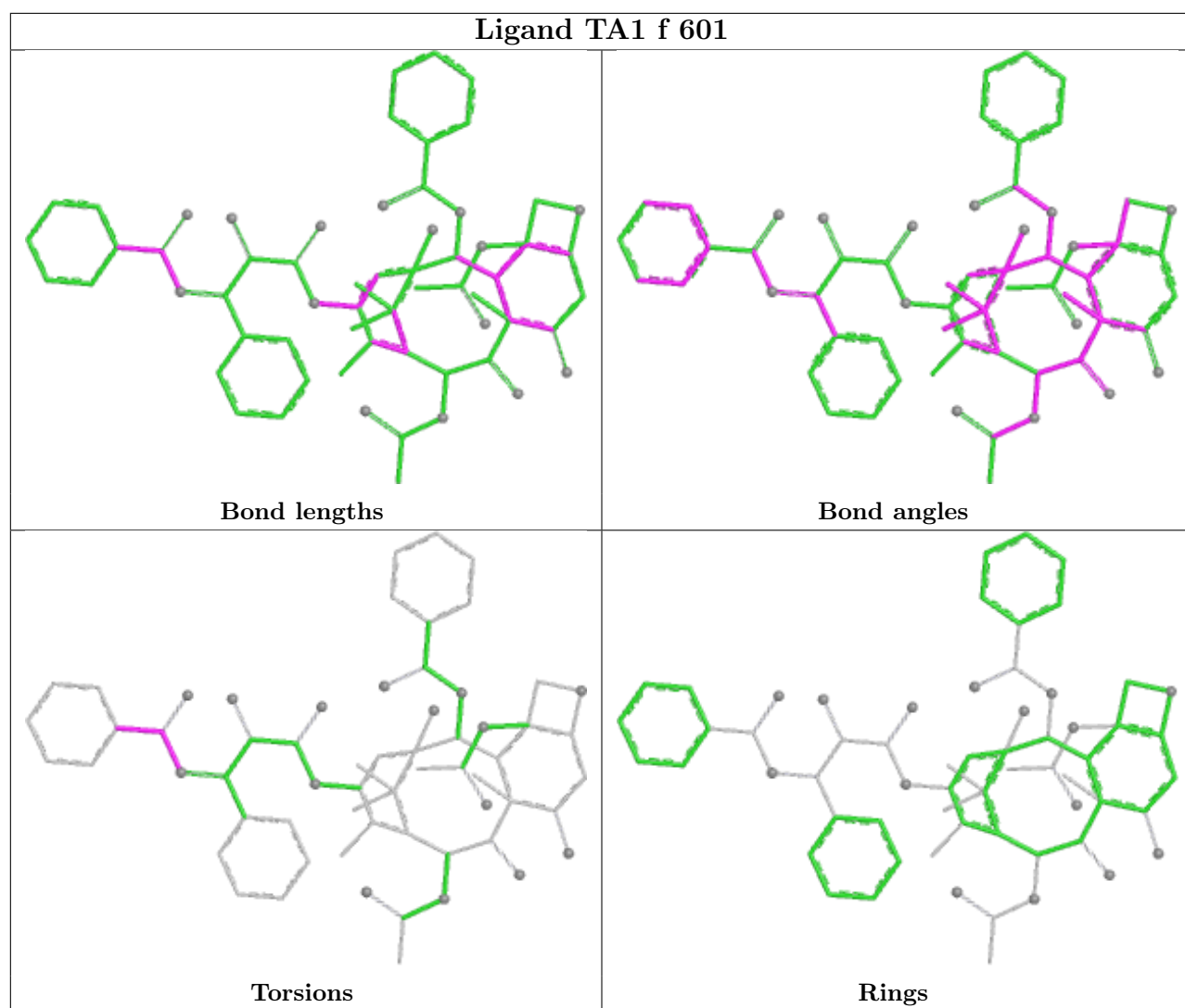


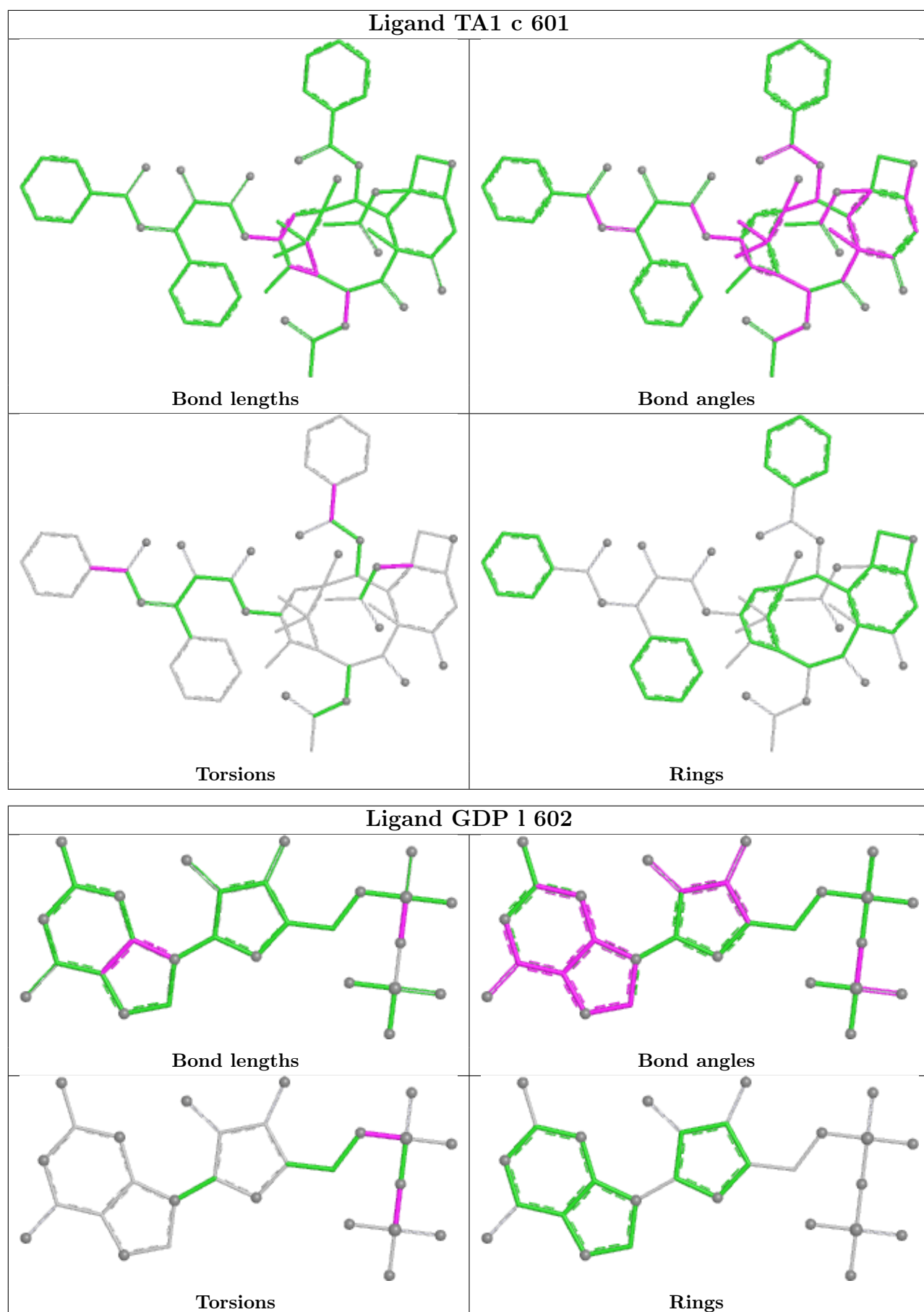
Rings



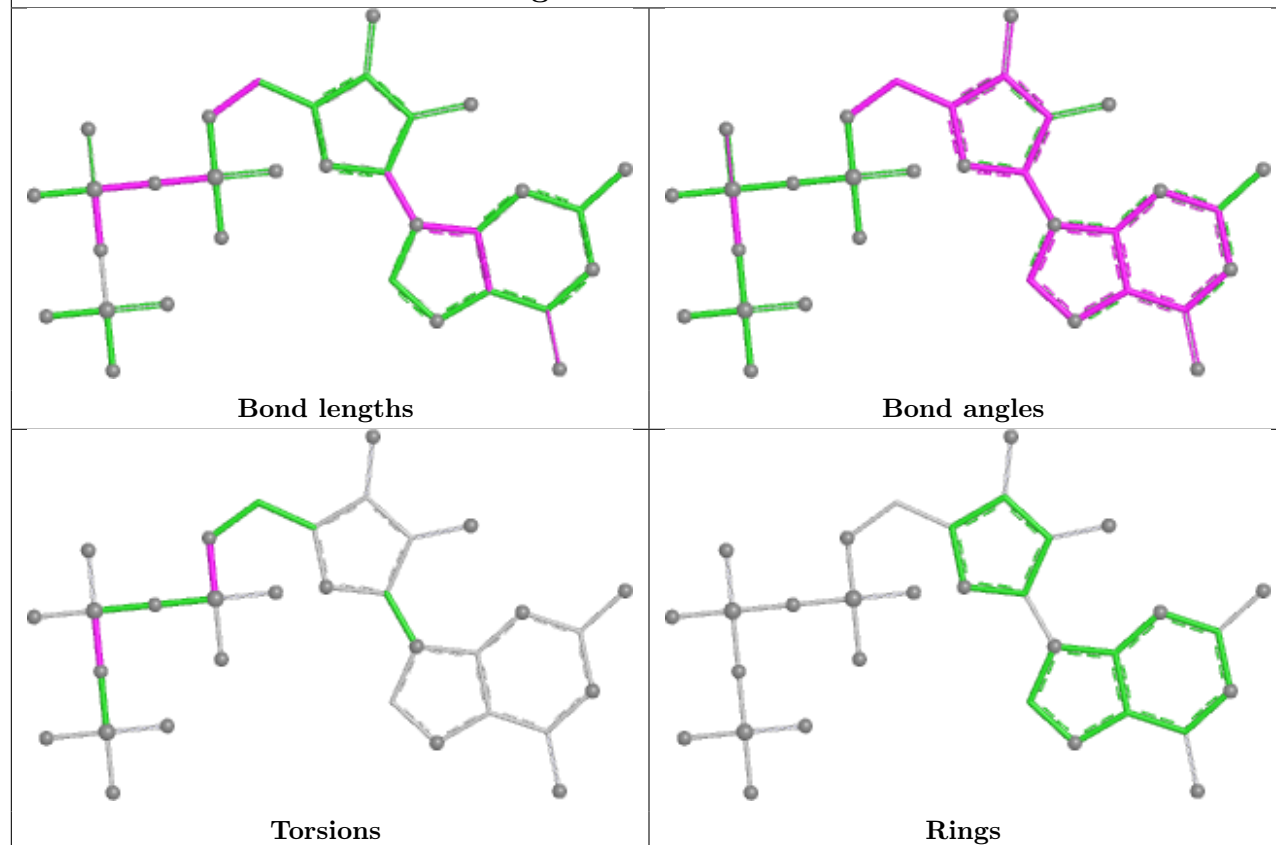




