



# Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 11:44 PM EST

PDB ID : 7M18  
EMDB ID : EMD-23615  
Title : HeLa-tubulin in complex with cryptophycin 1  
Authors : Eren, E.  
Deposited on : 2021-03-12  
Resolution : 3.38 Å (reported)  
Based on initial model : 6S8L

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

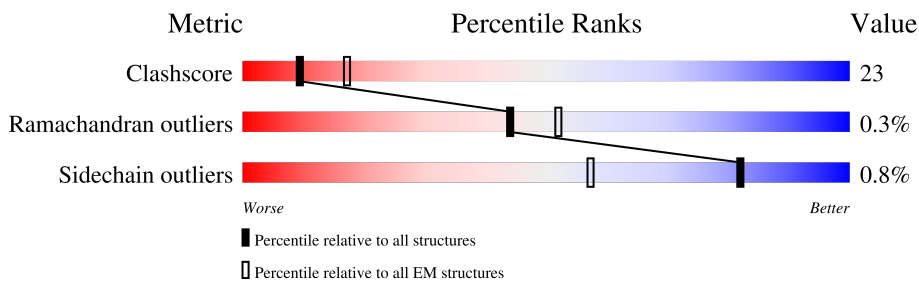
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.38 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	B	450	
1	D	450	
1	F	450	
1	H	450	
1	J	450	
1	L	450	
1	N	450	
1	P	450	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	A	451	 56% 41%
2	C	451	 56% 41%
2	E	451	 56% 41%
2	G	451	 56% 40%
2	I	451	 56% 41%
2	K	451	 56% 41%
2	M	451	 56% 41%
2	O	451	 56% 41%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 54064 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-3 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	D	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	F	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	H	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	J	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	L	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	N	427	Total 3312	C 2084	N 568	O 635	S 25	1	0
1	P	427	Total 3312	C 2084	N 568	O 635	S 25	1	0

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

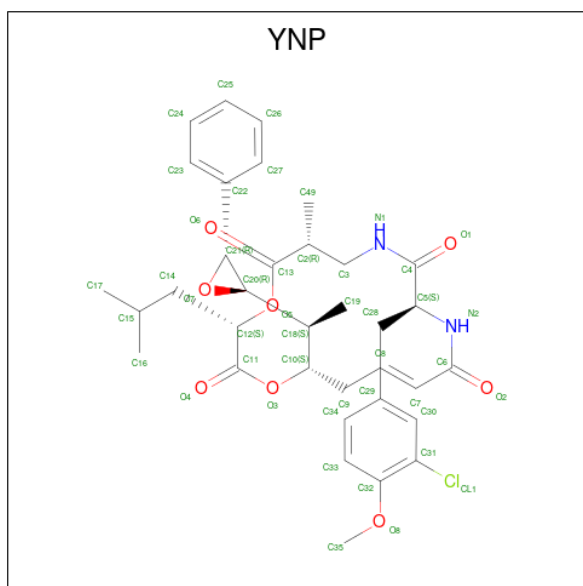
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	436	Total 3340	C 2117	N 570	O 633	S 20	0	0
2	C	436	Total 3340	C 2117	N 570	O 633	S 20	0	0
2	E	436	Total 3340	C 2117	N 570	O 633	S 20	0	0
2	G	436	Total 3340	C 2117	N 570	O 633	S 20	0	0
2	I	436	Total 3340	C 2117	N 570	O 633	S 20	0	0
2	K	436	Total 3340	C 2117	N 570	O 633	S 20	0	0
2	M	436	Total 3340	C 2117	N 570	O 633	S 20	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	O	436	3340	2117	570	633	20	0	0

- Molecule 3 is Cryptophycin 1 (three-letter code: YNP) (formula:  $C_{35}H_{43}ClN_2O_8$ ).



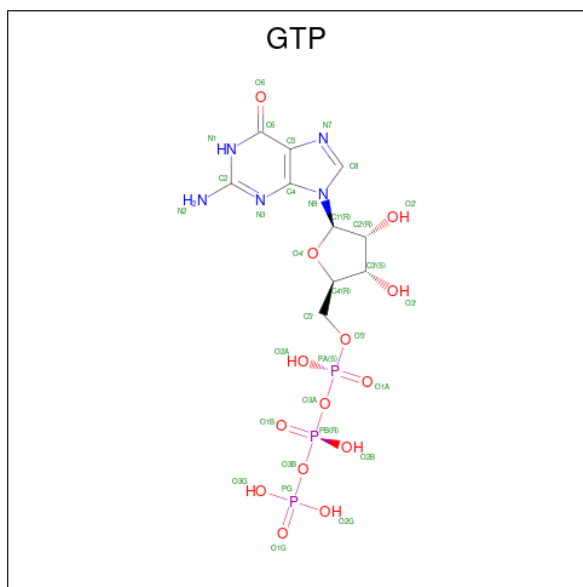
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Cl	N	O	
3	B	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	D	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	F	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	H	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	J	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	L	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	N	1	Total 46	C 35	Cl 1	N 2	O 8	0
3	P	1	Total 46	C 35	Cl 1	N 2	O 8	0

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	B	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	F	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	J	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	N	1	Total	C	N	O	P	0
			28	10	5	11	2	
4	P	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).

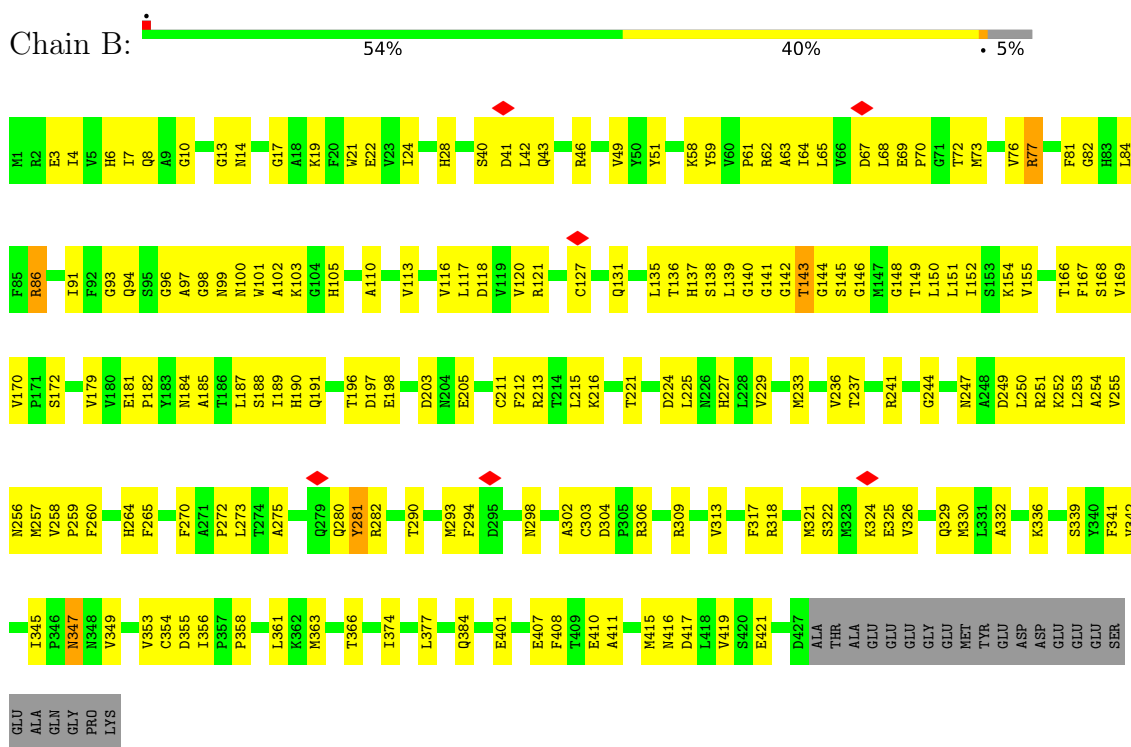


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
5	A	1	Total 32	C 10	N 5	O 14	P 3	0
5	C	1	Total 32	C 10	N 5	O 14	P 3	0
5	E	1	Total 32	C 10	N 5	O 14	P 3	0
5	G	1	Total 32	C 10	N 5	O 14	P 3	0
5	I	1	Total 32	C 10	N 5	O 14	P 3	0
5	K	1	Total 32	C 10	N 5	O 14	P 3	0
5	M	1	Total 32	C 10	N 5	O 14	P 3	0
5	O	1	Total 32	C 10	N 5	O 14	P 3	0