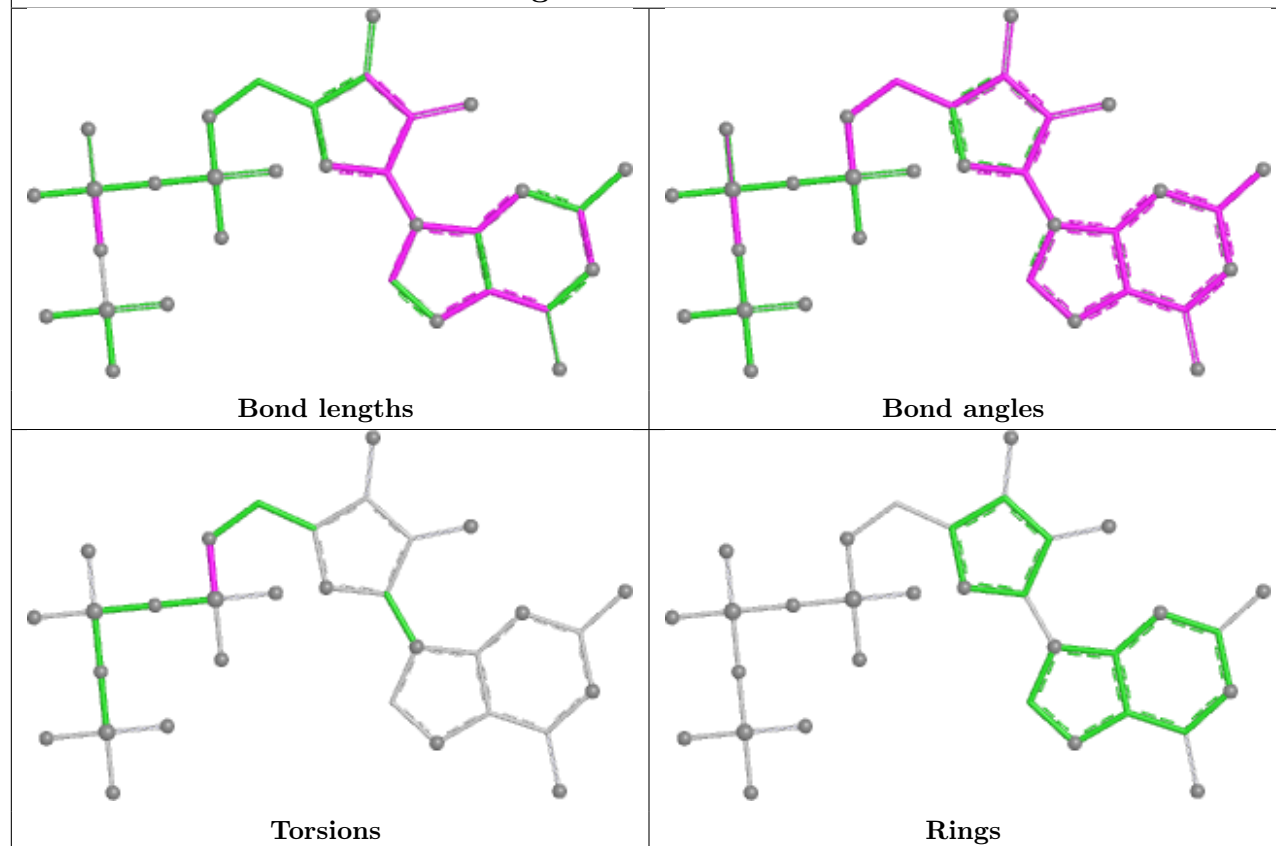


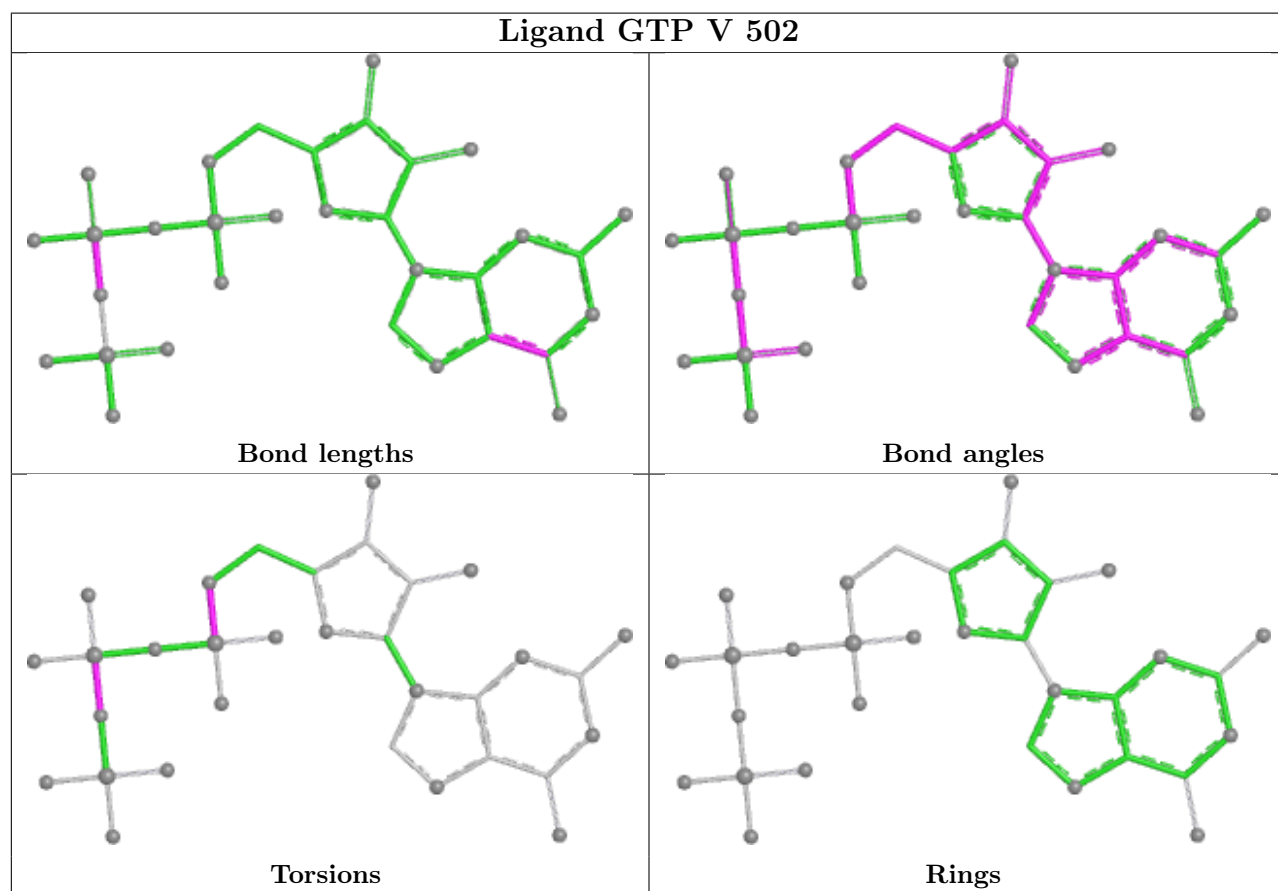
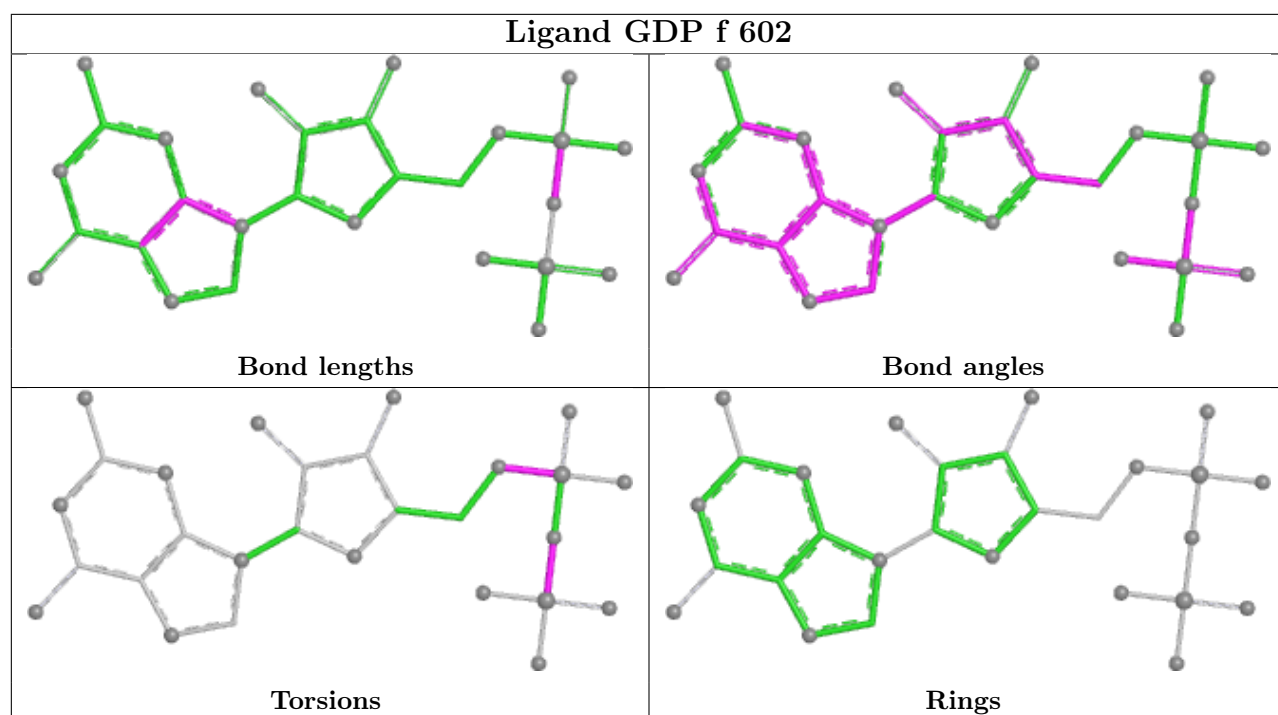


Ligand GTP P 502

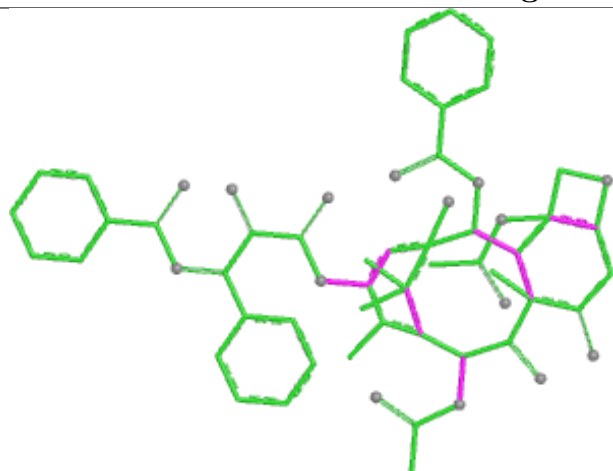


Ligand GTP T 502

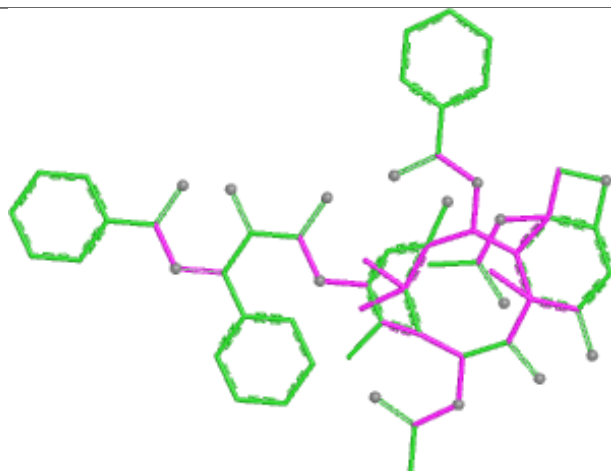




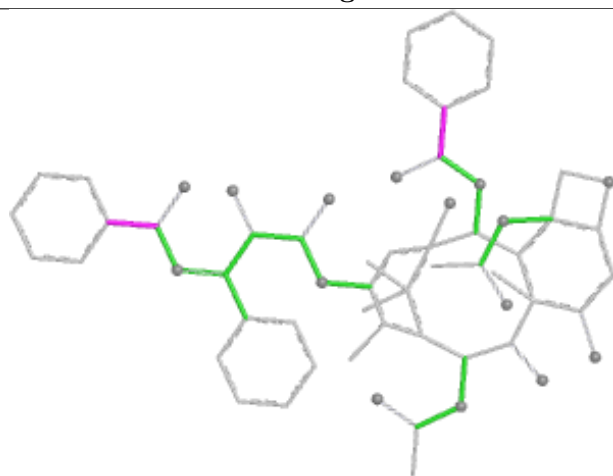
Ligand TA1 d 601



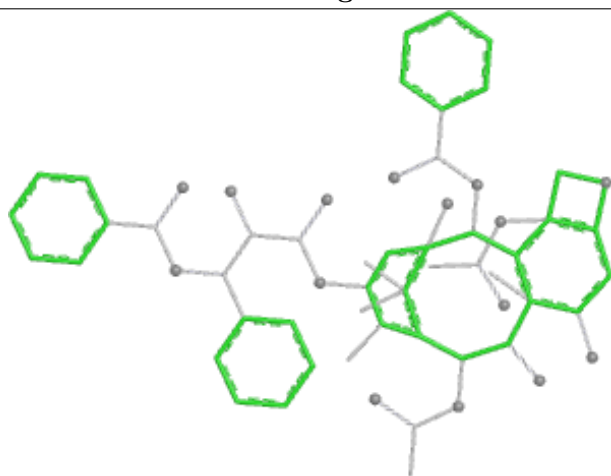
Bond lengths



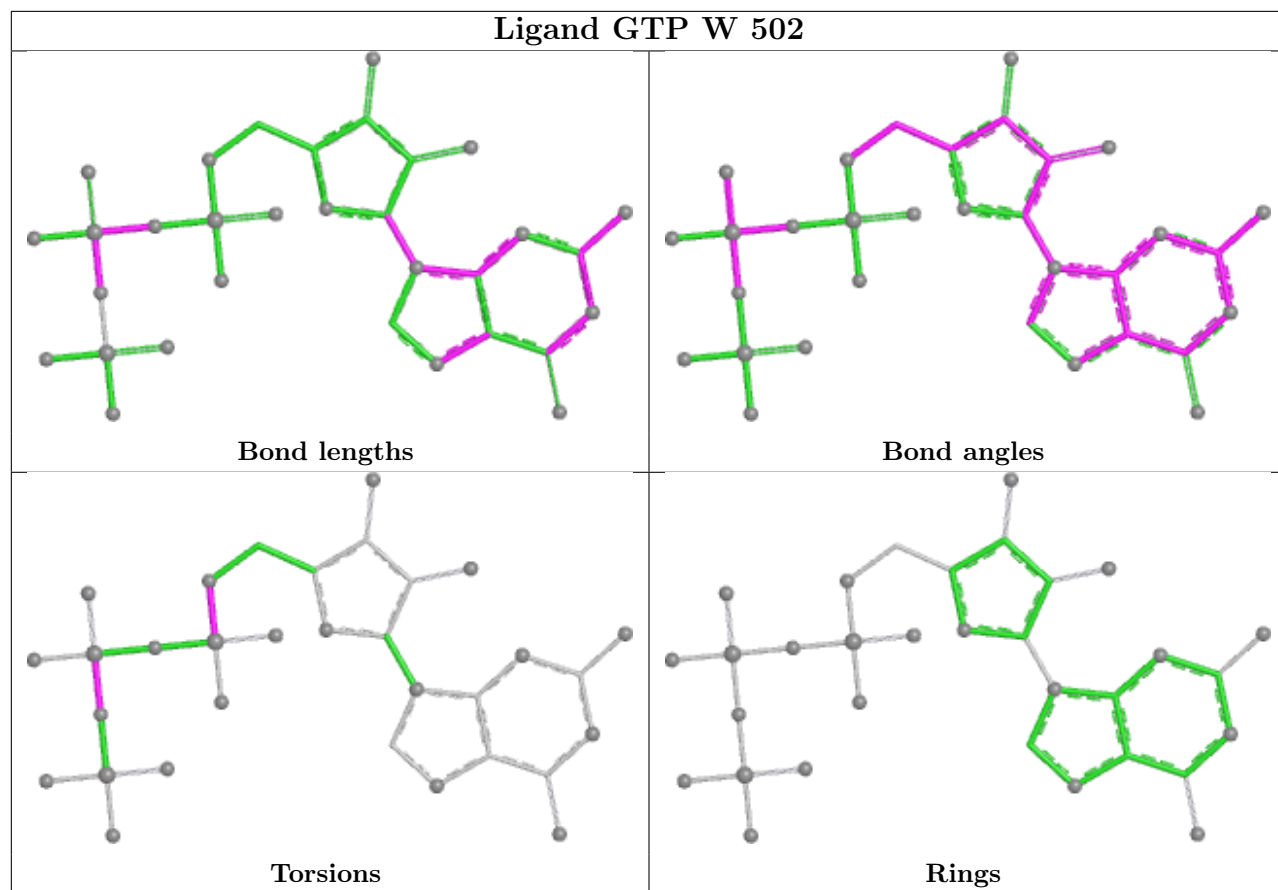
Bond angles

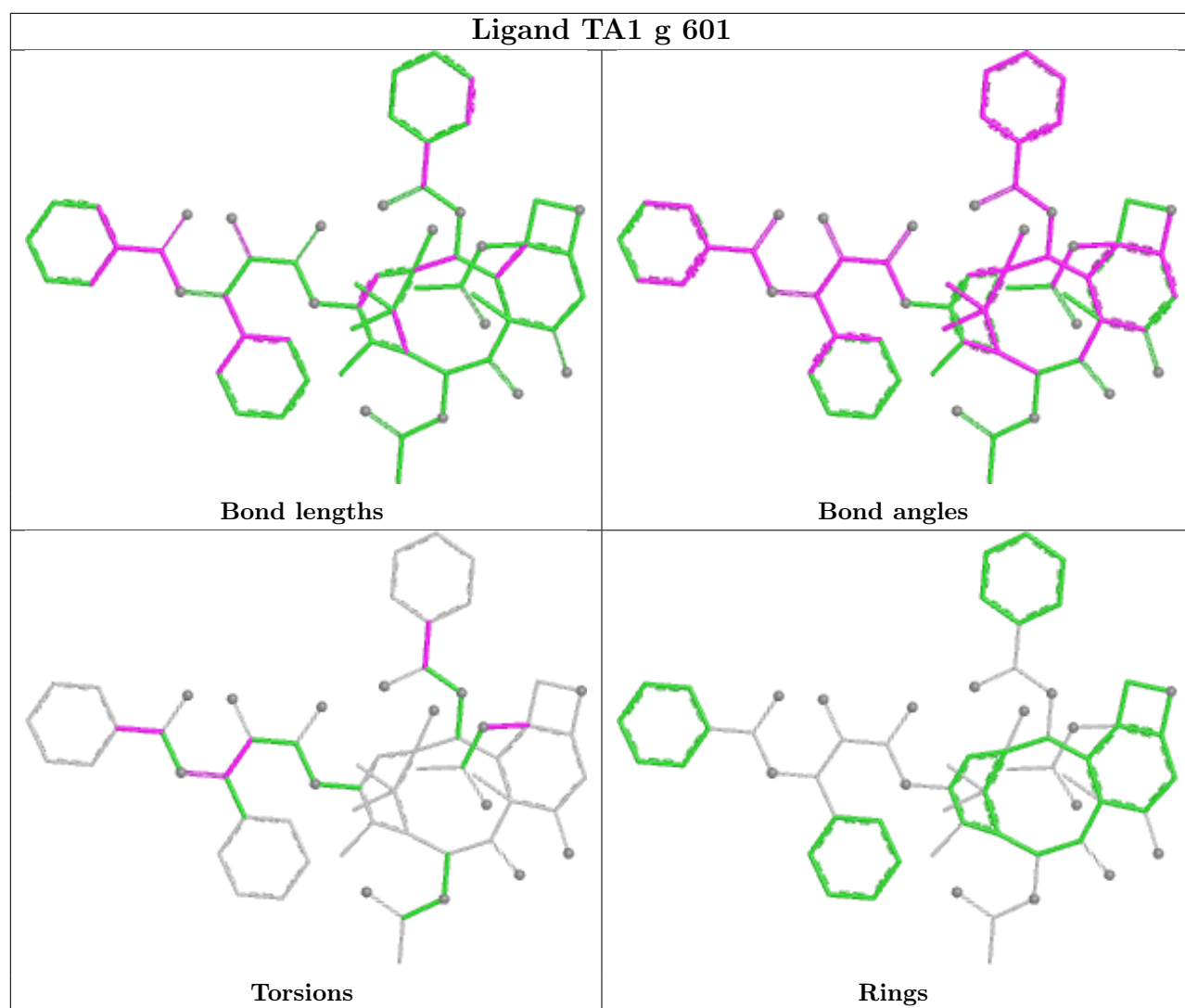


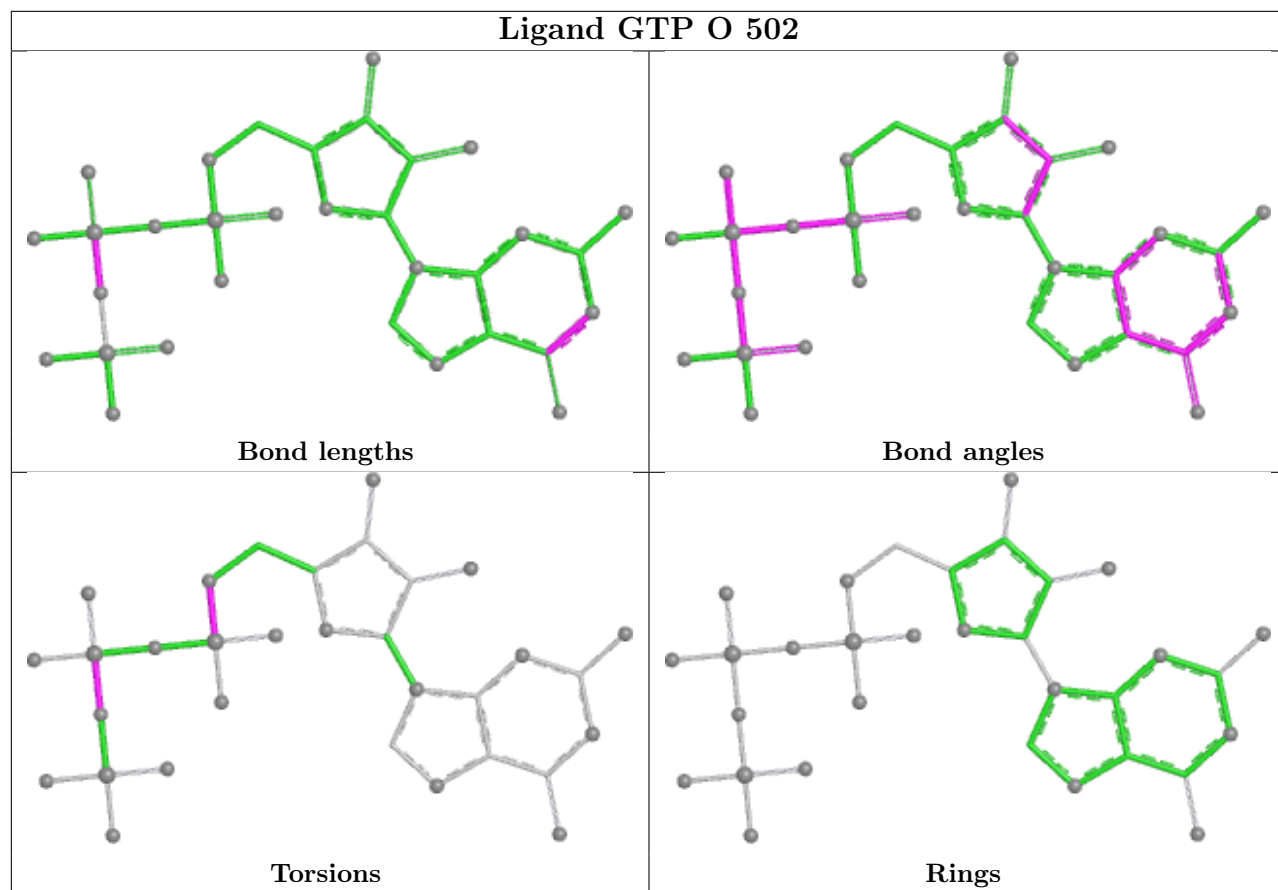
Torsions

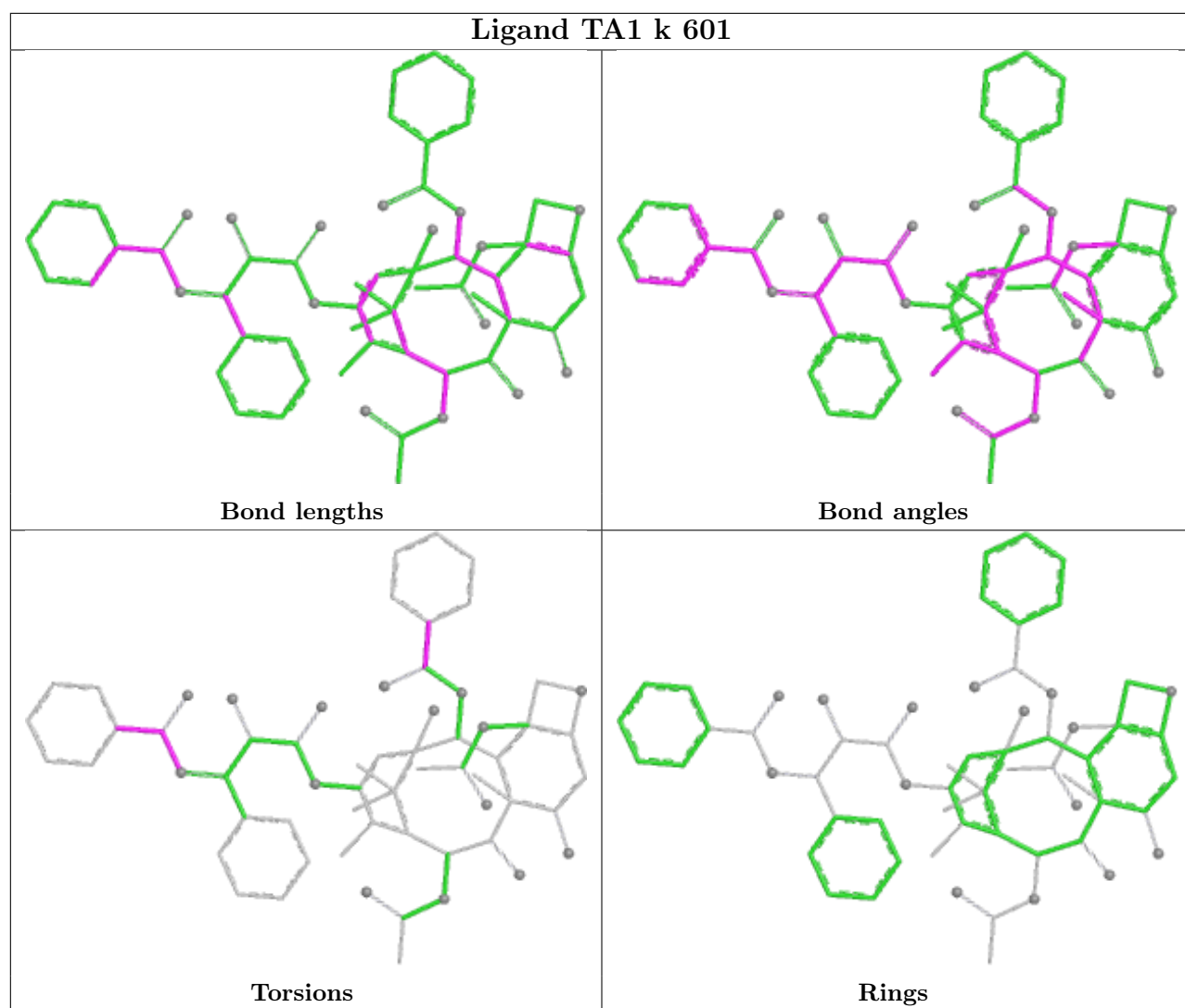


Rings

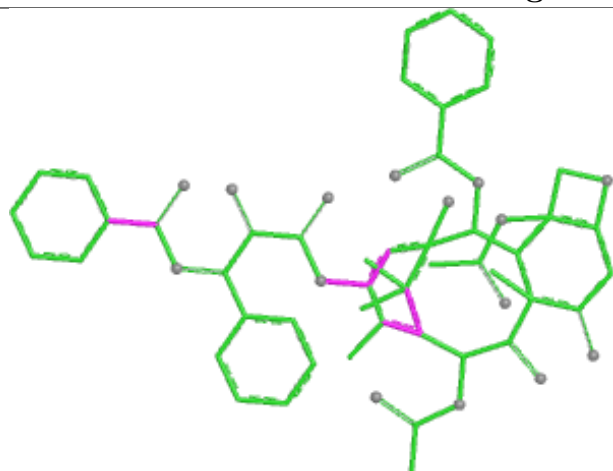




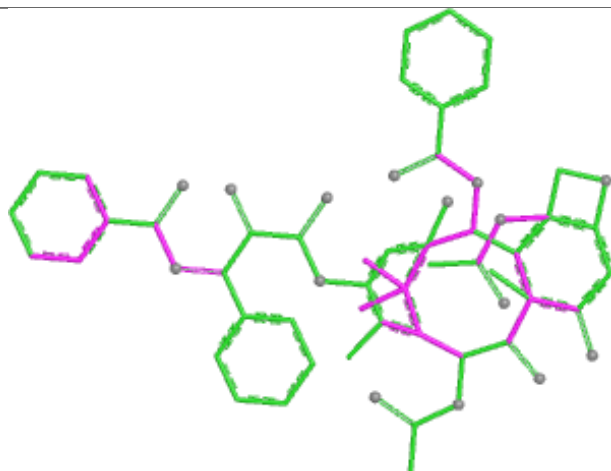




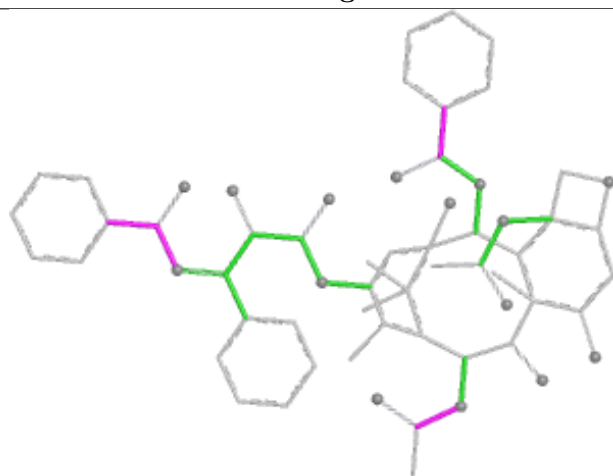
Ligand TA1 i 601



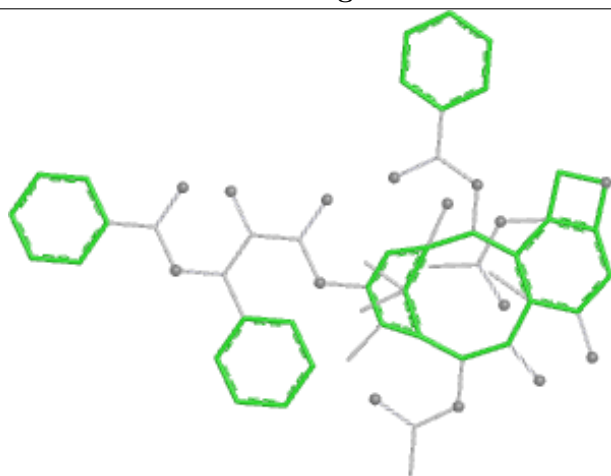
Bond lengths



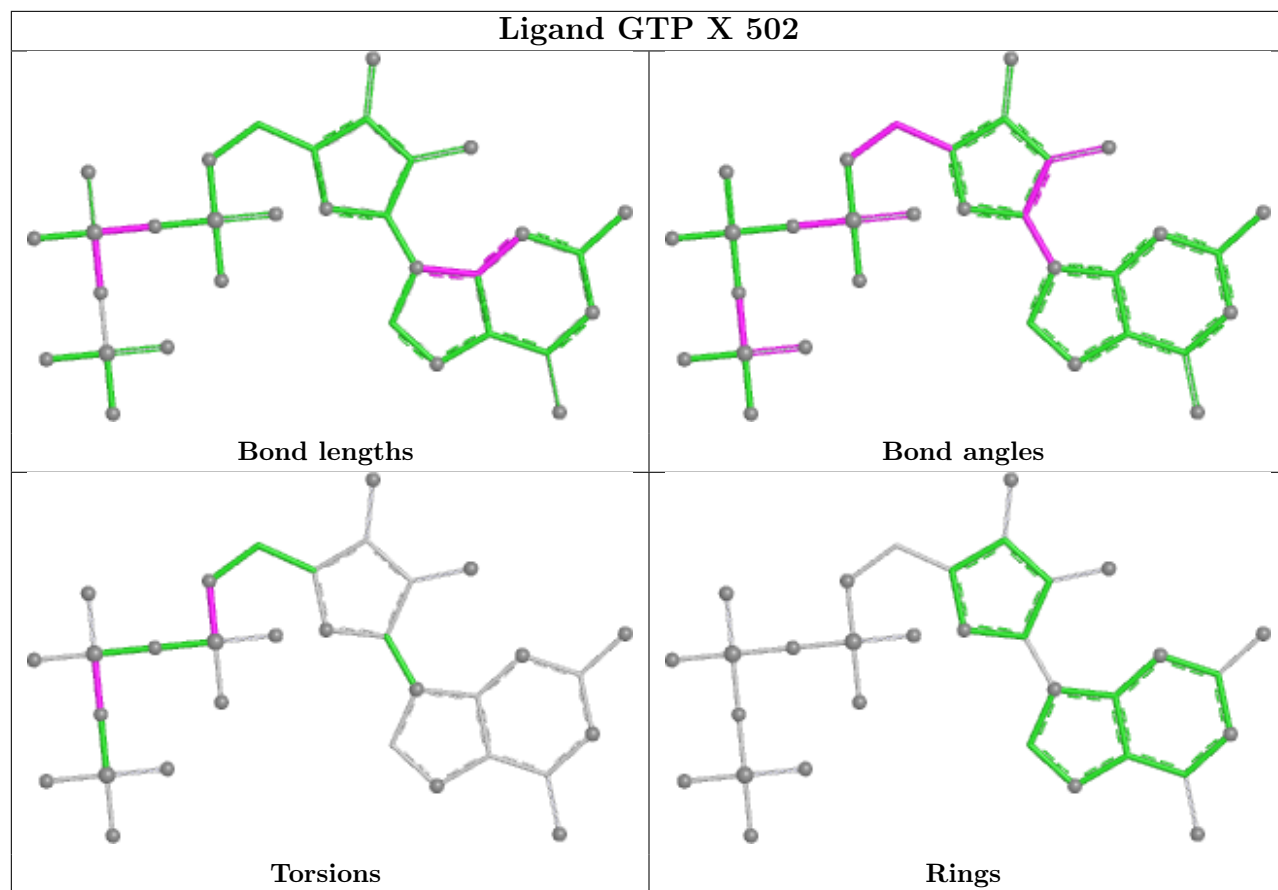
Bond angles

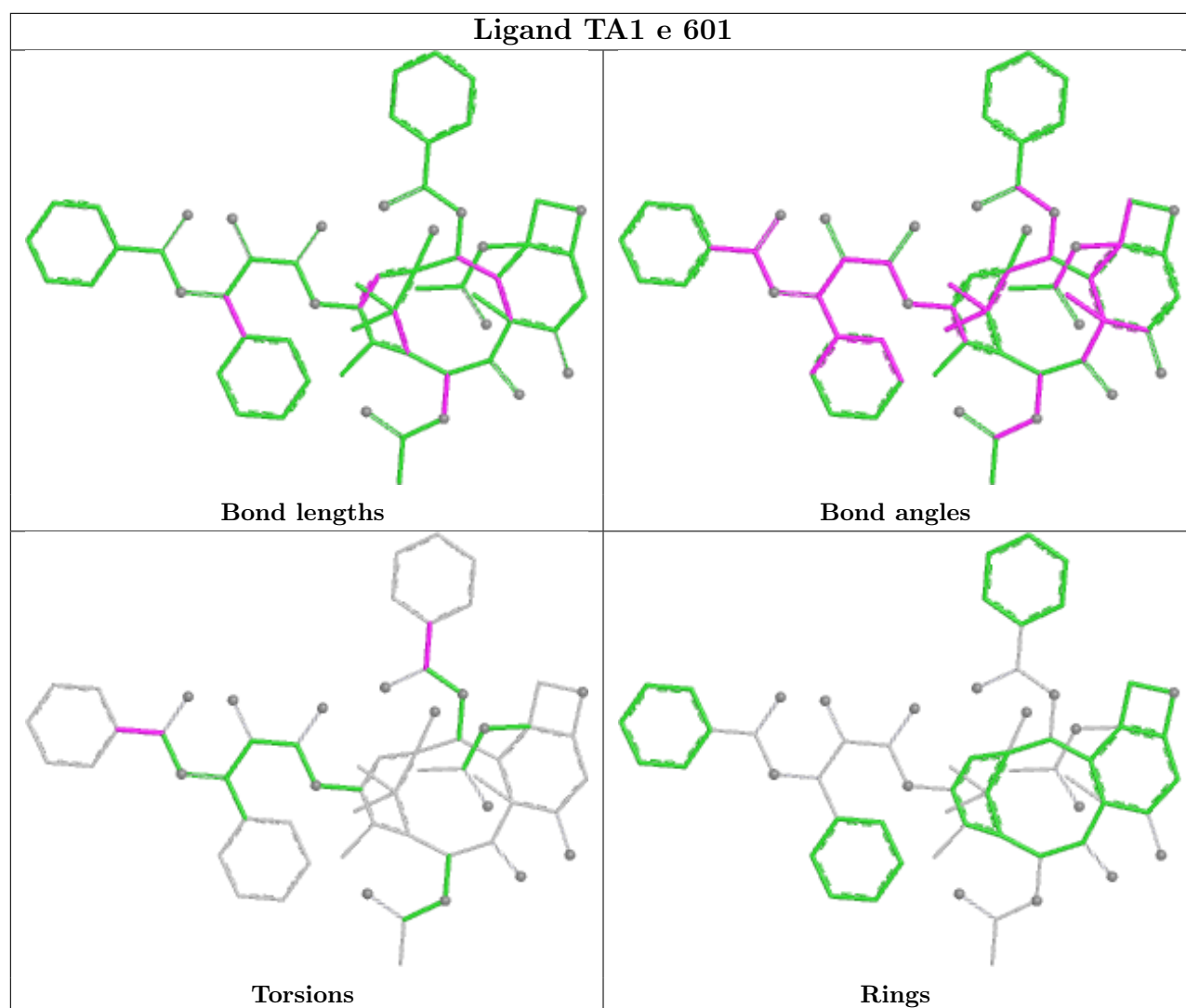


Torsions