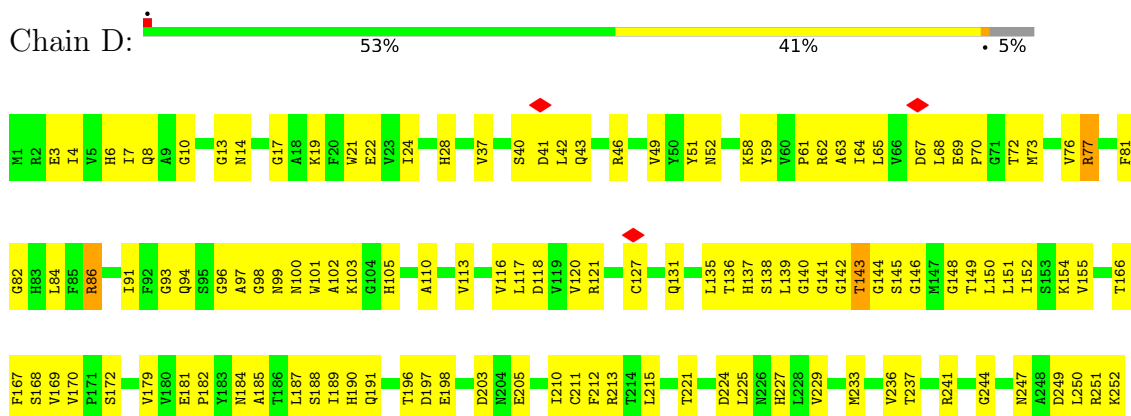
### 3 Residue-property plots

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

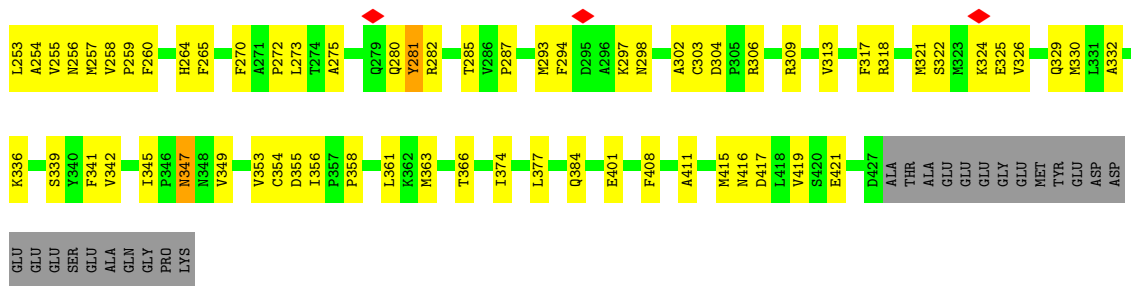
#### • Molecule 1: Tubulin beta-3 chain



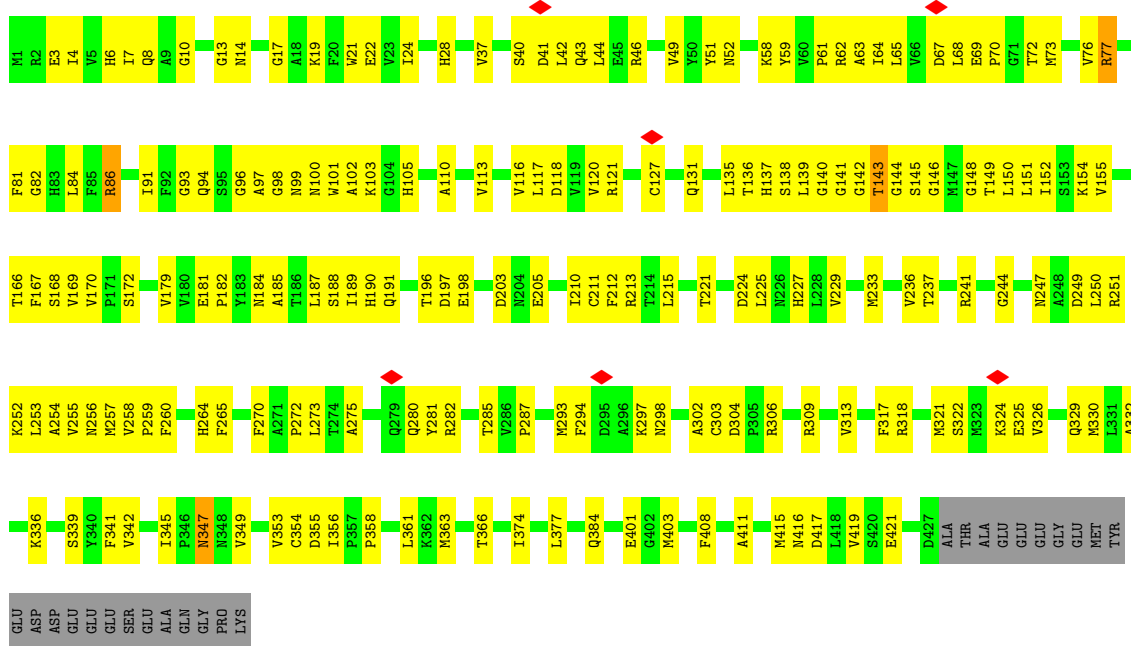
#### • Molecule 1: Tubulin beta-3 chain



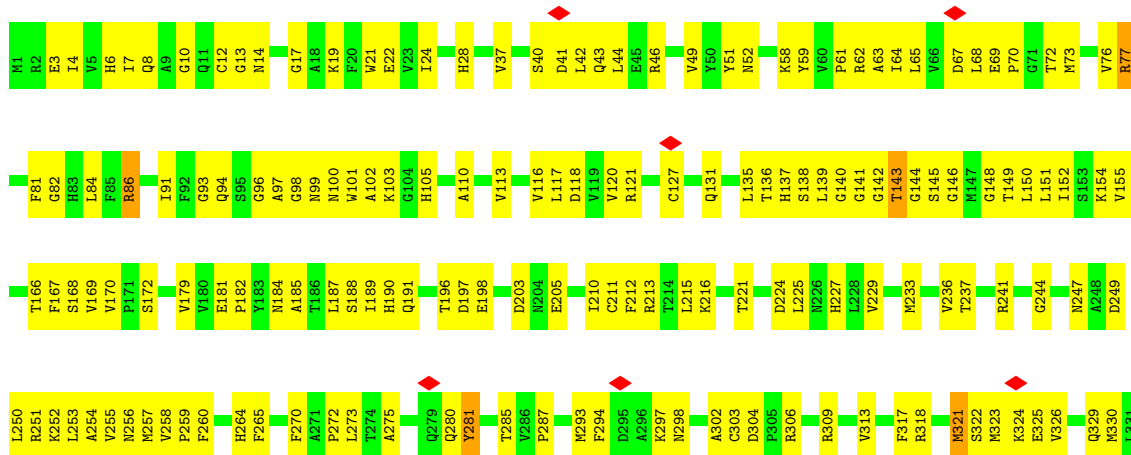


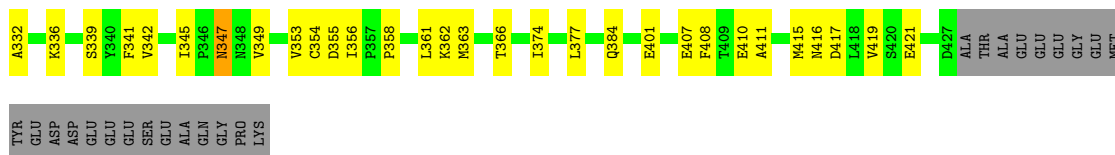


• Molecule 1: Tubulin beta-3 chain

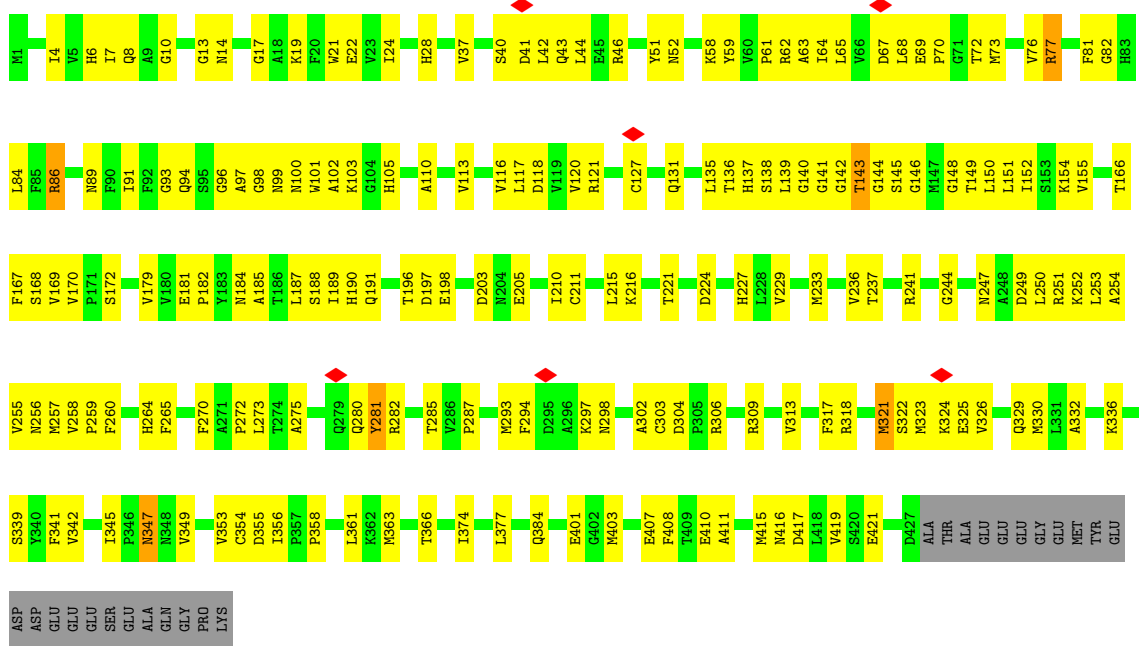


• Molecule 1: Tubulin beta-3 chain

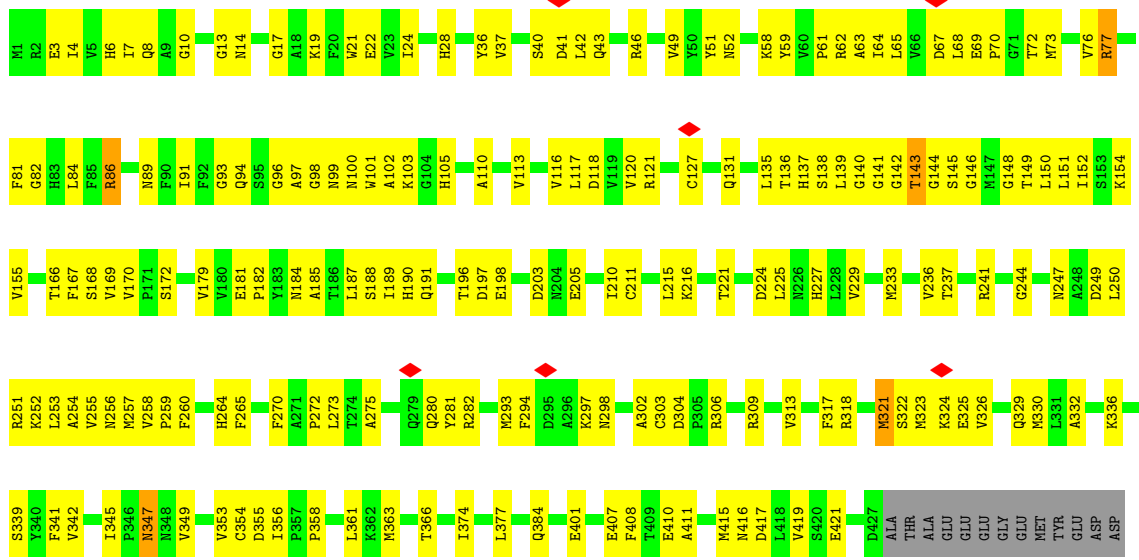




• Molecule 1: Tubulin beta-3 chain



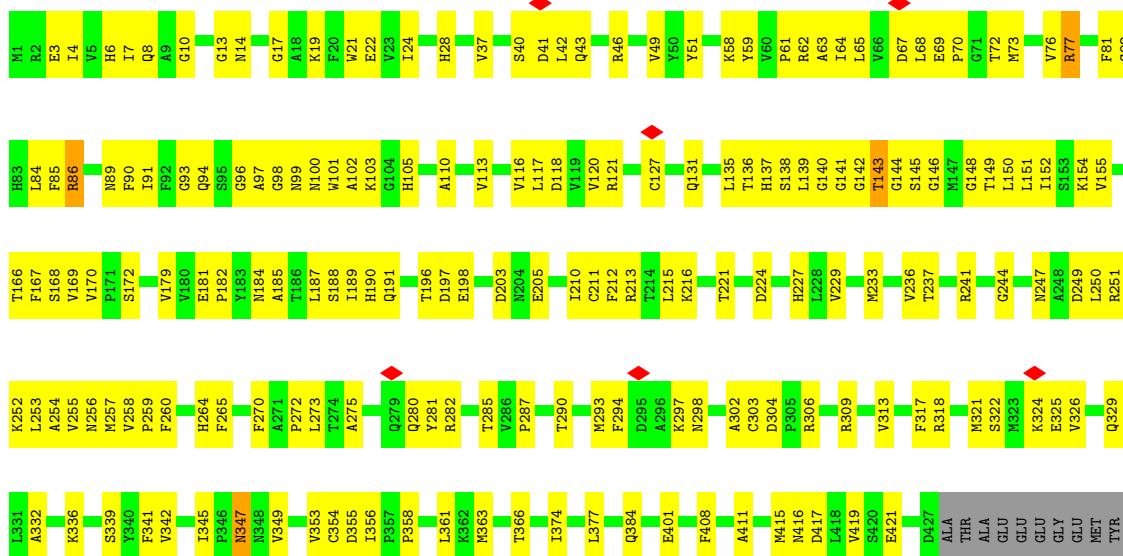
• Molecule 1: Tubulin beta-3 chain



GLU  
GLU  
GLU  
SER  
SER  
GLU  
ALA  
GLN  
GLY  
PRO  
LYS

- Molecule 1: Tubulin beta-3 chain

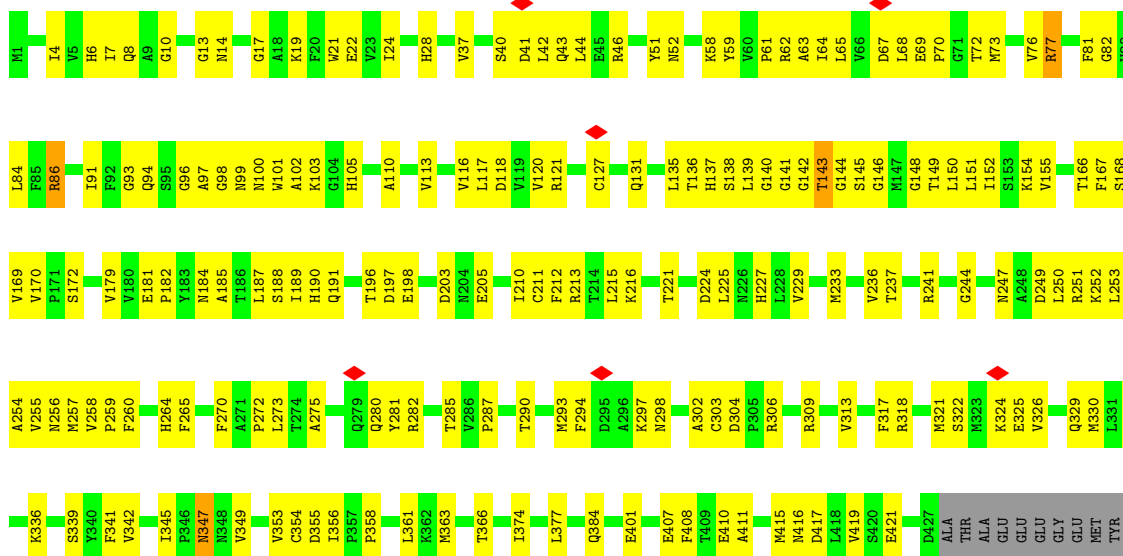
Chain N: 



GLU  
ASP  
ASP  
GLU  
GLU  
GLU  
SER  
GLU  
ALA  
GLN  
PRO  
LYS

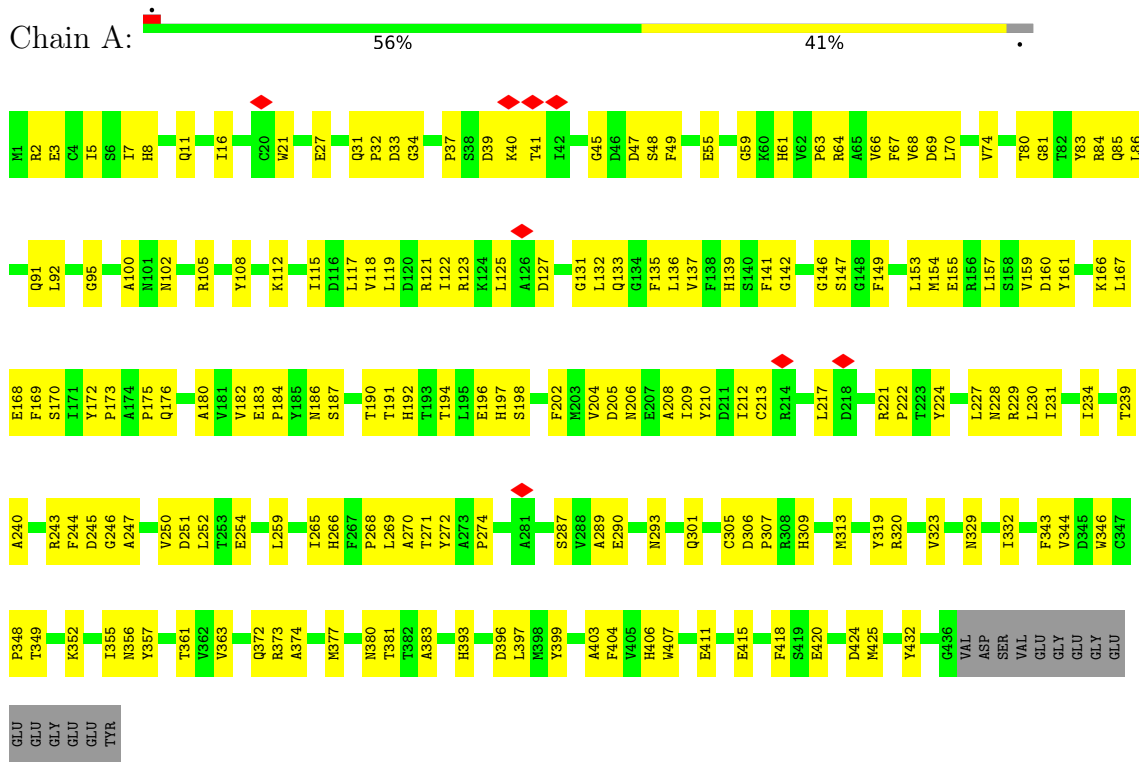
- Molecule 1: Tubulin beta-3 chain

Chain P: 

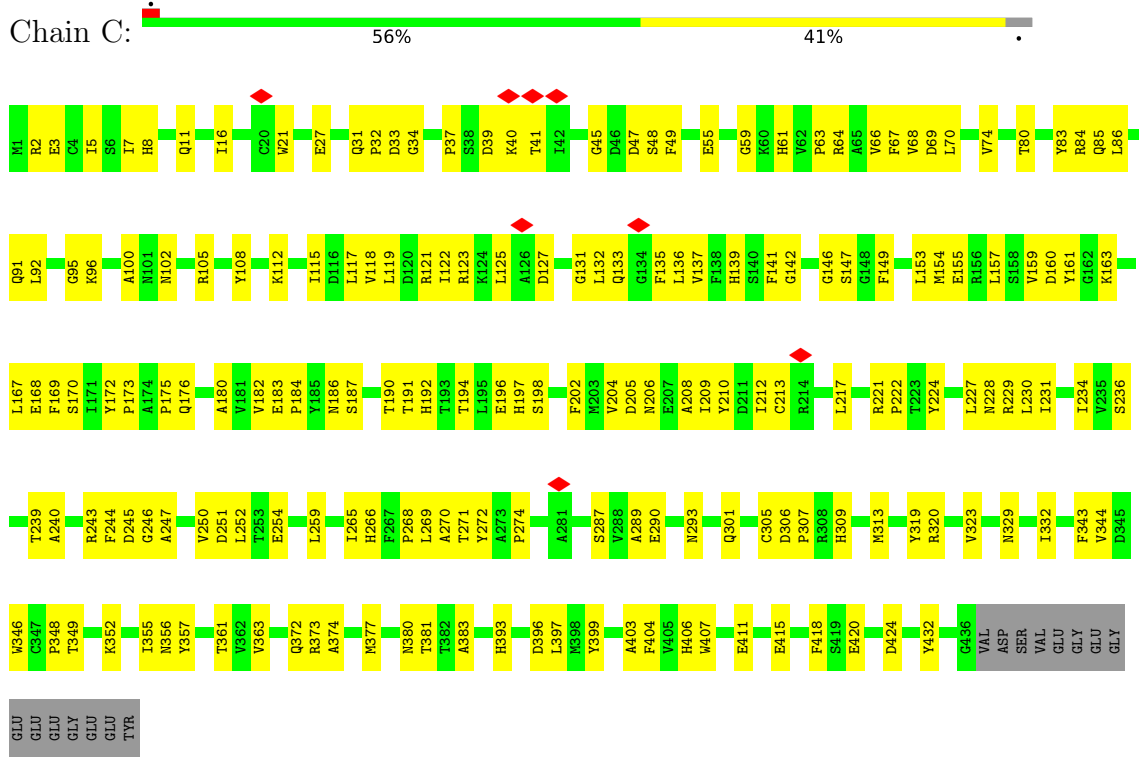


GLU  
ASP  
ASP  
GLU  
GLU  
GLU  
SER  
GLU  
ALA  
GLN  
PRO  
LYS

- Molecule 2: Tubulin alpha-1B chain

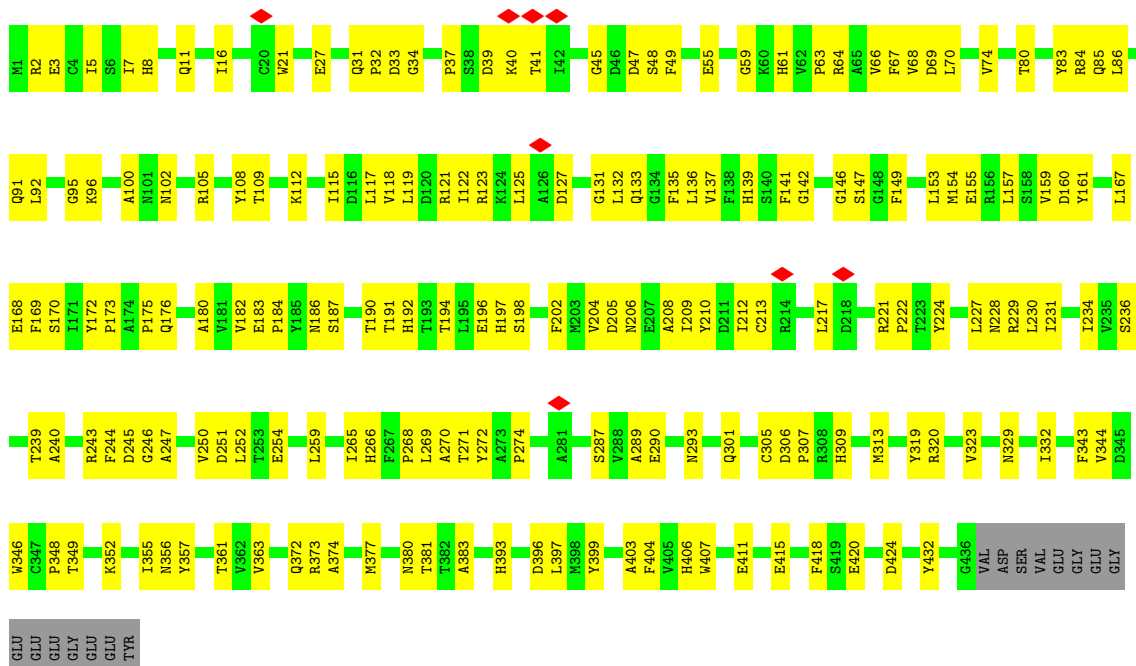


• Molecule 2: Tubulin alpha-1B chain

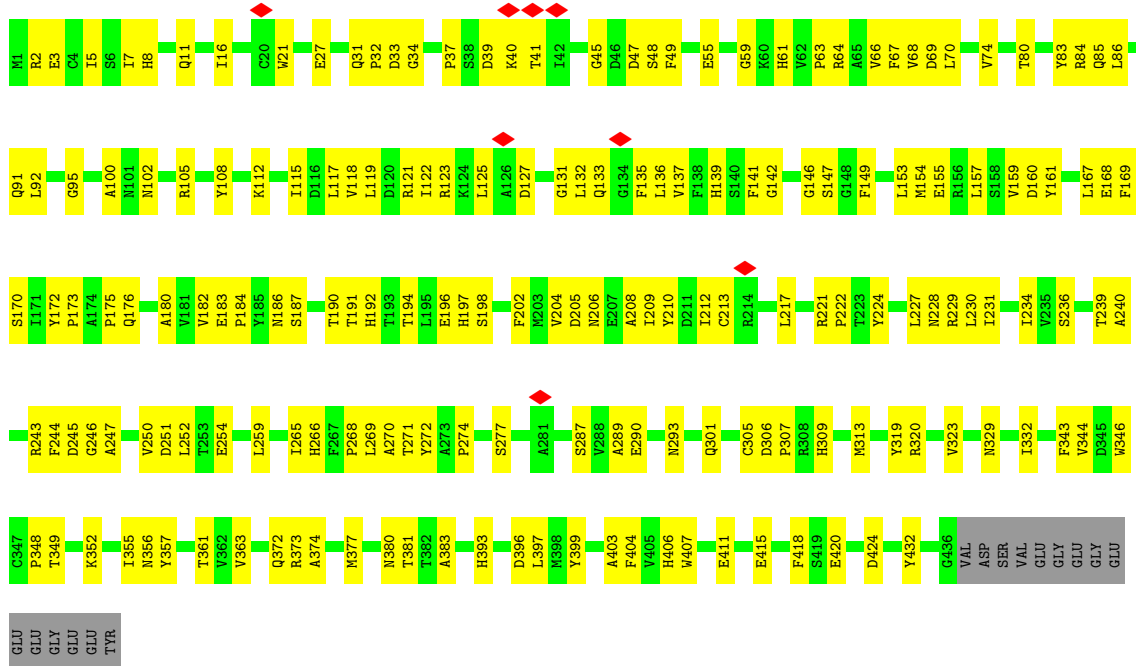


• Molecule 2: Tubulin alpha-1B chain



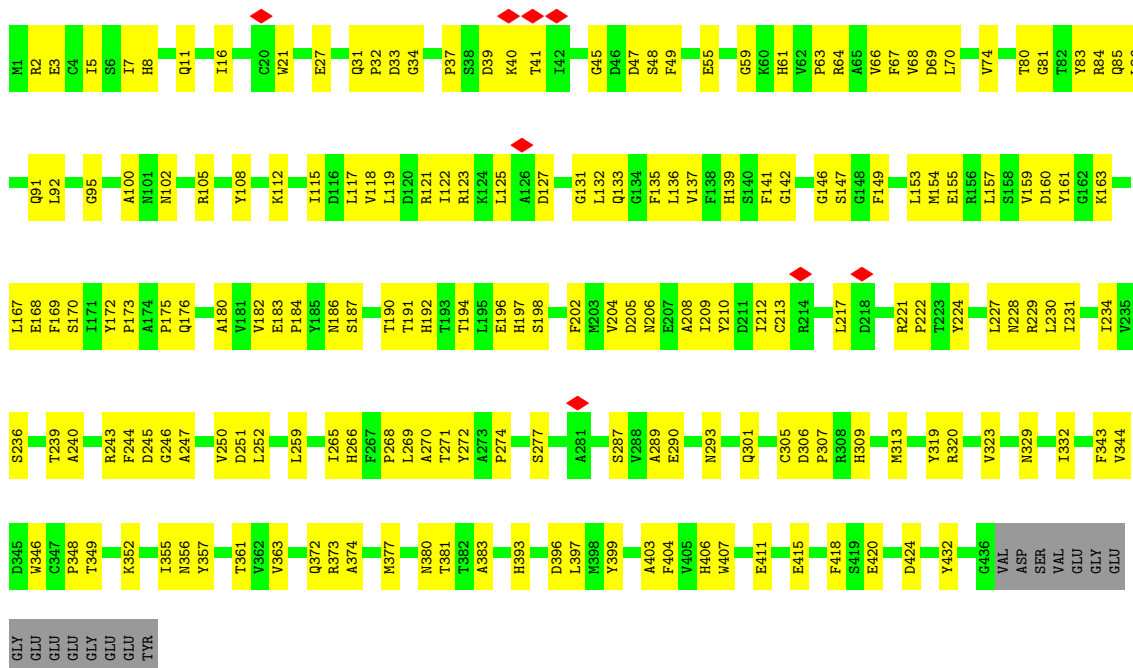


• Molecule 2: Tubulin alpha-1B chain

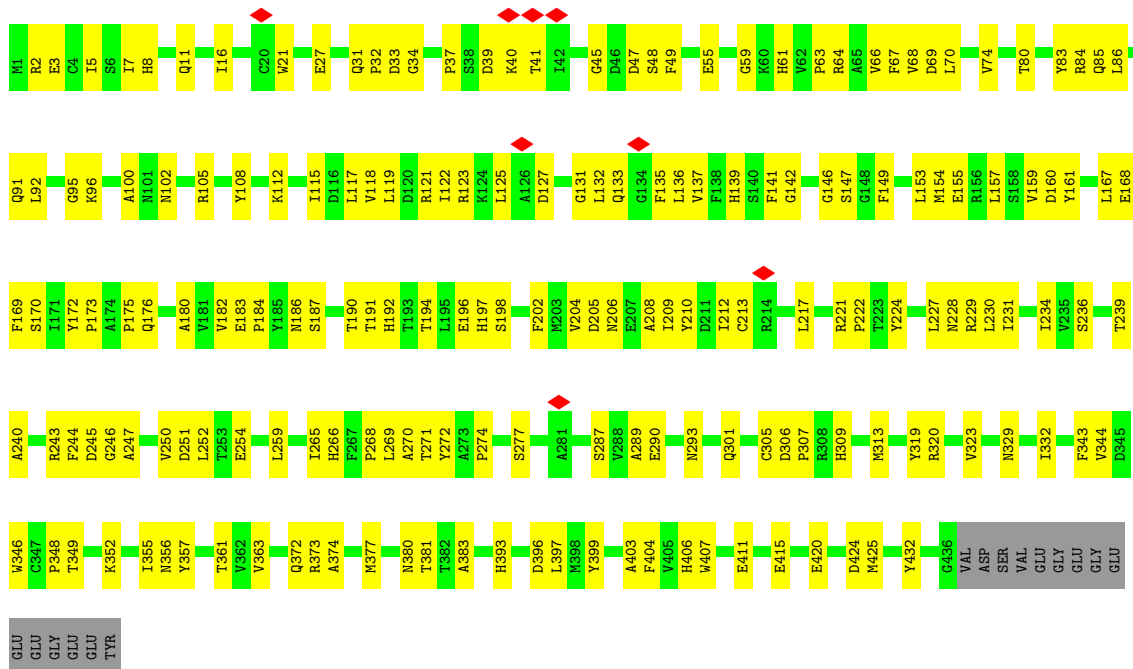


• Molecule 2: Tubulin alpha-1B chain



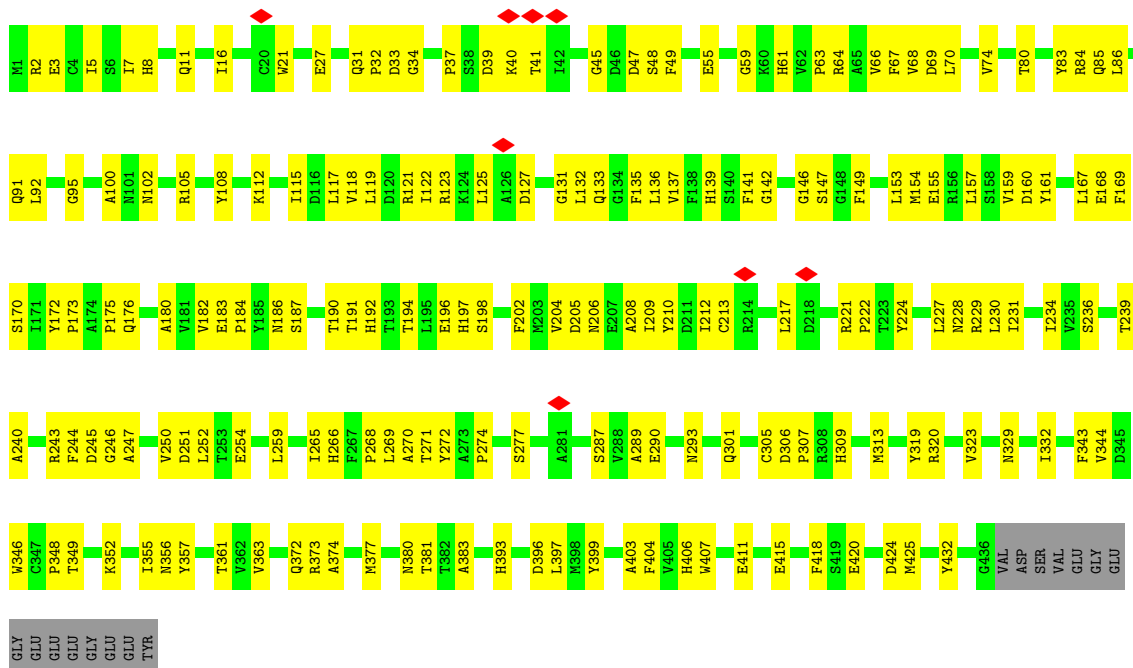


• Molecule 2: Tubulin alpha-1B chain

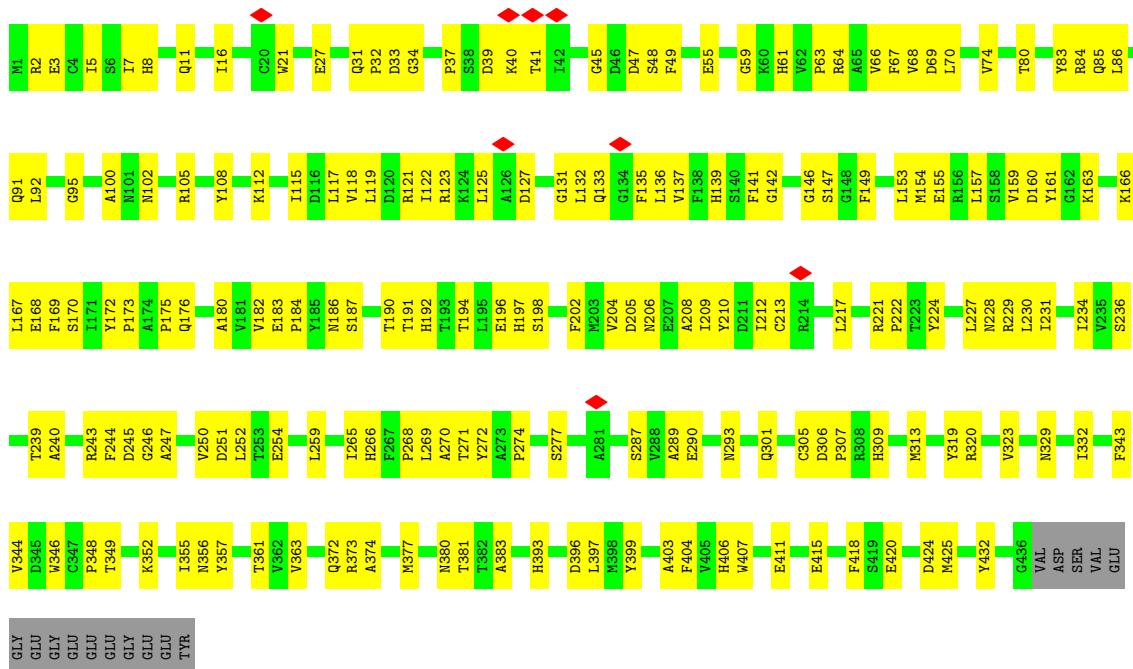


• Molecule 2: Tubulin alpha-1B chain





• Molecule 2: Tubulin alpha-1B chain



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of particles used	18899	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	66	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	35.696	Depositor
Minimum map value	-15.714	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.484	Depositor
Recommended contour level	4.5	Depositor
Map size ( $\text{\AA}$ )	635.99994, 635.99994, 635.99994	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.06, 1.06, 1.06	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: YNP, GTP, 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	B	0.29	0/3389	0.52	0/4596
1	D	0.29	0/3389	0.52	0/4596
1	F	0.29	0/3389	0.52	0/4596
1	H	0.29	0/3389	0.52	0/4596
1	J	0.29	0/3389	0.52	0/4596
1	L	0.29	0/3389	0.52	0/4596
1	N	0.29	0/3389	0.52	0/4596
1	P	0.29	0/3389	0.52	0/4596
2	A	0.28	0/3417	0.50	0/4650
2	C	0.28	0/3417	0.50	0/4650
2	E	0.28	0/3417	0.50	0/4650
2	G	0.28	0/3417	0.50	0/4650
2	I	0.28	0/3417	0.50	0/4650
2	K	0.28	0/3417	0.50	0/4650
2	M	0.28	0/3417	0.50	0/4650
2	O	0.28	0/3417	0.50	0/4650
All	All	0.28	0/54448	0.51	0/73968

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3312	0	3174	167	0
1	D	3312	0	3174	171	0
1	F	3312	0	3174	171	0
1	H	3312	0	3174	175	0
1	J	3312	0	3174	172	0
1	L	3312	0	3174	170	0
1	N	3312	0	3174	170	0
1	P	3312	0	3174	168	0
2	A	3340	0	3212	144	0
2	C	3340	0	3212	143	0
2	E	3340	0	3212	144	0
2	G	3340	0	3212	144	0
2	I	3340	0	3212	143	0
2	K	3340	0	3212	143	0
2	M	3340	0	3212	144	0
2	O	3340	0	3212	144	0
3	B	46	0	0	1	0
3	D	46	0	0	1	0
3	F	46	0	0	1	0
3	H	46	0	0	1	0
3	J	46	0	0	1	0
3	L	46	0	0	1	0
3	N	46	0	0	1	0
3	P	46	0	0	1	0
4	B	28	0	12	4	0
4	D	28	0	12	4	0
4	F	28	0	12	4	0
4	H	28	0	12	4	0
4	J	28	0	12	3	0
4	L	28	0	12	4	0
4	N	28	0	12	3	0
4	P	28	0	12	4	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
5	E	32	0	12	0	0
5	G	32	0	12	0	0
5	I	32	0	12	0	0
5	K	32	0	12	0	0
5	M	32	0	12	0	0
5	O	32	0	12	0	0
All	All	54064	0	51280	2373	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 23.