Rings





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	R	1
1	e	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	43:GLY	C	44:GLY	N	1.98
1	e	294:PHE	C	295:ASP	N	1.83

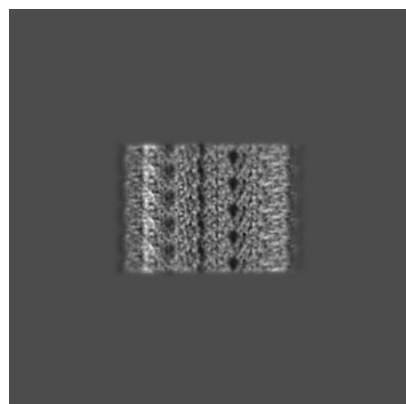
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16435. These allow visual inspection of the internal detail of the map and identification of artifacts.

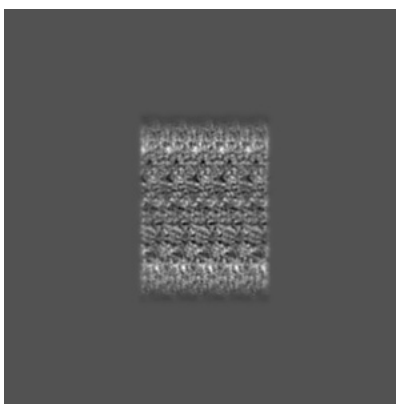
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

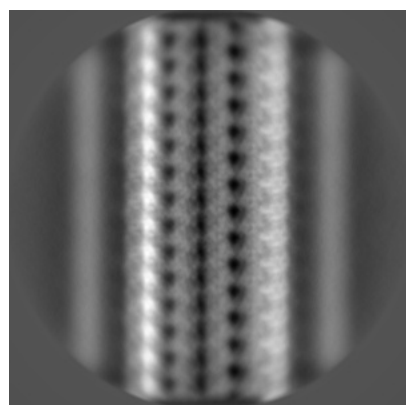


Y

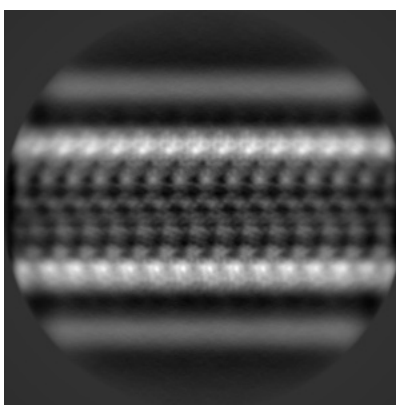


Z

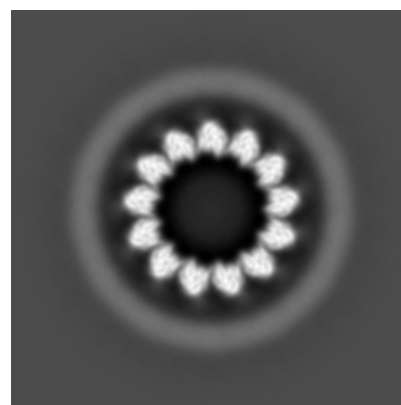
6.1.2 Raw map



X



Y

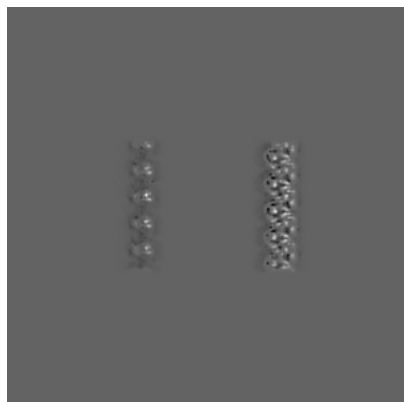


Z

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

6.2 Central slices [i](#)