All (2373) 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)
1:B:259:PRO:O	2:O:406:HIS:CE1	1.73	1.42
2:A:406:HIS:CE1	1:D:259:PRO:O	1.73	1.42
2:E:406:HIS:CE1	1:H:259:PRO:O	1.73	1.41
2:C:406:HIS:CE1	1:F:259:PRO:O	1.73	1.40
2:G:406:HIS:CE1	1:J:259:PRO:O	1.73	1.40
2:I:406:HIS:CE1	1:L:259:PRO:O	1.73	1.39
2:M:406:HIS:CE1	1:P:259:PRO:O	1.73	1.39
2:K:406:HIS:CE1	1:N:259:PRO:O	1.73	1.38
2:K:406:HIS:HE1	1:N:259:PRO:O	0.97	1.30
2:G:406:HIS:HE1	1:J:259:PRO:O	0.97	1.28
1:B:259:PRO:O	2:O:406:HIS:HE1	0.97	1.26
2:I:406:HIS:HE1	1:L:259:PRO:O	0.97	1.25
2:E:406:HIS:HE1	1:H:259:PRO:O	0.97	1.25
2:A:406:HIS:HE1	1:D:259:PRO:O	0.97	1.25
2:M:406:HIS:HE1	1:P:259:PRO:O	0.97	1.25
2:C:406:HIS:HE1	1:F:259:PRO:O	0.97	1.22
1:P:103:LYS:HZ2	1:P:143:THR:CG2	1.55	1.19
1:L:103:LYS:HZ2	1:L:143:THR:CG2	1.59	1.16
1:F:103:LYS:HZ2	1:F:143:THR:CG2	1.68	1.07
2:E:407:TRP:HE1	1:H:258:VAL:HG13	1.21	1.05
2:G:407:TRP:HE1	1:J:258:VAL:HG13	1.21	1.05
2:C:407:TRP:HE1	1:F:258:VAL:HG13	1.21	1.05
2:A:407:TRP:HE1	1:D:258:VAL:HG13	1.21	1.04
2:I:407:TRP:HE1	1:L:258:VAL:HG13	1.21	1.04
1:B:103:LYS:HZ2	1:B:143:THR:CG2	1.70	1.04
1:B:103:LYS:HZ2	1:B:143:THR:HG22	1.23	1.03
1:H:103:LYS:HZ2	1:H:143:THR:CG2	1.71	1.03
1:F:103:LYS:HZ2	1:F:143:THR:HG22	1.22	1.02
1:N:103:LYS:HZ2	1:N:143:THR:HG22	1.24	1.02
1:B:258:VAL:HG13	2:O:407:TRP:HE1	1.21	1.02
1:D:103:LYS:HZ2	1:D:143:THR:CG2	1.73	1.02
1:J:103:LYS:HZ2	1:J:143:THR:CG2	1.71	1.02
2:K:407:TRP:HE1	1:N:258:VAL:HG13	1.21	1.02
1:N:103:LYS:HZ2	1:N:143:THR:CG2	1.71	1.02
1:L:103:LYS:HZ2	1:L:143:THR:HG22	1.19	1.02
1:J:103:LYS:HZ2	1:J:143:THR:HG22	1.24	1.01
1:D:103:LYS:HZ2	1:D:143:THR:HG22	1.25	1.00
2:M:407:TRP:HE1	1:P:258:VAL:HG13	1.21	0.99
1:P:103:LYS:HZ2	1:P:143:THR:HG22	1.18	0.99
1:H:103:LYS:HZ2	1:H:143:THR:HG22	1.24	0.99

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:103:LYS:NZ	1:D:143:THR:CG2	2.28	0.97
1:F:103:LYS:NZ	1:F:143:THR:CG2	2.28	0.97
1:H:103:LYS:NZ	1:H:143:THR:CG2	2.28	0.97
1:B:103:LYS:NZ	1:B:143:THR:CG2	2.28	0.97
1:J:103:LYS:NZ	1:J:143:THR:CG2	2.28	0.96
1:N:103:LYS:NZ	1:N:143:THR:CG2	2.28	0.96
1:B:347:ASN:OD1	2:O:175:PRO:HB3	1.66	0.96
1:P:103:LYS:NZ	1:P:143:THR:CG2	2.28	0.96
2:K:175:PRO:HB3	1:N:347:ASN:OD1	1.66	0.95
2:M:175:PRO:HB3	1:P:347:ASN:OD1	1.66	0.95
2:K:406:HIS:HE1	1:N:259:PRO:C	1.70	0.95
2:M:406:HIS:HE1	1:P:259:PRO:C	1.70	0.95
2:E:175:PRO:HB3	1:H:347:ASN:OD1	1.66	0.95
1:L:103:LYS:NZ	1:L:143:THR:CG2	2.28	0.95
2:G:175:PRO:HB3	1:J:347:ASN:OD1	1.66	0.95
2:I:175:PRO:HB3	1:L:347:ASN:OD1	1.66	0.95
2:I:406:HIS:HE1	1:L:259:PRO:C	1.70	0.95
2:G:406:HIS:HE1	1:J:259:PRO:C	1.70	0.95
1:B:259:PRO:C	2:O:406:HIS:HE1	1.70	0.95
2:E:406:HIS:HE1	1:H:259:PRO:C	1.70	0.95
2:A:175:PRO:HB3	1:D:347:ASN:OD1	1.66	0.94
2:C:406:HIS:HE1	1:F:259:PRO:C	1.70	0.94
2:A:406:HIS:HE1	1:D:259:PRO:C	1.70	0.94
2:C:175:PRO:HB3	1:F:347:ASN:OD1	1.66	0.94
3:P:501:YNP:CL1	3:P:501:YNP:C35	2.55	0.92
3:D:501:YNP:C35	3:D:501:YNP:CL1	2.55	0.92
3:N:501:YNP:CL1	3:N:501:YNP:C35	2.55	0.92
3:B:501:YNP:C35	3:B:501:YNP:CL1	2.55	0.92
3:H:501:YNP:CL1	3:H:501:YNP:C35	2.55	0.91
3:L:501:YNP:C35	3:L:501:YNP:CL1	2.55	0.91
3:J:501:YNP:C35	3:J:501:YNP:CL1	2.55	0.91
3:F:501:YNP:CL1	3:F:501:YNP:C35	2.55	0.90
1:B:97:ALA:HA	1:B:143:THR:HG23	1.57	0.86
1:J:97:ALA:HA	1:J:143:THR:HG23	1.57	0.86
1:P:97:ALA:HA	1:P:143:THR:HG23	1.57	0.85
1:H:97:ALA:HA	1:H:143:THR:HG23	1.57	0.85
1:H:97:ALA:HB1	1:H:142:GLY:O	1.77	0.85
1:B:97:ALA:HB1	1:B:142:GLY:O	1.77	0.85
1:J:97:ALA:HB1	1:J:142:GLY:O	1.77	0.85
1:F:97:ALA:HA	1:F:143:THR:HG23	1.57	0.85
1:N:97:ALA:HA	1:N:143:THR:HG23	1.57	0.85

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:97:ALA:HB1	1:P:142:GLY:O	1.77	0.85
1:L:97:ALA:HB1	1:L:142:GLY:O	1.77	0.85
1:D:97:ALA:HA	1:D:143:THR:HG23	1.57	0.84
1:F:97:ALA:HB1	1:F:142:GLY:O	1.77	0.84
1:L:97:ALA:HA	1:L:143:THR:HG23	1.57	0.84
1:N:97:ALA:HB1	1:N:142:GLY:O	1.77	0.83
1:D:97:ALA:HB1	1:D:142:GLY:O	1.77	0.83
1:N:98:GLY:O	1:N:142:GLY:HA2	1.80	0.82
1:P:98:GLY:O	1:P:142:GLY:HA2	1.80	0.82
1:J:98:GLY:O	1:J:142:GLY:HA2	1.80	0.82
1:D:98:GLY:O	1:D:142:GLY:HA2	1.80	0.81
1:L:98:GLY:O	1:L:142:GLY:HA2	1.80	0.81
1:F:98:GLY:O	1:F:142:GLY:HA2	1.80	0.81
1:B:98:GLY:O	1:B:142:GLY:HA2	1.80	0.80
1:J:181:GLU:HA	1:J:184:ASN:HD22	1.47	0.80
1:H:98:GLY:O	1:H:142:GLY:HA2	1.80	0.80
1:N:181:GLU:HA	1:N:184:ASN:HD22	1.47	0.79
1:P:181:GLU:HA	1:P:184:ASN:HD22	1.47	0.79
1:L:181:GLU:HA	1:L:184:ASN:HD22	1.47	0.79
1:P:113:VAL:HG11	1:P:150:LEU:HD21	1.65	0.79
1:J:113:VAL:HG11	1:J:150:LEU:HD21	1.65	0.79
2:C:407:TRP:NE1	1:F:258:VAL:HG13	1.98	0.79
2:G:372:GLN:HG2	2:G:373:ARG:HD2	1.65	0.79
2:C:372:GLN:HG2	2:C:373:ARG:HD2	1.65	0.78
1:L:113:VAL:HG11	1:L:150:LEU:HD21	1.65	0.78
1:F:181:GLU:HA	1:F:184:ASN:HD22	1.47	0.78
2:E:372:GLN:HG2	2:E:373:ARG:HD2	1.65	0.78
2:I:372:GLN:HG2	2:I:373:ARG:HD2	1.65	0.78
2:K:372:GLN:HG2	2:K:373:ARG:HD2	1.65	0.78
1:N:113:VAL:HG11	1:N:150:LEU:HD21	1.65	0.78
1:D:181:GLU:HA	1:D:184:ASN:HD22	1.47	0.78
1:H:113:VAL:HG11	1:H:150:LEU:HD21	1.65	0.78
1:D:113:VAL:HG11	1:D:150:LEU:HD21	1.65	0.78
1:H:181:GLU:HA	1:H:184:ASN:HD22	1.47	0.78
1:B:181:GLU:HA	1:B:184:ASN:HD22	1.47	0.78
2:A:372:GLN:HG2	2:A:373:ARG:HD2	1.65	0.78
1:F:113:VAL:HG11	1:F:150:LEU:HD21	1.65	0.78
2:M:372:GLN:HG2	2:M:373:ARG:HD2	1.65	0.78
1:B:113:VAL:HG11	1:B:150:LEU:HD21	1.65	0.77
2:G:406:HIS:CE1	1:J:260:PHE:HA	2.20	0.77
2:O:372:GLN:HG2	2:O:373:ARG:HD2	1.65	0.77

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:PHE:HA	2:O:406:HIS:CE1	2.20	0.77
2:C:406:HIS:CE1	1:F:260:PHE:HA	2.20	0.77
1:B:258:VAL:HG13	2:O:407:TRP:NE1	1.98	0.77
2:E:407:TRP:NE1	1:H:258:VAL:HG13	1.98	0.77
2:M:407:TRP:NE1	1:P:258:VAL:HG13	1.98	0.77
2:M:406:HIS:CE1	1:P:260:PHE:HA	2.20	0.77
2:E:406:HIS:CE1	1:H:260:PHE:HA	2.20	0.76
2:I:407:TRP:NE1	1:L:258:VAL:HG13	1.98	0.76
2:A:381:THR:HG22	2:A:383:ALA:H	1.50	0.76
2:A:406:HIS:CE1	1:D:260:PHE:HA	2.20	0.76
2:I:406:HIS:CE1	1:L:260:PHE:HA	2.20	0.76
2:K:406:HIS:CE1	1:N:260:PHE:HA	2.20	0.76
2:A:407:TRP:NE1	1:D:258:VAL:HG13	1.98	0.76
2:C:381:THR:HG22	2:C:383:ALA:H	1.50	0.76
2:E:381:THR:HG22	2:E:383:ALA:H	1.50	0.75
2:K:407:TRP:NE1	1:N:258:VAL:HG13	1.98	0.75
2:G:381:THR:HG22	2:G:383:ALA:H	1.50	0.74
2:I:381:THR:HG22	2:I:383:ALA:H	1.50	0.74
2:O:381:THR:HG22	2:O:383:ALA:H	1.50	0.74
2:G:407:TRP:NE1	1:J:258:VAL:HG13	1.98	0.74
1:J:97:ALA:HA	1:J:143:THR:CG2	2.18	0.74
1:H:97:ALA:HA	1:H:143:THR:CG2	2.18	0.74
2:K:381:THR:HG22	2:K:383:ALA:H	1.50	0.73
1:F:97:ALA:HA	1:F:143:THR:CG2	2.18	0.73
1:J:236:VAL:HA	1:J:366:THR:HG21	1.70	0.73
1:D:97:ALA:HA	1:D:143:THR:CG2	2.18	0.73
2:M:381:THR:HG22	2:M:383:ALA:H	1.50	0.73
1:L:236:VAL:HA	1:L:366:THR:HG21	1.70	0.73
1:D:179:VAL:HG21	2:C:348:PRO:HD2	1.71	0.73
1:P:97:ALA:HA	1:P:143:THR:CG2	2.18	0.73
1:L:97:ALA:HA	1:L:143:THR:CG2	2.18	0.73
1:H:236:VAL:HA	1:H:366:THR:HG21	1.70	0.73
1:N:97:ALA:HA	1:N:143:THR:CG2	2.18	0.73
1:N:236:VAL:HA	1:N:366:THR:HG21	1.70	0.73
2:O:154:MET:HE3	2:O:194:THR:HA	1.71	0.73
1:B:97:ALA:HA	1:B:143:THR:CG2	2.18	0.72
1:P:179:VAL:HG21	2:O:348:PRO:HD2	1.71	0.72
1:F:179:VAL:HG21	2:E:348:PRO:HD2	1.71	0.72
2:I:154:MET:HE3	2:I:194:THR:HA	1.71	0.72
1:B:179:VAL:HG21	2:A:348:PRO:HD2	1.71	0.72
1:D:236:VAL:HA	1:D:366:THR:HG21	1.70	0.72

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:154:MET:HE3	2:G:194:THR:HA	1.71	0.72
2:A:224:TYR:O	2:A:228:ASN:HB2	1.90	0.72
2:E:224:TYR:O	2:E:228:ASN:HB2	1.90	0.72
1:P:10:GLY:O	1:P:14:ASN:ND2	2.22	0.72
2:O:224:TYR:O	2:O:228:ASN:HB2	1.90	0.72
2:C:224:TYR:O	2:C:228:ASN:HB2	1.90	0.72
2:E:154:MET:HE3	2:E:194:THR:HA	1.71	0.72
1:H:179:VAL:HG21	2:G:348:PRO:HD2	1.71	0.72
2:G:224:TYR:O	2:G:228:ASN:HB2	1.90	0.72
1:B:236:VAL:HA	1:B:366:THR:HG21	1.70	0.72
1:N:179:VAL:HG21	2:M:348:PRO:HD2	1.71	0.71
1:P:236:VAL:HA	1:P:366:THR:HG21	1.70	0.71
1:F:236:VAL:HA	1:F:366:THR:HG21	1.70	0.71
2:M:224:TYR:O	2:M:228:ASN:HB2	1.90	0.71
2:K:154:MET:HE3	2:K:194:THR:HA	1.71	0.71
2:M:154:MET:HE3	2:M:194:THR:HA	1.71	0.71
2:A:154:MET:HE3	2:A:194:THR:HA	1.71	0.71
1:J:179:VAL:HG21	2:I:348:PRO:HD2	1.71	0.71
2:I:224:TYR:O	2:I:228:ASN:HB2	1.90	0.71
1:L:179:VAL:HG21	2:K:348:PRO:HD2	1.71	0.71
1:D:138:SER:HA	1:D:169:VAL:H	1.56	0.71
1:B:10:GLY:O	1:B:14:ASN:ND2	2.22	0.70
2:C:154:MET:HE3	2:C:194:THR:HA	1.71	0.70
1:F:138:SER:HA	1:F:169:VAL:H	1.56	0.70
1:P:138:SER:HA	1:P:169:VAL:H	1.56	0.70
1:L:10:GLY:O	1:L:14:ASN:ND2	2.22	0.70
1:B:138:SER:HA	1:B:169:VAL:H	1.56	0.70
2:K:224:TYR:O	2:K:228:ASN:HB2	1.90	0.70
2:G:259:LEU:O	2:G:380:ASN:ND2	2.25	0.70
2:E:259:LEU:O	2:E:380:ASN:ND2	2.25	0.70
1:L:63:ALA:O	1:L:86:ARG:NH1	2.25	0.70
1:N:138:SER:HA	1:N:169:VAL:H	1.56	0.70
1:B:63:ALA:O	1:B:86:ARG:NH1	2.25	0.70
1:F:63:ALA:O	1:F:86:ARG:NH1	2.25	0.70
2:I:259:LEU:O	2:I:380:ASN:ND2	2.25	0.70
1:P:150:LEU:HG	1:P:154:LYS:NZ	2.07	0.70
1:H:150:LEU:HG	1:H:154:LYS:NZ	2.07	0.69
2:O:259:LEU:O	2:O:380:ASN:ND2	2.25	0.69
1:J:63:ALA:O	1:J:86:ARG:NH1	2.25	0.69
1:L:138:SER:HA	1:L:169:VAL:H	1.56	0.69
1:J:138:SER:HA	1:J:169:VAL:H	1.56	0.69

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:259:LEU:O	2:K:380:ASN:ND2	2.25	0.69
1:N:150:LEU:HG	1:N:154:LYS:NZ	2.07	0.69
2:M:259:LEU:O	2:M:380:ASN:ND2	2.25	0.69
2:C:259:LEU:O	2:C:380:ASN:ND2	2.25	0.69
1:F:150:LEU:HG	1:F:154:LYS:NZ	2.07	0.69
1:D:10:GLY:O	1:D:14:ASN:ND2	2.22	0.69
1:H:138:SER:HA	1:H:169:VAL:H	1.56	0.69
1:J:150:LEU:HG	1:J:154:LYS:NZ	2.07	0.69
1:D:150:LEU:HG	1:D:154:LYS:NZ	2.07	0.69
2:A:259:LEU:O	2:A:380:ASN:ND2	2.25	0.69
1:L:150:LEU:HG	1:L:154:LYS:NZ	2.07	0.69
1:D:63:ALA:O	1:D:86:ARG:NH1	2.25	0.69
2:E:182:VAL:O	2:E:186:ASN:ND2	2.26	0.69
1:B:150:LEU:HG	1:B:154:LYS:NZ	2.07	0.68
1:D:189:ILE:HG12	1:D:415:MET:HE1	1.75	0.68
2:C:182:VAL:O	2:C:186:ASN:ND2	2.26	0.68
1:P:63:ALA:O	1:P:86:ARG:NH1	2.25	0.68
1:H:63:ALA:O	1:H:86:ARG:NH1	2.25	0.68
2:A:182:VAL:O	2:A:186:ASN:ND2	2.26	0.68
2:C:32:PRO:O	2:C:85:GLN:NE2	2.27	0.68
2:M:32:PRO:O	2:M:85:GLN:NE2	2.27	0.68
1:F:10:GLY:O	1:F:14:ASN:ND2	2.22	0.68
2:K:182:VAL:O	2:K:186:ASN:ND2	2.26	0.68
2:O:182:VAL:O	2:O:186:ASN:ND2	2.26	0.68
1:J:68:LEU:HA	1:J:93:GLY:HA3	1.76	0.68
2:K:32:PRO:O	2:K:85:GLN:NE2	2.27	0.68
1:B:68:LEU:HA	1:B:93:GLY:HA3	1.76	0.68
2:A:32:PRO:O	2:A:85:GLN:NE2	2.27	0.68
1:F:68:LEU:HA	1:F:93:GLY:HA3	1.76	0.68
2:G:182:VAL:O	2:G:186:ASN:ND2	2.26	0.68
1:N:63:ALA:O	1:N:86:ARG:NH1	2.25	0.68
1:N:68:LEU:HA	1:N:93:GLY:HA3	1.76	0.68
2:O:32:PRO:O	2:O:85:GLN:NE2	2.27	0.68
2:I:32:PRO:O	2:I:85:GLN:NE2	2.27	0.68
2:I:119:LEU:HD23	2:I:122:ILE:HD11	1.76	0.68
1:D:68:LEU:HA	1:D:93:GLY:HA3	1.76	0.67
2:G:119:LEU:HD23	2:G:122:ILE:HD11	1.76	0.67
1:P:8:GLN:HE22	1:P:17:GLY:HA3	1.59	0.67
2:K:119:LEU:HD23	2:K:122:ILE:HD11	1.76	0.67
2:G:32:PRO:O	2:G:85:GLN:NE2	2.27	0.67
1:L:8:GLN:HE22	1:L:17:GLY:HA3	1.59	0.67

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:68:LEU:HA	1:L:93:GLY:HA3	1.76	0.67
1:P:189:ILE:HG12	1:P:415:MET:HE1	1.77	0.67
1:B:189:ILE:HG12	1:B:415:MET:HE1	1.75	0.67
1:D:8:GLN:HE22	1:D:17:GLY:HA3	1.59	0.67
2:E:32:PRO:O	2:E:85:GLN:NE2	2.27	0.67
2:E:119:LEU:HD23	2:E:122:ILE:HD11	1.76	0.67
1:J:8:GLN:HE22	1:J:17:GLY:HA3	1.59	0.67
1:N:189:ILE:HG12	1:N:415:MET:HE1	1.76	0.67
2:M:182:VAL:O	2:M:186:ASN:ND2	2.26	0.67
2:I:182:VAL:O	2:I:186:ASN:ND2	2.26	0.67
1:N:28:HIS:O	1:N:43:GLN:NE2	2.28	0.67
2:M:119:LEU:HD23	2:M:122:ILE:HD11	1.76	0.67
1:B:101:TRP:HE1	1:B:146:GLY:HA2	1.60	0.67
1:H:10:GLY:O	1:H:14:ASN:ND2	2.22	0.67
1:N:8:GLN:HE22	1:N:17:GLY:HA3	1.59	0.67
1:D:101:TRP:HE1	1:D:146:GLY:HA2	1.60	0.66
1:N:10:GLY:O	1:N:14:ASN:ND2	2.22	0.66
1:P:101:TRP:HE1	1:P:146:GLY:HA2	1.60	0.66
2:O:119:LEU:HD23	2:O:122:ILE:HD11	1.76	0.66
1:B:8:GLN:HE22	1:B:17:GLY:HA3	1.59	0.66
1:D:28:HIS:O	1:D:43:GLN:NE2	2.28	0.66
1:F:8:GLN:HE22	1:F:17:GLY:HA3	1.59	0.66
1:H:68:LEU:HA	1:H:93:GLY:HA3	1.76	0.66
2:A:119:LEU:HD23	2:A:122:ILE:HD11	1.76	0.66
1:L:28:HIS:O	1:L:43:GLN:NE2	2.28	0.66
2:C:119:LEU:HD23	2:C:122:ILE:HD11	1.76	0.66
1:P:68:LEU:HA	1:P:93:GLY:HA3	1.76	0.66
1:F:28:HIS:O	1:F:43:GLN:NE2	2.28	0.66
1:N:101:TRP:HE1	1:N:146:GLY:HA2	1.60	0.66
1:B:28:HIS:O	1:B:43:GLN:NE2	2.28	0.66
1:J:28:HIS:O	1:J:43:GLN:NE2	2.28	0.66
1:L:101:TRP:HE1	1:L:146:GLY:HA2	1.60	0.66
1:F:101:TRP:HE1	1:F:146:GLY:HA2	1.60	0.66
2:M:407:TRP:HE1	1:P:258:VAL:CG1	2.05	0.66
1:H:28:HIS:O	1:H:43:GLN:NE2	2.28	0.66
1:H:8:GLN:HE22	1:H:17:GLY:HA3	1.59	0.66
2:K:64:ARG:HB2	2:K:125:LEU:HD11	1.78	0.66
1:P:28:HIS:O	1:P:43:GLN:NE2	2.28	0.66
2:K:123:ARG:NH1	2:K:127:ASP:OD2	2.29	0.65
2:O:123:ARG:NH1	2:O:127:ASP:OD2	2.29	0.65
1:B:258:VAL:CG1	2:O:407:TRP:HE1	2.05	0.65