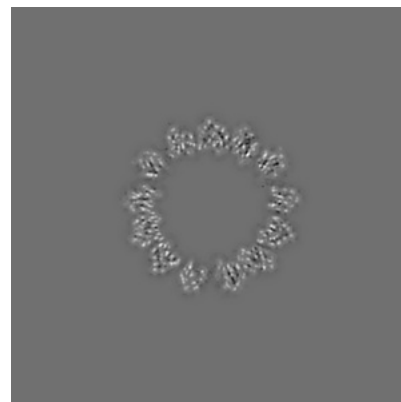
6.2.1 Primary map



X Index: 160

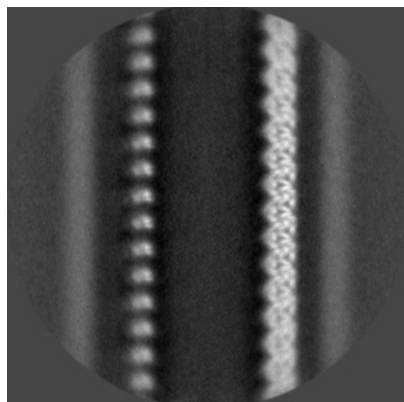


Y Index: 160

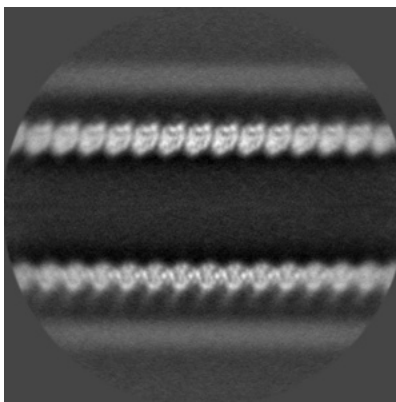


Z Index: 160

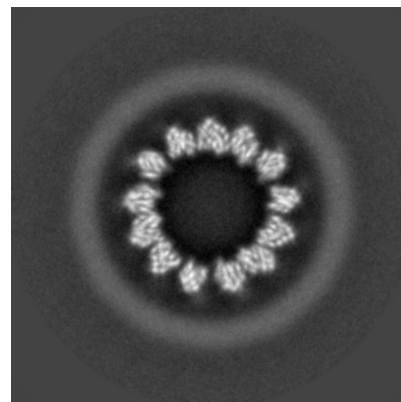
6.2.2 Raw map



X Index: 160



Y Index: 160



Z Index: 160

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: 111

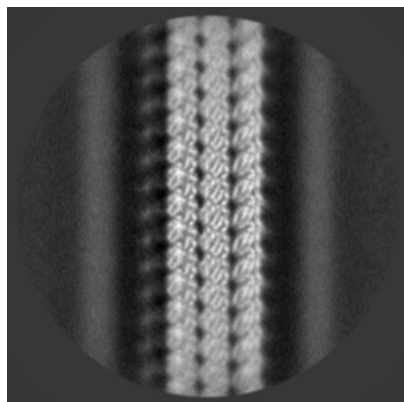


Y Index: 109

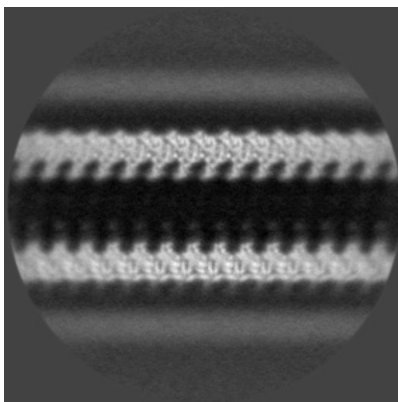


Z Index: 159

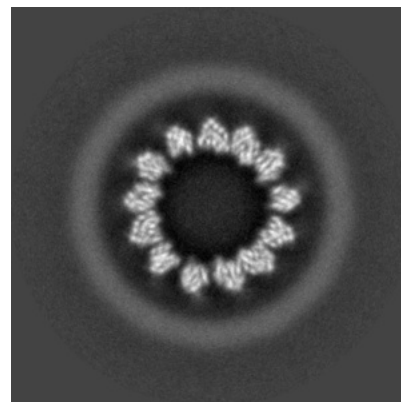
6.3.2 Raw map



X Index: 213



Y Index: 196

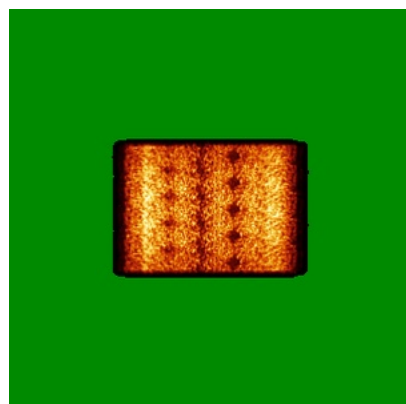


Z Index: 141

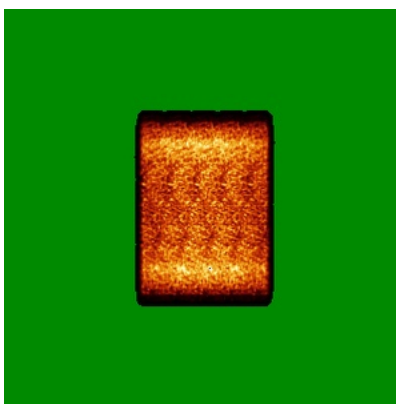
The images above show the largest variance slices of the map in three orthogonal directions.

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

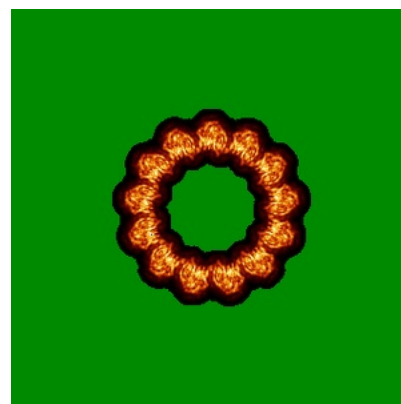
6.4.1 Primary map



X

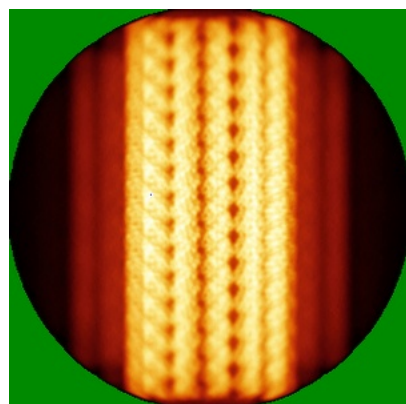


Y

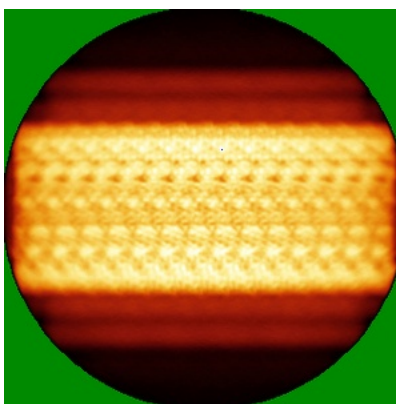


Z

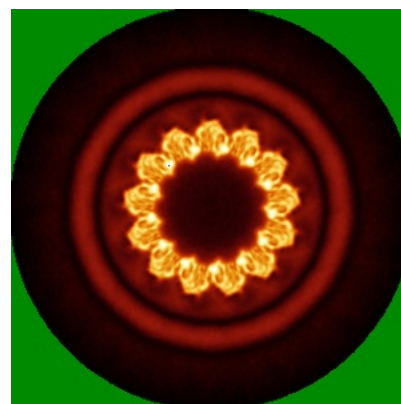
6.4.2 Raw map



X



Y

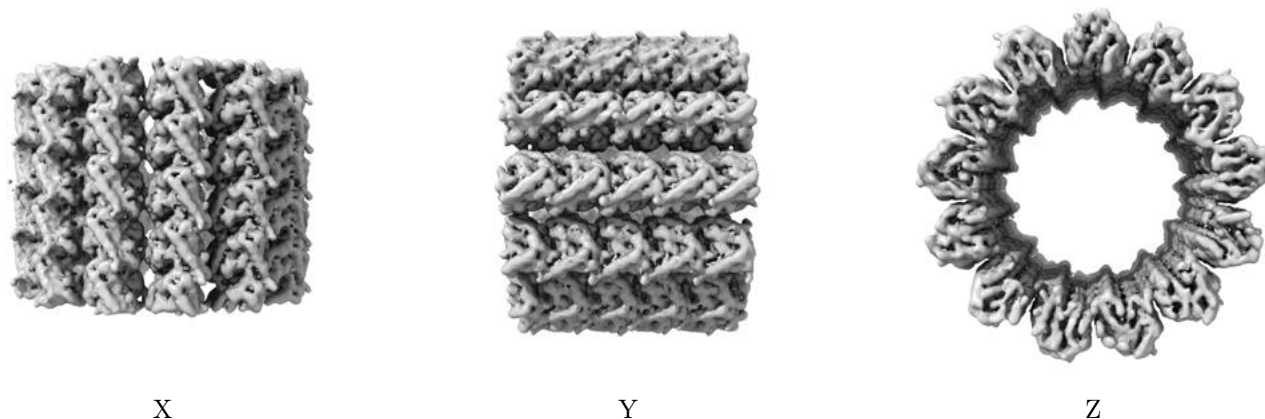


Z

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

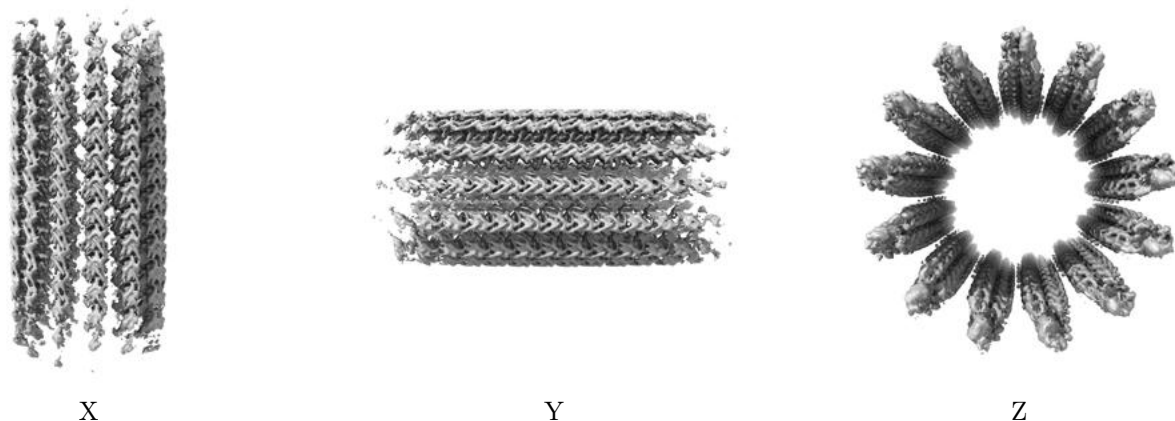
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

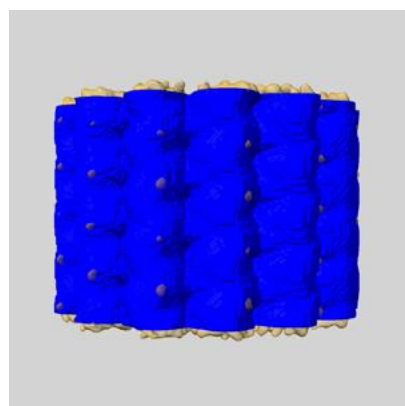
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

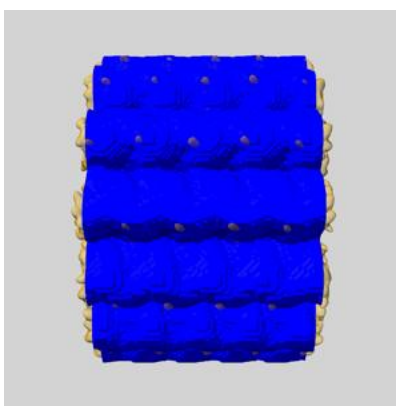
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

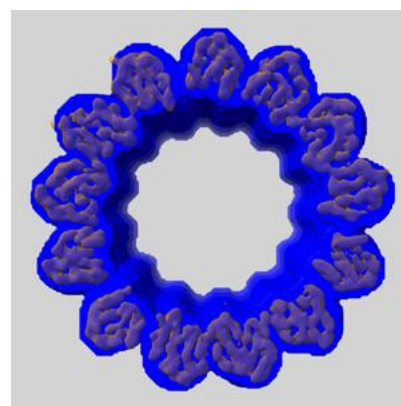
6.6.1 emd_16435_msk_1.map [i](#)