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:309:ARG:NH1	1:J:339:SER:O	2.30	0.65
2:A:407:TRP:HE1	1:D:258:VAL:CG1	2.05	0.65
1:F:309:ARG:NH1	1:F:339:SER:O	2.30	0.65
1:H:309:ARG:NH1	1:H:339:SER:O	2.30	0.65
2:I:123:ARG:NH1	2:I:127:ASP:OD2	2.29	0.65
2:O:102:ASN:OD1	2:O:105:ARG:N	2.30	0.65
1:H:101:TRP:HE1	1:H:146:GLY:HA2	1.60	0.65
1:H:189:ILE:HG12	1:H:415:MET:HE1	1.78	0.65
2:M:123:ARG:NH1	2:M:127:ASP:OD2	2.29	0.65
2:A:102:ASN:OD1	2:A:105:ARG:N	2.30	0.65
2:C:123:ARG:NH1	2:C:127:ASP:OD2	2.29	0.65
1:L:309:ARG:NH1	1:L:339:SER:O	2.30	0.65
2:K:102:ASN:OD1	2:K:105:ARG:N	2.30	0.65
2:C:407:TRP:HE1	1:F:258:VAL:CG1	2.05	0.65
2:E:123:ARG:NH1	2:E:127:ASP:OD2	2.29	0.65
1:J:189:ILE:HG12	1:J:415:MET:HE1	1.77	0.65
2:I:64:ARG:HB2	2:I:125:LEU:HD11	1.78	0.65
1:P:97:ALA:HB2	1:P:143:THR:OG1	1.97	0.65
1:P:309:ARG:NH1	1:P:339:SER:O	2.30	0.65
1:B:309:ARG:NH1	1:B:339:SER:O	2.30	0.65
2:A:123:ARG:NH1	2:A:127:ASP:OD2	2.29	0.65
1:D:97:ALA:HB2	1:D:143:THR:OG1	1.97	0.65
1:J:101:TRP:HE1	1:J:146:GLY:HA2	1.60	0.65
1:F:97:ALA:HB2	1:F:143:THR:OG1	1.97	0.65
1:F:189:ILE:HG12	1:F:415:MET:HE1	1.79	0.65
1:J:97:ALA:HB2	1:J:143:THR:OG1	1.97	0.65
1:N:97:ALA:HB2	1:N:143:THR:OG1	1.97	0.65
1:N:309:ARG:NH1	1:N:339:SER:O	2.30	0.65
2:M:11:GLN:HG3	2:M:74:VAL:HG21	1.79	0.65
1:B:102:ALA:HA	1:B:105:HIS:HB3	1.79	0.65
1:D:309:ARG:NH1	1:D:339:SER:O	2.30	0.65
1:H:97:ALA:HB2	1:H:143:THR:OG1	1.97	0.65
1:J:102:ALA:HA	1:J:105:HIS:HB3	1.79	0.65
2:K:11:GLN:HG3	2:K:74:VAL:HG21	1.79	0.65
1:B:252:LYS:HA	1:B:255:VAL:HG22	1.79	0.64
2:A:11:GLN:HG3	2:A:74:VAL:HG21	1.79	0.64
1:D:97:ALA:HA	1:D:103:LYS:HZ1	1.62	0.64
2:G:123:ARG:NH1	2:G:127:ASP:OD2	2.29	0.64
2:O:11:GLN:HG3	2:O:74:VAL:HG21	1.79	0.64
1:D:102:ALA:HA	1:D:105:HIS:HB3	1.79	0.64
1:L:102:ALA:HA	1:L:105:HIS:HB3	1.79	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:64:ARG:HB2	2:O:125:LEU:HD11	1.78	0.64
2:C:102:ASN:OD1	2:C:105:ARG:N	2.30	0.64
2:E:64:ARG:HB2	2:E:125:LEU:HD11	1.78	0.64
1:H:102:ALA:HA	1:H:105:HIS:HB3	1.79	0.64
1:L:97:ALA:HB2	1:L:143:THR:OG1	1.97	0.64
2:M:64:ARG:HB2	2:M:125:LEU:HD11	1.78	0.64
1:P:102:ALA:HA	1:P:105:HIS:HB3	1.79	0.64
2:A:64:ARG:HB2	2:A:125:LEU:HD11	1.78	0.64
2:C:11:GLN:HG3	2:C:74:VAL:HG21	1.79	0.64
1:F:118:ASP:OD1	1:F:121:ARG:NH2	2.30	0.64
2:M:245:ASP:OD1	2:M:246:GLY:N	2.31	0.64
1:F:102:ALA:HA	1:F:105:HIS:HB3	1.79	0.64
2:E:11:GLN:HG3	2:E:74:VAL:HG21	1.79	0.64
1:H:118:ASP:OD1	1:H:121:ARG:NH2	2.30	0.64
2:G:64:ARG:HB2	2:G:125:LEU:HD11	1.78	0.64
1:N:236:VAL:HG13	1:N:237:THR:HG23	1.80	0.64
1:P:118:ASP:OD1	1:P:121:ARG:NH2	2.30	0.64
2:C:64:ARG:HB2	2:C:125:LEU:HD11	1.78	0.64
2:E:407:TRP:HE1	1:H:258:VAL:CG1	2.05	0.64
2:I:11:GLN:HG3	2:I:74:VAL:HG21	1.79	0.64
1:B:97:ALA:HB2	1:B:143:THR:OG1	1.97	0.64
2:A:245:ASP:OD1	2:A:246:GLY:N	2.31	0.64
2:E:102:ASN:OD1	2:E:105:ARG:N	2.30	0.64
2:G:245:ASP:OD1	2:G:246:GLY:N	2.31	0.64
1:J:10:GLY:O	1:J:14:ASN:ND2	2.22	0.64
2:I:245:ASP:OD1	2:I:246:GLY:N	2.31	0.64
1:N:102:ALA:HA	1:N:105:HIS:HB3	1.79	0.64
2:C:245:ASP:OD1	2:C:246:GLY:N	2.31	0.64
2:E:306:ASP:OD1	2:E:309:HIS:ND1	2.29	0.64
1:H:68:LEU:HD12	1:H:143:THR:CG2	2.28	0.64
1:L:236:VAL:HG13	1:L:237:THR:HG23	1.80	0.64
1:P:236:VAL:HG13	1:P:237:THR:HG23	1.80	0.64
1:F:249:ASP:OD1	1:F:250:LEU:N	2.31	0.64
2:G:11:GLN:HG3	2:G:74:VAL:HG21	1.79	0.64
2:K:245:ASP:OD1	2:K:246:GLY:N	2.31	0.64
2:O:55:GLU:HB3	2:O:59:GLY:HA2	1.80	0.64
2:O:245:ASP:OD1	2:O:246:GLY:N	2.31	0.64
1:B:118:ASP:OD1	1:B:121:ARG:NH2	2.30	0.63
1:L:252:LYS:HA	1:L:255:VAL:HG22	1.79	0.63
1:N:118:ASP:OD1	1:N:121:ARG:NH2	2.30	0.63
1:P:252:LYS:HA	1:P:255:VAL:HG22	1.79	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:ASP:OD1	1:B:250:LEU:N	2.31	0.63
2:A:306:ASP:OD1	2:A:309:HIS:ND1	2.29	0.63
1:D:68:LEU:HD12	1:D:143:THR:CG2	2.28	0.63
2:C:407:TRP:CZ2	1:F:254:ALA:HB1	2.34	0.63
1:L:68:LEU:HD12	1:L:143:THR:CG2	2.28	0.63
1:L:189:ILE:HG12	1:L:415:MET:HE1	1.78	0.63
2:M:102:ASN:OD1	2:M:105:ARG:N	2.30	0.63
1:B:254:ALA:HB1	2:O:407:TRP:CZ2	2.34	0.63
2:A:55:GLU:HB3	2:A:59:GLY:HA2	1.81	0.63
1:H:97:ALA:HA	1:H:103:LYS:HZ1	1.63	0.63
2:G:102:ASN:OD1	2:G:105:ARG:N	2.30	0.63
1:J:252:LYS:HA	1:J:255:VAL:HG22	1.79	0.63
2:I:407:TRP:CZ2	1:L:254:ALA:HB1	2.34	0.63
1:D:118:ASP:OD1	1:D:121:ARG:NH2	2.30	0.63
1:F:252:LYS:HA	1:F:255:VAL:HG22	1.79	0.63
1:H:249:ASP:OD1	1:H:250:LEU:N	2.31	0.63
1:J:236:VAL:HG13	1:J:237:THR:HG23	1.80	0.63
2:K:407:TRP:CZ2	1:N:254:ALA:HB1	2.34	0.63
1:N:97:ALA:HA	1:N:103:LYS:HZ1	1.63	0.63
2:E:407:TRP:CZ2	1:H:254:ALA:HB1	2.34	0.63
1:H:252:LYS:HA	1:H:255:VAL:HG22	1.79	0.63
2:M:55:GLU:HB3	2:M:59:GLY:HA2	1.81	0.63
2:M:407:TRP:CZ2	1:P:254:ALA:HB1	2.34	0.63
1:P:68:LEU:HD12	1:P:143:THR:CG2	2.28	0.63
1:D:252:LYS:HA	1:D:255:VAL:HG22	1.79	0.63
1:F:68:LEU:HD12	1:F:143:THR:CG2	2.28	0.63
1:F:236:VAL:HG13	1:F:237:THR:HG23	1.80	0.63
2:E:245:ASP:OD1	2:E:246:GLY:N	2.31	0.63
1:J:145:SER:HG	1:J:188:SER:CB	2.12	0.63
1:J:68:LEU:HD12	1:J:143:THR:CG2	2.28	0.63
1:J:97:ALA:HA	1:J:103:LYS:HZ1	1.63	0.63
1:L:249:ASP:OD1	1:L:250:LEU:N	2.31	0.63
1:B:97:ALA:HA	1:B:103:LYS:HZ1	1.64	0.63
1:H:145:SER:HG	1:H:188:SER:CB	2.12	0.63
1:N:249:ASP:OD1	1:N:250:LEU:N	2.31	0.63
1:B:68:LEU:HD12	1:B:143:THR:CG2	2.28	0.63
1:J:118:ASP:OD1	1:J:121:ARG:NH2	2.30	0.63
2:C:55:GLU:HB3	2:C:59:GLY:HA2	1.80	0.62
1:J:249:ASP:OD1	1:J:250:LEU:N	2.31	0.62
1:N:68:LEU:HD12	1:N:143:THR:CG2	2.28	0.62
1:N:103:LYS:HZ1	1:N:143:THR:CG2	2.12	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:249:ASP:OD1	1:D:250:LEU:N	2.31	0.62
2:K:323:VAL:HG23	2:K:355:ILE:HG21	1.81	0.62
2:G:407:TRP:CZ2	1:J:254:ALA:HB1	2.34	0.62
2:K:55:GLU:HB3	2:K:59:GLY:HA2	1.80	0.62
1:D:236:VAL:HG13	1:D:237:THR:HG23	1.80	0.62
2:G:407:TRP:HE1	1:J:258:VAL:CG1	2.05	0.62
1:L:118:ASP:OD1	1:L:121:ARG:NH2	2.30	0.62
1:L:145:SER:HG	1:L:188:SER:CB	2.12	0.62
1:N:252:LYS:HA	1:N:255:VAL:HG22	1.79	0.62
2:A:407:TRP:CZ2	1:D:254:ALA:HB1	2.34	0.62
1:B:236:VAL:HG13	1:B:237:THR:HG23	1.80	0.62
2:G:323:VAL:HG23	2:G:355:ILE:HG21	1.81	0.62
2:C:406:HIS:CE1	1:F:260:PHE:CA	2.83	0.62
1:H:236:VAL:HG13	1:H:237:THR:HG23	1.80	0.62
2:E:55:GLU:HB3	2:E:59:GLY:HA2	1.81	0.61
1:J:103:LYS:HZ1	1:J:143:THR:CG2	2.12	0.61
2:I:55:GLU:HB3	2:I:59:GLY:HA2	1.81	0.61
2:I:102:ASN:OD1	2:I:105:ARG:N	2.30	0.61
1:P:249:ASP:OD1	1:P:250:LEU:N	2.31	0.61
2:E:406:HIS:CE1	1:H:260:PHE:CA	2.83	0.61
2:M:406:HIS:CE1	1:P:260:PHE:CA	2.83	0.61
2:O:323:VAL:HG23	2:O:355:ILE:HG21	1.81	0.61
1:F:97:ALA:HA	1:F:103:LYS:HZ1	1.65	0.61
2:G:55:GLU:HB3	2:G:59:GLY:HA2	1.80	0.61
2:G:343:PHE:HB3	2:G:349:THR:HG21	1.82	0.61
1:N:145:SER:HG	1:N:188:SER:CB	2.13	0.61
2:A:406:HIS:CE1	1:D:260:PHE:CA	2.83	0.61
2:E:343:PHE:HB3	2:E:349:THR:HG21	1.82	0.61
1:B:260:PHE:CA	2:O:406:HIS:CE1	2.83	0.61
1:F:145:SER:HG	1:F:188:SER:CB	2.14	0.61
1:H:97:ALA:CB	1:H:143:THR:OG1	2.49	0.61
2:G:406:HIS:CE1	1:J:260:PHE:CA	2.83	0.61
2:I:323:VAL:HG23	2:I:355:ILE:HG21	1.82	0.61
2:I:343:PHE:HB3	2:I:349:THR:HG21	1.82	0.61
1:N:97:ALA:CB	1:N:143:THR:OG1	2.49	0.61
1:P:97:ALA:CB	1:P:143:THR:OG1	2.49	0.61
2:C:343:PHE:HB3	2:C:349:THR:HG21	1.82	0.61
1:J:97:ALA:CB	1:J:143:THR:OG1	2.49	0.61
2:I:406:HIS:CE1	1:L:260:PHE:CA	2.83	0.61
2:K:406:HIS:CE1	1:N:260:PHE:CA	2.83	0.61
1:F:97:ALA:CB	1:F:143:THR:OG1	2.49	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:306:ASP:OD1	2:I:309:HIS:ND1	2.29	0.61
1:L:97:ALA:CB	1:L:143:THR:OG1	2.49	0.61
1:P:145:SER:HG	1:P:188:SER:CB	2.13	0.61
2:O:3:GLU:N	2:O:131:GLY:O	2.34	0.61
1:B:97:ALA:CB	1:B:143:THR:OG1	2.49	0.61
1:B:99:ASN:ND2	1:B:141:GLY:O	2.34	0.61
2:C:306:ASP:OD1	2:C:309:HIS:ND1	2.29	0.61
1:N:99:ASN:ND2	1:N:141:GLY:O	2.34	0.61
1:P:99:ASN:ND2	1:P:141:GLY:O	2.34	0.61
2:O:172:TYR:N	2:O:204:VAL:O	2.34	0.61
2:I:407:TRP:HE1	1:L:258:VAL:CG1	2.05	0.60
1:L:99:ASN:ND2	1:L:141:GLY:O	2.34	0.60
2:A:172:TYR:N	2:A:204:VAL:O	2.34	0.60
2:A:323:VAL:HG23	2:A:355:ILE:HG21	1.82	0.60
1:F:145:SER:OG	1:F:188:SER:CB	2.50	0.60
2:M:3:GLU:N	2:M:131:GLY:O	2.34	0.60
2:M:306:ASP:OD1	2:M:309:HIS:ND1	2.29	0.60
2:A:3:GLU:N	2:A:131:GLY:O	2.34	0.60
1:D:294:PHE:O	1:D:306:ARG:NH2	2.34	0.60
2:C:323:VAL:HG23	2:C:355:ILE:HG21	1.81	0.60
1:J:294:PHE:O	1:J:306:ARG:NH2	2.34	0.60
2:I:3:GLU:N	2:I:131:GLY:O	2.34	0.60
1:D:145:SER:OG	1:D:188:SER:CB	2.50	0.60
2:C:3:GLU:N	2:C:131:GLY:O	2.34	0.60
1:H:145:SER:OG	1:H:188:SER:CB	2.50	0.60
2:G:3:GLU:N	2:G:131:GLY:O	2.34	0.60
1:J:99:ASN:ND2	1:J:141:GLY:O	2.34	0.60
1:L:237:THR:OG1	1:L:241:ARG:NH1	2.35	0.60
2:M:323:VAL:HG23	2:M:355:ILE:HG21	1.82	0.60
2:M:343:PHE:HB3	2:M:349:THR:HG21	1.82	0.60
1:B:294:PHE:O	1:B:306:ARG:NH2	2.34	0.60
2:A:251:ASP:OD1	2:A:252:LEU:N	2.35	0.60
1:D:103:LYS:HZ1	1:D:143:THR:CG2	2.11	0.60
2:C:172:TYR:N	2:C:204:VAL:O	2.34	0.60
1:H:237:THR:OG1	1:H:241:ARG:NH1	2.35	0.60
1:L:145:SER:OG	1:L:188:SER:CB	2.50	0.60
1:B:145:SER:OG	1:B:188:SER:CB	2.50	0.60
1:D:97:ALA:CB	1:D:143:THR:OG1	2.49	0.60
1:F:294:PHE:O	1:F:306:ARG:NH2	2.34	0.60
1:H:294:PHE:O	1:H:306:ARG:NH2	2.34	0.60
1:J:145:SER:OG	1:J:188:SER:CB	2.50	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:251:ASP:OD1	2:I:252:LEU:N	2.35	0.60
1:L:294:PHE:O	1:L:306:ARG:NH2	2.34	0.60
2:K:137:VAL:HB	2:K:168:GLU:HA	1.84	0.60
2:K:251:ASP:OD1	2:K:252:LEU:N	2.35	0.60
2:O:251:ASP:OD1	2:O:252:LEU:N	2.35	0.60
1:D:99:ASN:ND2	1:D:141:GLY:O	2.34	0.60
1:N:145:SER:OG	1:N:188:SER:CB	2.50	0.60
2:M:137:VAL:HB	2:M:168:GLU:HA	1.84	0.60
2:A:343:PHE:HB3	2:A:349:THR:HG21	1.82	0.60
2:E:172:TYR:N	2:E:204:VAL:O	2.34	0.60
1:H:103:LYS:HZ1	1:H:143:THR:CG2	2.12	0.60
2:I:137:VAL:HB	2:I:168:GLU:HA	1.84	0.60
2:K:3:GLU:N	2:K:131:GLY:O	2.34	0.60
1:N:237:THR:OG1	1:N:241:ARG:NH1	2.35	0.60
2:E:323:VAL:HG23	2:E:355:ILE:HG21	1.82	0.60
1:H:294:PHE:HB3	1:H:306:ARG:HH12	1.67	0.60
1:J:237:THR:OG1	1:J:241:ARG:NH1	2.35	0.60
2:K:343:PHE:HB3	2:K:349:THR:HG21	1.82	0.60
1:P:237:THR:OG1	1:P:241:ARG:NH1	2.35	0.60
2:O:244:PHE:HB2	2:O:356:ASN:HD21	1.67	0.60
1:B:103:LYS:HZ1	1:B:143:THR:CG2	2.14	0.60
1:P:46:ARG:NH1	1:P:241:ARG:O	2.34	0.60
2:A:244:PHE:HB2	2:A:356:ASN:HD21	1.67	0.59
2:C:251:ASP:OD1	2:C:252:LEU:N	2.35	0.59
1:F:237:THR:OG1	1:F:241:ARG:NH1	2.35	0.59
2:E:3:GLU:N	2:E:131:GLY:O	2.34	0.59
1:H:140:GLY:HA3	4:H:502:GDP:H4'	1.84	0.59
1:N:46:ARG:NH1	1:N:241:ARG:O	2.34	0.59
1:P:145:SER:OG	1:P:188:SER:CB	2.50	0.59
1:P:294:PHE:O	1:P:306:ARG:NH2	2.34	0.59
2:O:137:VAL:HB	2:O:168:GLU:HA	1.84	0.59
1:H:170:VAL:HG21	1:H:377:LEU:HD11	1.84	0.59
1:J:140:GLY:HA3	4:J:502:GDP:H4'	1.85	0.59
1:J:294:PHE:HB3	1:J:306:ARG:HH12	1.67	0.59
1:L:140:GLY:HA3	4:L:502:GDP:H4'	1.84	0.59
2:K:244:PHE:HB2	2:K:356:ASN:HD21	1.67	0.59
2:K:407:TRP:HE1	1:N:258:VAL:CG1	2.05	0.59
1:N:294:PHE:O	1:N:306:ARG:NH2	2.34	0.59
2:O:306:ASP:OD1	2:O:309:HIS:ND1	2.29	0.59
1:D:145:SER:HG	1:D:188:SER:CB	2.15	0.59
2:G:251:ASP:OD1	2:G:252:LEU:N	2.35	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:8:HIS:HB2	2:K:67:PHE:HA	1.84	0.59
2:K:239:THR:HG23	2:K:243:ARG:HH11	1.68	0.59
2:O:343:PHE:HB3	2:O:349:THR:HG21	1.82	0.59
1:B:145:SER:HG	1:B:188:SER:CB	2.15	0.59
1:D:244:GLY:O	1:D:247:ASN:ND2	2.36	0.59
2:E:244:PHE:HB2	2:E:356:ASN:HD21	1.67	0.59
2:G:239:THR:HG23	2:G:243:ARG:HH11	1.68	0.59
2:G:244:PHE:HB2	2:G:356:ASN:HD21	1.67	0.59
1:B:244:GLY:O	1:B:247:ASN:ND2	2.36	0.59
1:F:140:GLY:HA3	4:F:502:GDP:H4'	1.85	0.59
2:I:239:THR:HG23	2:I:243:ARG:HH11	1.68	0.59
2:K:306:ASP:OD1	2:K:309:HIS:ND1	2.29	0.59
2:M:239:THR:HG23	2:M:243:ARG:HH11	1.68	0.59
1:F:99:ASN:ND2	1:F:141:GLY:O	2.34	0.59
1:F:294:PHE:HB3	1:F:306:ARG:HH12	1.67	0.59
1:H:244:GLY:O	1:H:247:ASN:ND2	2.36	0.59
2:G:137:VAL:HB	2:G:168:GLU:HA	1.84	0.59
2:G:172:TYR:N	2:G:204:VAL:O	2.34	0.59
1:B:150:LEU:HG	1:B:154:LYS:HZ1	1.67	0.59
1:H:99:ASN:ND2	1:H:141:GLY:O	2.34	0.59
1:J:244:GLY:O	1:J:247:ASN:ND2	2.36	0.59
1:L:244:GLY:O	1:L:247:ASN:ND2	2.36	0.59
1:N:140:GLY:HA3	4:N:502:GDP:H4'	1.85	0.59
1:B:46:ARG:NH1	1:B:241:ARG:O	2.34	0.59
1:B:237:THR:OG1	1:B:241:ARG:NH1	2.35	0.59
2:C:8:HIS:HB2	2:C:67:PHE:HA	1.84	0.59
2:E:251:ASP:OD1	2:E:252:LEU:N	2.35	0.59
1:L:46:ARG:NH1	1:L:241:ARG:O	2.34	0.59
1:L:294:PHE:HB3	1:L:306:ARG:HH12	1.67	0.59
1:F:46:ARG:NH1	1:F:241:ARG:O	2.34	0.59
2:M:8:HIS:HB2	2:M:67:PHE:HA	1.84	0.59
2:M:244:PHE:HB2	2:M:356:ASN:HD21	1.67	0.59
2:M:251:ASP:OD1	2:M:252:LEU:N	2.35	0.59
1:P:140:GLY:HA3	4:P:502:GDP:H4'	1.84	0.59
1:D:294:PHE:HB3	1:D:306:ARG:HH12	1.67	0.58
1:N:244:GLY:O	1:N:247:ASN:ND2	2.36	0.58
2:A:137:VAL:HB	2:A:168:GLU:HA	1.84	0.58
1:D:170:VAL:HG21	1:D:377:LEU:HD11	1.84	0.58
2:I:244:PHE:HB2	2:I:356:ASN:HD21	1.67	0.58
2:O:239:THR:HG23	2:O:243:ARG:HH11	1.68	0.58
1:B:294:PHE:HB3	1:B:306:ARG:HH12	1.67	0.58