X



Y

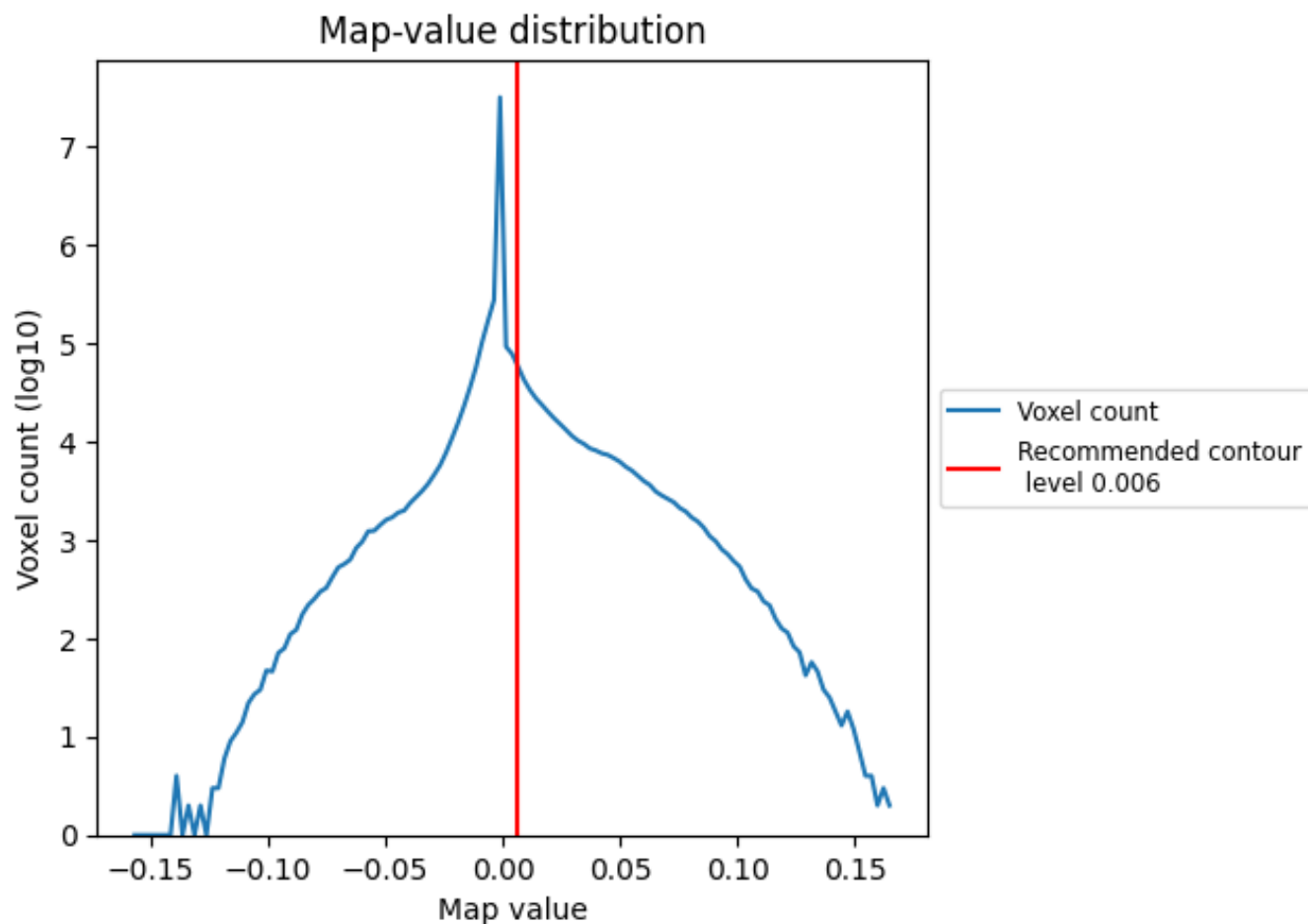


Z

7 Map analysis [i](#)

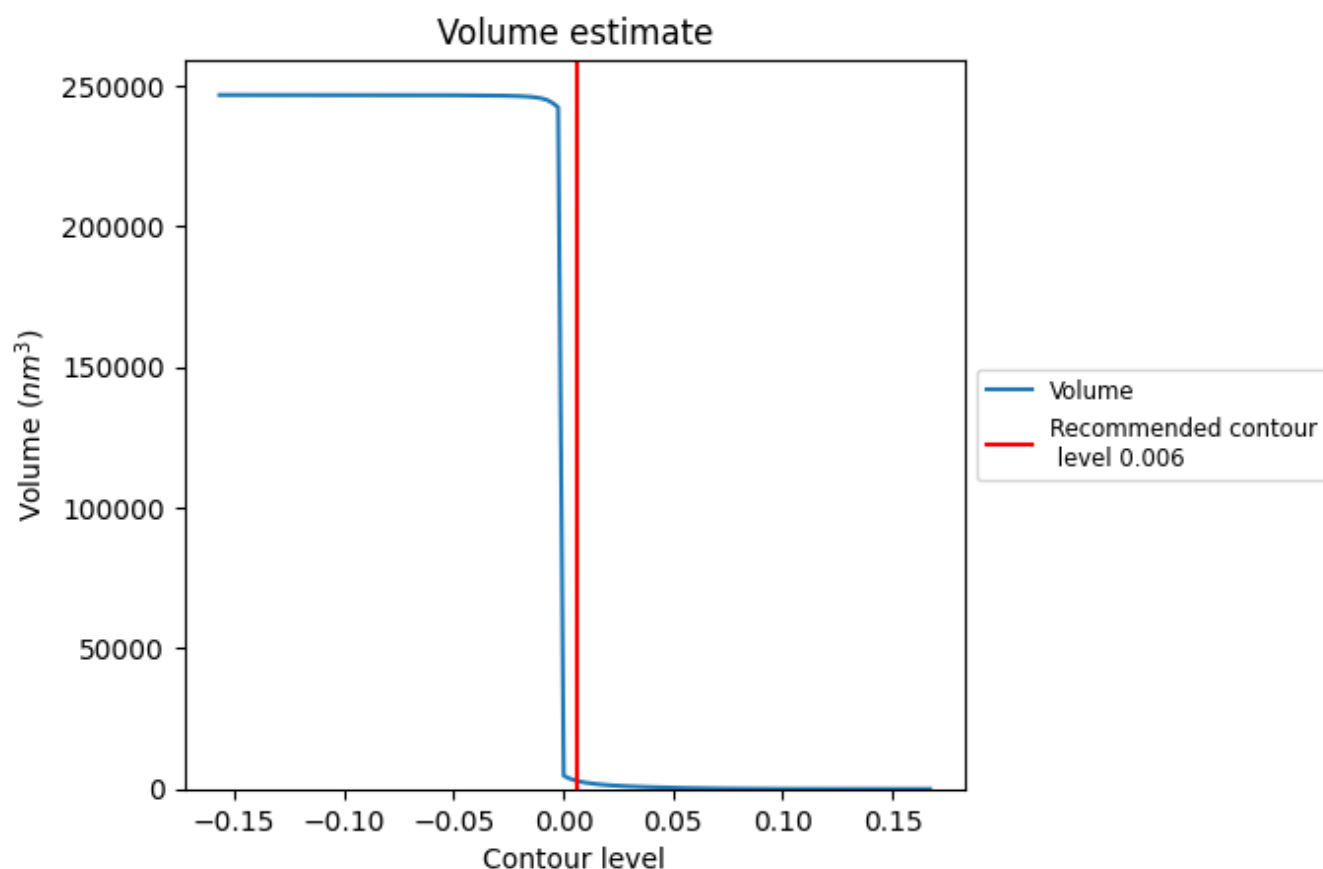
This section contains the results of statistical analysis of the map.

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.

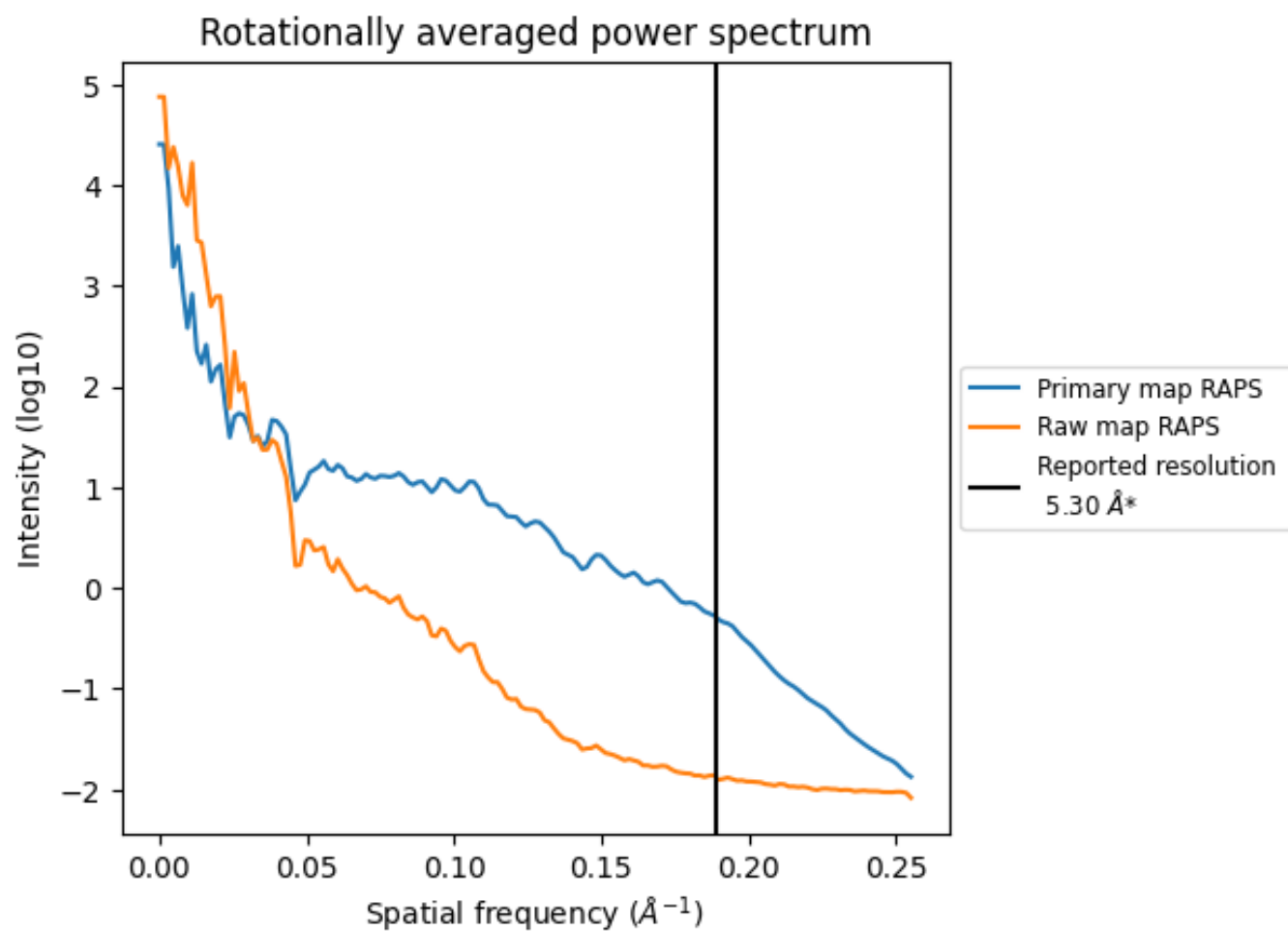
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2953 nm^3 ; this corresponds to an approximate mass of 2668 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 [i](#)

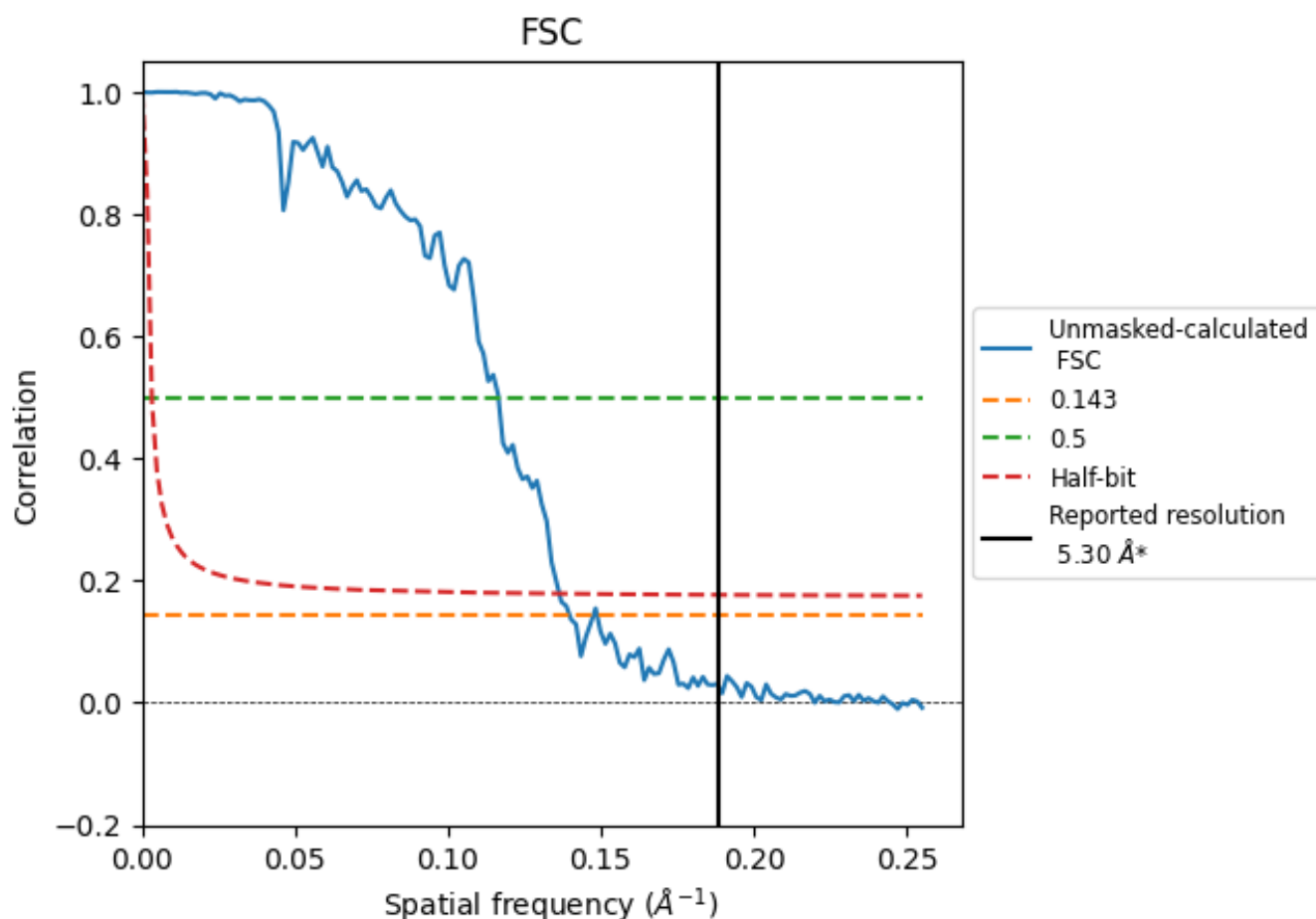


*Reported resolution corresponds to spatial frequency of 0.189 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.189 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