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:239:THR:HG23	2:E:243:ARG:HH11	1.68	0.58
2:I:172:TYR:N	2:I:204:VAL:O	2.34	0.58
1:P:294:PHE:HB3	1:P:306:ARG:HH12	1.67	0.58
1:B:140:GLY:HA3	4:B:502:GDP:H4'	1.85	0.58
2:E:8:HIS:HB2	2:E:67:PHE:HA	1.84	0.58
1:D:237:THR:OG1	1:D:241:ARG:NH1	2.35	0.58
2:C:244:PHE:HB2	2:C:356:ASN:HD21	1.67	0.58
1:F:244:GLY:O	1:F:247:ASN:ND2	2.36	0.58
2:E:137:VAL:HB	2:E:168:GLU:HA	1.84	0.58
1:H:46:ARG:NH1	1:H:241:ARG:O	2.34	0.58
2:G:306:ASP:OD1	2:G:309:HIS:ND1	2.29	0.58
1:J:170:VAL:HG21	1:J:377:LEU:HD11	1.84	0.58
1:L:170:VAL:HG21	1:L:377:LEU:HD11	1.84	0.58
1:P:170:VAL:HG21	1:P:377:LEU:HD11	1.84	0.58
1:D:140:GLY:HA3	4:D:502:GDP:H4'	1.84	0.58
2:G:8:HIS:HB2	2:G:67:PHE:HA	1.84	0.58
1:L:150:LEU:HG	1:L:154:LYS:HZ3	1.67	0.58
2:O:8:HIS:HB2	2:O:67:PHE:HA	1.84	0.58
2:C:137:VAL:HB	2:C:168:GLU:HA	1.84	0.58
1:P:244:GLY:O	1:P:247:ASN:ND2	2.36	0.58
1:H:73:MET:O	1:H:77:ARG:HD3	2.04	0.58
2:K:172:TYR:N	2:K:204:VAL:O	2.34	0.58
1:N:170:VAL:HG21	1:N:377:LEU:HD11	1.84	0.58
2:A:8:HIS:HB2	2:A:67:PHE:HA	1.84	0.58
1:F:170:VAL:HG21	1:F:377:LEU:HD11	1.84	0.58
2:I:8:HIS:HB2	2:I:67:PHE:HA	1.84	0.58
1:P:150:LEU:HG	1:P:154:LYS:HZ3	1.68	0.58
1:B:170:VAL:HG21	1:B:377:LEU:HD11	1.84	0.58
2:A:239:THR:HG23	2:A:243:ARG:HH11	1.68	0.58
1:J:96:GLY:O	1:J:103:LYS:NZ	2.37	0.58
1:L:73:MET:O	1:L:77:ARG:HD3	2.04	0.58
1:J:73:MET:O	1:J:77:ARG:HD3	2.04	0.57
1:N:294:PHE:HB3	1:N:306:ARG:HH12	1.67	0.57
1:H:96:GLY:O	1:H:103:LYS:NZ	2.37	0.57
1:F:73:MET:O	1:F:77:ARG:HD3	2.04	0.57
1:J:46:ARG:NH1	1:J:241:ARG:O	2.34	0.57
2:M:172:TYR:N	2:M:204:VAL:O	2.34	0.57
2:M:289:ALA:O	2:M:293:ASN:ND2	2.38	0.57
2:C:239:THR:HG23	2:C:243:ARG:HH11	1.68	0.57
1:P:73:MET:O	1:P:77:ARG:HD3	2.04	0.57
2:C:411:GLU:N	2:C:411:GLU:OE1	2.38	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:289:ALA:O	2:K:293:ASN:ND2	2.38	0.57
2:A:411:GLU:OE1	2:A:411:GLU:N	2.38	0.57
2:E:289:ALA:O	2:E:293:ASN:ND2	2.38	0.57
1:J:249:ASP:O	1:J:253:LEU:N	2.26	0.57
1:N:73:MET:O	1:N:77:ARG:HD3	2.04	0.57
2:O:411:GLU:OE1	2:O:411:GLU:N	2.38	0.57
1:B:96:GLY:O	1:B:103:LYS:NZ	2.37	0.57
1:D:46:ARG:NH1	1:D:241:ARG:O	2.34	0.57
2:M:411:GLU:OE1	2:M:411:GLU:N	2.38	0.57
2:E:411:GLU:OE1	2:E:411:GLU:N	2.38	0.57
2:G:407:TRP:HZ2	1:J:254:ALA:HB1	1.70	0.57
1:J:103:LYS:NZ	1:J:143:THR:HG23	2.19	0.57
2:I:411:GLU:OE1	2:I:411:GLU:N	2.38	0.57
2:A:289:ALA:O	2:A:293:ASN:ND2	2.38	0.57
1:D:73:MET:O	1:D:77:ARG:HD3	2.04	0.57
2:C:407:TRP:HZ2	1:F:254:ALA:HB1	1.70	0.57
1:F:169:VAL:HG11	4:F:502:GDP:HN22	1.70	0.57
1:J:169:VAL:HG11	4:J:502:GDP:HN22	1.70	0.57
2:O:289:ALA:O	2:O:293:ASN:ND2	2.38	0.57
2:G:198:SER:OG	2:G:266:HIS:NE2	2.31	0.56
2:G:289:ALA:O	2:G:293:ASN:ND2	2.38	0.56
2:I:407:TRP:HZ2	1:L:254:ALA:HB1	1.70	0.56
2:M:407:TRP:HZ2	1:P:254:ALA:HB1	1.70	0.56
1:P:96:GLY:O	1:P:103:LYS:NZ	2.37	0.56
1:D:8:GLN:NE2	1:D:13:GLY:O	2.37	0.56
1:D:96:GLY:O	1:D:103:LYS:NZ	2.37	0.56
2:O:198:SER:OG	2:O:266:HIS:NE2	2.31	0.56
1:B:73:MET:O	1:B:77:ARG:HD3	2.04	0.56
1:D:185:ALA:O	1:D:189:ILE:HG22	2.06	0.56
2:G:411:GLU:OE1	2:G:411:GLU:N	2.38	0.56
2:K:411:GLU:N	2:K:411:GLU:OE1	2.38	0.56
1:N:148:GLY:O	1:N:152:ILE:HG12	2.05	0.56
1:P:148:GLY:O	1:P:152:ILE:HG12	2.05	0.56
2:I:289:ALA:O	2:I:293:ASN:ND2	2.38	0.56
1:N:270:PHE:O	1:N:298:ASN:ND2	2.39	0.56
1:B:185:ALA:O	1:B:189:ILE:HG22	2.06	0.56
2:A:407:TRP:HZ2	1:D:254:ALA:HB1	1.70	0.56
2:C:108:TYR:O	2:C:112:LYS:NZ	2.29	0.56
1:F:103:LYS:HZ1	1:F:143:THR:CG2	2.16	0.56
1:F:185:ALA:O	1:F:189:ILE:HG22	2.06	0.56
1:H:8:GLN:NE2	1:H:13:GLY:O	2.37	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:169:VAL:HG11	4:H:502:GDP:HN22	1.70	0.56
1:J:270:PHE:O	1:J:298:ASN:ND2	2.39	0.56
1:L:148:GLY:O	1:L:152:ILE:HG12	2.05	0.56
1:J:148:GLY:O	1:J:152:ILE:HG12	2.05	0.56
1:J:417:ASP:O	1:J:421:GLU:HG2	2.06	0.56
2:M:16:ILE:HG12	2:M:231:ILE:HD11	1.88	0.56
1:D:148:GLY:O	1:D:152:ILE:HG12	2.05	0.56
2:C:289:ALA:O	2:C:293:ASN:ND2	2.38	0.56
1:H:185:ALA:O	1:H:189:ILE:HG22	2.06	0.56
2:I:16:ILE:HG12	2:I:231:ILE:HD11	1.88	0.56
1:B:148:GLY:O	1:B:152:ILE:HG12	2.05	0.56
1:F:8:GLN:NE2	1:F:13:GLY:O	2.37	0.56
1:H:417:ASP:O	1:H:421:GLU:HG2	2.06	0.56
2:K:407:TRP:HZ2	1:N:254:ALA:HB1	1.70	0.56
1:J:185:ALA:O	1:J:189:ILE:HG22	2.06	0.56
1:L:169:VAL:HG11	4:L:502:GDP:HN22	1.70	0.56
1:N:249:ASP:O	1:N:253:LEU:N	2.26	0.56
1:P:417:ASP:O	1:P:421:GLU:HG2	2.06	0.56
1:D:417:ASP:O	1:D:421:GLU:HG2	2.06	0.56
1:F:148:GLY:O	1:F:152:ILE:HG12	2.05	0.56
1:F:417:ASP:O	1:F:421:GLU:HG2	2.06	0.56
1:L:8:GLN:NE2	1:L:13:GLY:O	2.37	0.56
1:N:169:VAL:HG11	4:N:502:GDP:HN22	1.70	0.56
1:N:417:ASP:O	1:N:421:GLU:HG2	2.06	0.56
1:B:8:GLN:NE2	1:B:13:GLY:O	2.37	0.55
1:L:417:ASP:O	1:L:421:GLU:HG2	2.06	0.55
1:N:96:GLY:O	1:N:103:LYS:NZ	2.37	0.55
1:P:169:VAL:HG11	4:P:502:GDP:HN22	1.70	0.55
2:O:16:ILE:HG12	2:O:231:ILE:HD11	1.88	0.55
1:B:169:VAL:HG11	4:B:502:GDP:HN22	1.70	0.55
1:B:417:ASP:O	1:B:421:GLU:HG2	2.06	0.55
1:P:185:ALA:O	1:P:189:ILE:HG22	2.06	0.55
2:A:16:ILE:HG12	2:A:231:ILE:HD11	1.88	0.55
1:H:148:GLY:O	1:H:152:ILE:HG12	2.05	0.55
1:F:96:GLY:O	1:F:103:LYS:NZ	2.37	0.55
2:G:16:ILE:HG12	2:G:231:ILE:HD11	1.88	0.55
1:J:8:GLN:NE2	1:J:13:GLY:O	2.37	0.55
1:L:103:LYS:NZ	1:L:143:THR:HG23	2.19	0.55
2:E:16:ILE:HG12	2:E:231:ILE:HD11	1.88	0.55
2:E:407:TRP:HZ2	1:H:254:ALA:HB1	1.70	0.55
1:J:139:LEU:HD12	1:J:170:VAL:HG12	1.89	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:176:GLN:OE1	2:I:176:GLN:N	2.40	0.55
1:F:139:LEU:HD12	1:F:170:VAL:HG12	1.89	0.55
2:E:39:ASP:OD2	2:E:45:GLY:N	2.40	0.55
1:J:144:GLY:HA3	4:J:502:GDP:O1A	2.07	0.55
2:K:176:GLN:OE1	2:K:176:GLN:N	2.40	0.55
1:P:139:LEU:HD12	1:P:170:VAL:HG12	1.89	0.55
1:P:270:PHE:O	1:P:298:ASN:ND2	2.39	0.55
1:B:62:ARG:NH1	1:B:127:CYS:SG	2.80	0.55
1:D:139:LEU:HD12	1:D:170:VAL:HG12	1.89	0.55
2:C:39:ASP:OD2	2:C:45:GLY:N	2.40	0.55
1:H:270:PHE:O	1:H:298:ASN:ND2	2.39	0.55
1:N:144:GLY:HA3	4:N:502:GDP:O1A	2.07	0.55
1:N:185:ALA:O	1:N:189:ILE:HG22	2.06	0.55
1:B:254:ALA:HB1	2:O:407:TRP:HZ2	1.70	0.55
1:B:270:PHE:O	1:B:298:ASN:ND2	2.39	0.55
2:A:39:ASP:OD2	2:A:45:GLY:N	2.40	0.55
1:D:169:VAL:HG11	4:D:502:GDP:HN22	1.70	0.55
2:I:39:ASP:OD2	2:I:45:GLY:N	2.40	0.55
1:L:270:PHE:O	1:L:298:ASN:ND2	2.39	0.55
1:N:62:ARG:NH1	1:N:127:CYS:SG	2.80	0.55
2:M:176:GLN:OE1	2:M:176:GLN:N	2.40	0.55
2:M:198:SER:OG	2:M:266:HIS:NE2	2.31	0.55
1:P:144:GLY:HA3	4:P:502:GDP:O1A	2.07	0.55
1:B:99:ASN:HD22	1:B:141:GLY:C	2.10	0.55
1:D:62:ARG:NH1	1:D:127:CYS:SG	2.80	0.55
1:D:270:PHE:O	1:D:298:ASN:ND2	2.39	0.55
1:H:144:GLY:HA3	4:H:502:GDP:O1A	2.07	0.55
1:L:62:ARG:NH1	1:L:127:CYS:SG	2.80	0.55
1:L:185:ALA:O	1:L:189:ILE:HG22	2.06	0.55
2:C:168:GLU:O	2:C:202:PHE:N	2.33	0.55
1:L:144:GLY:HA3	4:L:502:GDP:O1A	2.07	0.55
1:N:99:ASN:HD22	1:N:141:GLY:C	2.10	0.55
2:O:176:GLN:N	2:O:176:GLN:OE1	2.40	0.55
1:B:144:GLY:HA3	4:B:502:GDP:O1A	2.07	0.54