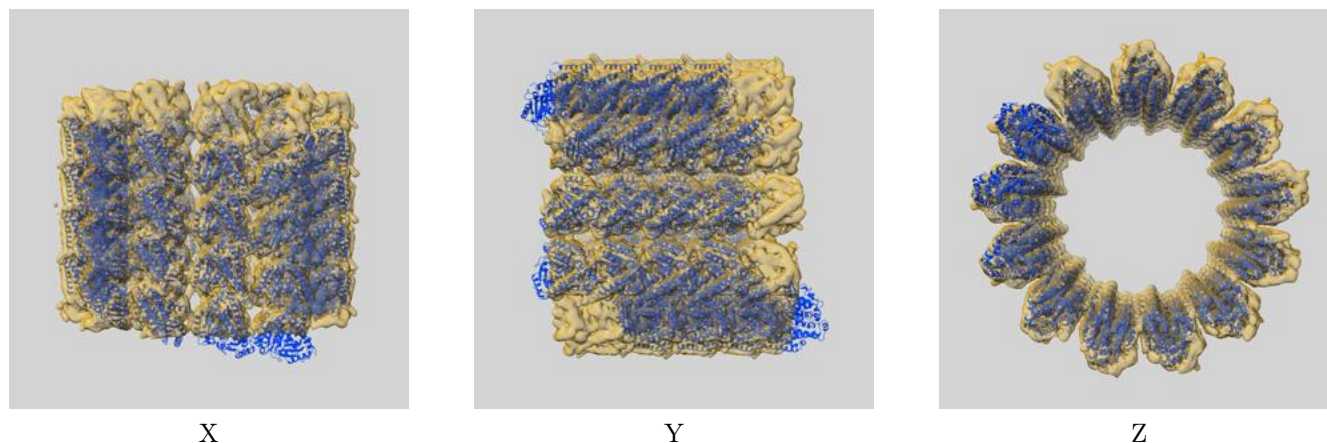
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.15	8.58	7.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.15 differs from the reported value 5.3 by more than 10 %

9 Map-model fit [i](#)

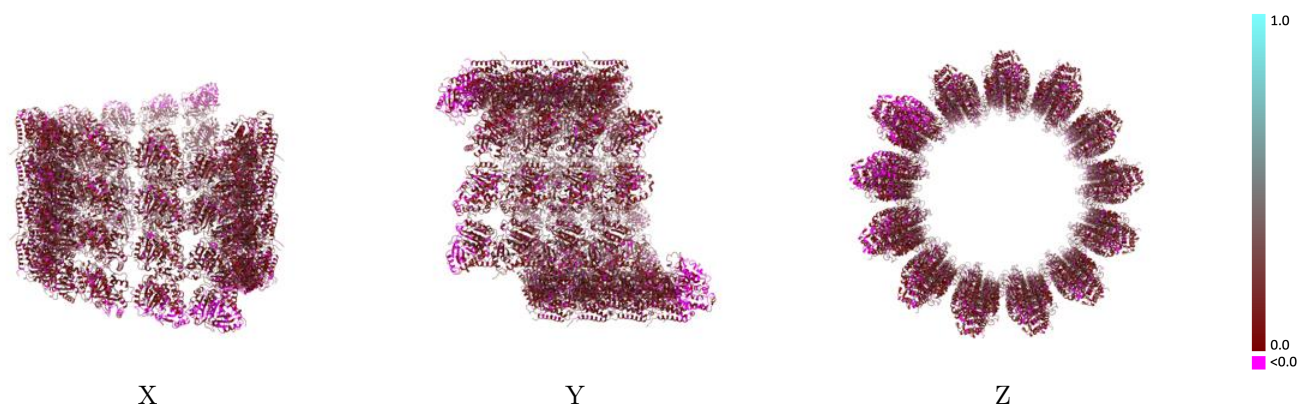
This section contains information regarding the fit between EMDB map EMD-16435 and PDB model 8C5C. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



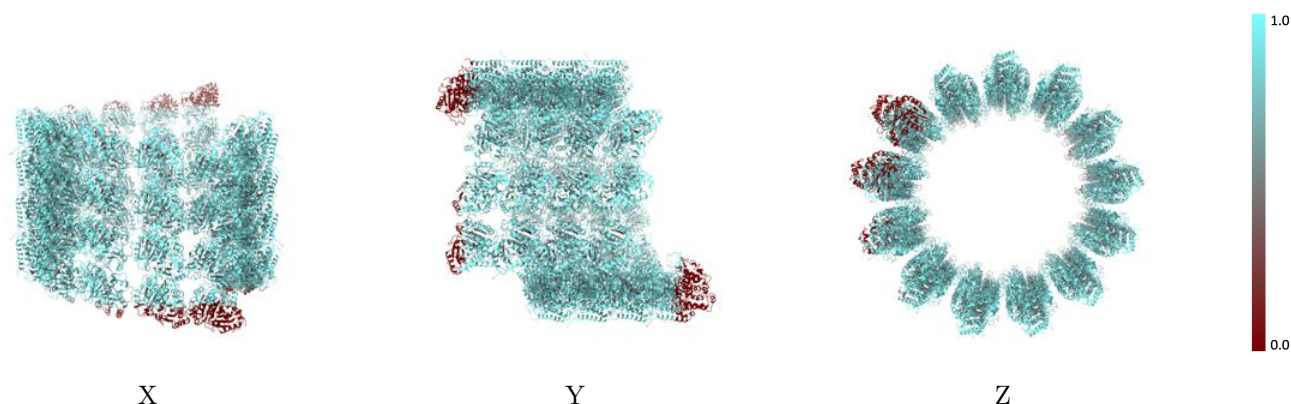
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



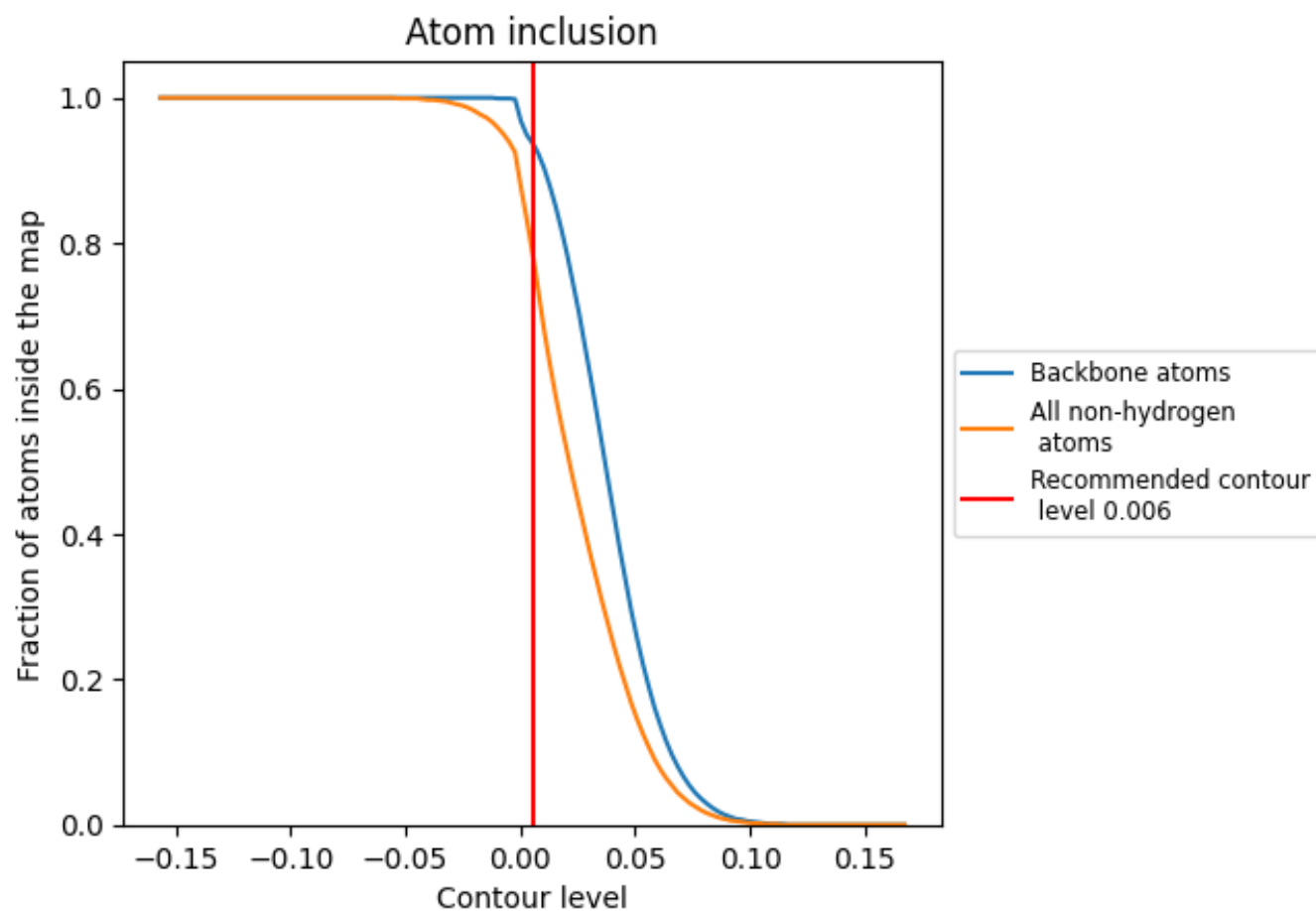
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7720	 0.1530
A	 0.5240	 0.0860
B	 0.3220	 0.0470
C	 0.8080	 0.1670
D	 0.8120	 0.1620
E	 0.8100	 0.1620
F	 0.8060	 0.1670
G	 0.8140	 0.1680
H	 0.8040	 0.1630
I	 0.8090	 0.1650
J	 0.8070	 0.1640
K	 0.8030	 0.1550
L	 0.7950	 0.1470
M	 0.7050	 0.1290
N	 0.8170	 0.1740
O	 0.8160	 0.1730
P	 0.8100	 0.1600
Q	 0.8140	 0.1630
R	 0.8090	 0.1650
S	 0.8120	 0.1610
T	 0.8120	 0.1650
U	 0.8150	 0.1680
V	 0.8110	 0.1690
W	 0.8130	 0.1680
X	 0.8150	 0.1710
Y	 0.8130	 0.1730
Z	 0.8240	 0.1750
a	 0.8180	 0.1650
b	 0.8080	 0.1580
c	 0.8120	 0.1690
d	 0.8080	 0.1700
e	 0.8030	 0.1680
f	 0.8150	 0.1720
g	 0.8170	 0.1720
h	 0.8130	 0.1750



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Chain	Atom inclusion	Q-score
i	 0.8090	 0.1700
j	 0.8140	 0.1740
k	 0.8150	 0.1740
l	 0.8110	 0.1700
m	 0.8200	 0.1750
n	 0.8130	 0.1670
o	 0.8020	 0.1670
p	 0.5880	 0.0790
q	 0.7550	 0.1220
r	 0.8070	 0.1470
s	 0.3060	 0.0360
t	 0.5120	 0.0650
u	 0.7100	 0.1120
v	 0.8010	 0.1460
w	 0.8170	 0.1540
x	 0.8090	 0.1590
y	 0.8090	 0.1630
z	 0.8010	 0.1680