1:F:99:ASN:HD22	1:F:141:GLY:C	2.10	0.54
2:G:39:ASP:OD2	2:G:45:GLY:N	2.40	0.54
2:K:16:ILE:HG12	2:K:231:ILE:HD11	1.88	0.54
2:K:39:ASP:OD2	2:K:45:GLY:N	2.40	0.54
2:M:39:ASP:OD2	2:M:45:GLY:N	2.40	0.54
1:P:99:ASN:HD22	1:P:141:GLY:C	2.10	0.54
1:D:67:ASP:OD2	1:D:72:THR:HB	2.08	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:176:GLN:OE1	2:C:176:GLN:N	2.40	0.54
1:F:103:LYS:NZ	1:F:143:THR:HG21	2.21	0.54
1:D:103:LYS:NZ	1:D:143:THR:HG23	2.19	0.54
1:F:270:PHE:O	1:F:298:ASN:ND2	2.39	0.54
1:H:67:ASP:OD2	1:H:72:THR:HB	2.08	0.54
2:G:176:GLN:N	2:G:176:GLN:OE1	2.40	0.54
1:J:150:LEU:HG	1:J:154:LYS:HZ1	1.72	0.54
1:P:67:ASP:OD2	1:P:72:THR:HB	2.08	0.54
1:B:67:ASP:OD2	1:B:72:THR:HB	2.08	0.54
1:D:99:ASN:HD22	1:D:141:GLY:C	2.10	0.54
1:N:103:LYS:NZ	1:N:143:THR:HG21	2.21	0.54
2:C:16:ILE:HG12	2:C:231:ILE:HD11	1.88	0.54
1:L:139:LEU:HD12	1:L:170:VAL:HG12	1.89	0.54
1:D:144:GLY:HA3	4:D:502:GDP:O1A	2.07	0.54
2:C:198:SER:OG	2:C:266:HIS:NE2	2.31	0.54
1:F:8:GLN:NE2	1:F:17:GLY:HA3	2.23	0.54
1:H:139:LEU:HD12	1:H:170:VAL:HG12	1.89	0.54
1:L:96:GLY:O	1:L:103:LYS:NZ	2.37	0.54
1:L:99:ASN:HD22	1:L:141:GLY:C	2.10	0.54
1:N:67:ASP:OD2	1:N:72:THR:HB	2.08	0.54
1:N:139:LEU:HD12	1:N:170:VAL:HG12	1.89	0.54
1:P:62:ARG:NH1	1:P:127:CYS:SG	2.80	0.54
1:B:139:LEU:HD12	1:B:170:VAL:HG12	1.89	0.54
2:A:393:HIS:O	2:A:397:LEU:HD23	2.08	0.54
1:H:8:GLN:NE2	1:H:17:GLY:HA3	2.23	0.54
1:H:62:ARG:NH1	1:H:127:CYS:SG	2.80	0.54
1:J:62:ARG:NH1	1:J:127:CYS:SG	2.80	0.54
1:J:67:ASP:OD2	1:J:72:THR:HB	2.08	0.54
1:P:8:GLN:NE2	1:P:13:GLY:O	2.37	0.54
1:F:62:ARG:NH1	1:F:127:CYS:SG	2.80	0.54
1:F:253:LEU:O	1:F:257:MET:HB2	2.08	0.54
2:E:176:GLN:OE1	2:E:176:GLN:N	2.40	0.54
2:G:393:HIS:O	2:G:397:LEU:HD23	2.08	0.54
1:J:99:ASN:HD22	1:J:141:GLY:C	2.10	0.54
2:M:393:HIS:O	2:M:397:LEU:HD23	2.08	0.54
1:P:249:ASP:O	1:P:253:LEU:N	2.26	0.54
2:O:39:ASP:OD2	2:O:45:GLY:N	2.40	0.54
2:O:393:HIS:O	2:O:397:LEU:HD23	2.08	0.54
2:C:393:HIS:O	2:C:397:LEU:HD23	2.08	0.54
1:F:144:GLY:HA3	4:F:502:GDP:O1A	2.07	0.54
1:H:253:LEU:O	1:H:257:MET:HB2	2.08	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:GLN:N	1:B:94:GLN:OE1	2.41	0.54
1:D:150:LEU:HG	1:D:154:LYS:HZ1	1.72	0.54
1:F:67:ASP:OD2	1:F:72:THR:HB	2.08	0.54
2:E:320:ARG:HG2	2:E:374:ALA:HB3	1.90	0.54
2:E:393:HIS:O	2:E:397:LEU:HD23	2.08	0.54
1:H:101:TRP:CZ3	1:H:187:LEU:HB3	2.44	0.54
2:G:5:ILE:HG12	2:G:132:LEU:HD13	1.90	0.54
2:G:196:GLU:N	2:G:196:GLU:OE1	2.42	0.54
2:G:320:ARG:HG2	2:G:374:ALA:HB3	1.90	0.54
2:I:393:HIS:O	2:I:397:LEU:HD23	2.08	0.54
2:A:176:GLN:OE1	2:A:176:GLN:N	2.40	0.53
1:D:8:GLN:NE2	1:D:17:GLY:HA3	2.23	0.53
2:I:5:ILE:HG12	2:I:132:LEU:HD13	1.90	0.53
2:I:196:GLU:OE1	2:I:196:GLU:N	2.42	0.53
2:I:221:ARG:CB	1:L:324:LYS:CB	2.86	0.53
1:L:69:GLU:HB3	1:L:96:GLY:HA2	1.90	0.53
2:K:196:GLU:OE1	2:K:196:GLU:N	2.42	0.53
1:B:101:TRP:CZ3	1:B:187:LEU:HB3	2.44	0.53
2:C:5:ILE:HG12	2:C:132:LEU:HD13	1.90	0.53
2:C:320:ARG:HG2	2:C:374:ALA:HB3	1.90	0.53
1:F:58:LYS:NZ	1:F:59:TYR:O	2.41	0.53
1:F:103:LYS:NZ	1:F:143:THR:HG23	2.19	0.53
2:E:5:ILE:HG12	2:E:132:LEU:HD13	1.90	0.53
1:H:99:ASN:HD22	1:H:141:GLY:C	2.10	0.53
1:J:58:LYS:NZ	1:J:59:TYR:O	2.41	0.53
2:M:196:GLU:OE1	2:M:196:GLU:N	2.42	0.53
2:M:221:ARG:CB	1:P:324:LYS:CB	2.86	0.53
2:A:5:ILE:HG12	2:A:132:LEU:HD13	1.90	0.53
1:D:253:LEU:O	1:D:257:MET:HB2	2.08	0.53
2:E:196:GLU:OE1	2:E:196:GLU:N	2.42	0.53
1:J:101:TRP:CZ3	1:J:187:LEU:HB3	2.44	0.53
2:I:320:ARG:HG2	2:I:374:ALA:HB3	1.90	0.53
2:C:196:GLU:OE1	2:C:196:GLU:N	2.42	0.53
2:C:208:ALA:O	2:C:212:ILE:HG12	2.09	0.53
1:H:103:LYS:NZ	1:H:143:THR:HG23	2.19	0.53
1:J:69:GLU:HB3	1:J:96:GLY:HA2	1.90	0.53
1:L:253:LEU:O	1:L:257:MET:HB2	2.08	0.53
2:A:221:ARG:CB	1:D:324:LYS:CB	2.86	0.53
1:J:103:LYS:NZ	1:J:143:THR:HG21	2.21	0.53
1:N:8:GLN:NE2	1:N:13:GLY:O	2.37	0.53
1:N:69:GLU:HB3	1:N:96:GLY:HA2	1.90	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:187:SER:O	2:M:191:THR:HG22	2.09	0.53
2:A:208:ALA:O	2:A:212:ILE:HG12	2.09	0.53
1:D:94:GLN:OE1	1:D:94:GLN:N	2.41	0.53
1:F:101:TRP:CZ3	1:F:187:LEU:HB3	2.44	0.53
1:L:101:TRP:CZ3	1:L:187:LEU:HB3	2.44	0.53
1:P:253:LEU:O	1:P:257:MET:HB2	2.08	0.53
1:B:8:GLN:NE2	1:B:17:GLY:HA3	2.23	0.53
2:E:187:SER:O	2:E:191:THR:HG22	2.09	0.53
2:E:208:ALA:O	2:E:212:ILE:HG12	2.09	0.53
1:J:253:LEU:O	1:J:257:MET:HB2	2.08	0.53
1:L:97:ALA:HA	1:L:103:LYS:HZ1	1.73	0.53
1:N:94:GLN:OE1	1:N:94:GLN:N	2.41	0.53
1:N:150:LEU:HG	1:N:154:LYS:HZ1	1.72	0.53
2:M:141:PHE:O	2:M:147:SER:OG	2.26	0.53
1:F:81:PHE:HA	1:F:84:LEU:HD23	1.91	0.53
1:F:94:GLN:OE1	1:F:94:GLN:N	2.41	0.53
2:E:221:ARG:CB	1:H:324:LYS:CB	2.86	0.53
1:H:4:ILE:HG12	1:H:131:GLN:HB3	1.91	0.53
1:H:69:GLU:HB3	1:H:96:GLY:HA2	1.90	0.53
1:J:81:PHE:HA	1:J:84:LEU:HD23	1.91	0.53
2:K:5:ILE:HG12	2:K:132:LEU:HD13	1.90	0.53
1:N:103:LYS:NZ	1:N:143:THR:HG23	2.19	0.53
1:P:101:TRP:CZ3	1:P:187:LEU:HB3	2.44	0.53
2:O:196:GLU:N	2:O:196:GLU:OE1	2.42	0.53
1:B:324:LYS:CB	2:O:221:ARG:CB	2.86	0.53
1:D:69:GLU:HB3	1:D:96:GLY:HA2	1.90	0.53
2:C:221:ARG:CB	1:F:324:LYS:CB	2.86	0.53
2:G:47:ASP:OD1	2:G:48:SER:N	2.41	0.53
2:G:187:SER:O	2:G:191:THR:HG22	2.09	0.53
1:L:67:ASP:OD2	1:L:72:THR:HB	2.08	0.53
2:K:393:HIS:O	2:K:397:LEU:HD23	2.08	0.53
1:N:101:TRP:CZ3	1:N:187:LEU:HB3	2.44	0.53
1:B:253:LEU:O	1:B:257:MET:HB2	2.08	0.53
2:A:55:GLU:HA	2:A:61:HIS:H	1.74	0.53
2:A:187:SER:O	2:A:191:THR:HG22	2.09	0.53
1:D:21:TRP:HZ3	1:D:51:TYR:HE1	1.57	0.53
1:F:21:TRP:HZ3	1:F:51:TYR:HE1	1.57	0.53
1:H:94:GLN:OE1	1:H:94:GLN:N	2.41	0.53
1:H:150:LEU:HG	1:H:154:LYS:HZ1	1.73	0.53
2:K:320:ARG:HG2	2:K:374:ALA:HB3	1.90	0.53
2:O:5:ILE:HG12	2:O:132:LEU:HD13	1.90	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:196:GLU:OE1	2:A:196:GLU:N	2.42	0.52
2:A:320:ARG:HG2	2:A:374:ALA:HB3	1.90	0.52
1:D:4:ILE:HG12	1:D:131:GLN:HB3	1.91	0.52
1:D:229:VAL:O	1:D:233:MET:HG3	2.09	0.52
1:H:326:VAL:HA	1:H:329:GLN:NE2	2.24	0.52
1:J:326:VAL:HA	1:J:329:GLN:NE2	2.24	0.52
1:L:94:GLN:OE1	1:L:94:GLN:N	2.41	0.52
2:K:221:ARG:CB	1:N:324:LYS:CB	2.86	0.52
1:P:81:PHE:HA	1:P:84:LEU:HD23	1.91	0.52
1:B:69:GLU:HB3	1:B:96:GLY:HA2	1.90	0.52
1:B:81:PHE:HA	1:B:84:LEU:HD23	1.91	0.52
1:D:101:TRP:CZ3	1:D:187:LEU:HB3	2.44	0.52
2:C:187:SER:O	2:C:191:THR:HG22	2.09	0.52
2:G:221:ARG:CB	1:J:324:LYS:CB	2.86	0.52
1:J:94:GLN:N	1:J:94:GLN:OE1	2.41	0.52
2:I:187:SER:O	2:I:191:THR:HG22	2.09	0.52
1:L:4:ILE:HG12	1:L:131:GLN:HB3	1.91	0.52
2:K:198:SER:OG	2:K:266:HIS:NE2	2.31	0.52
1:N:81:PHE:HA	1:N:84:LEU:HD23	1.91	0.52
1:P:229:VAL:O	1:P:233:MET:HG3	2.09	0.52
2:O:208:ALA:O	2:O:212:ILE:HG12	2.09	0.52
1:B:103:LYS:NZ	1:B:143:THR:HG21	2.21	0.52
1:B:249:ASP:O	1:B:253:LEU:N	2.26	0.52
2:C:141:PHE:O	2:C:147:SER:OG	2.26	0.52
1:F:303:CYS:SG	1:F:304:ASP:N	2.83	0.52
1:N:303:CYS:SG	1:N:304:ASP:N	2.83	0.52
2:O:168:GLU:O	2:O:202:PHE:N	2.33	0.52
1:B:21:TRP:HZ3	1:B:51:TYR:HE1	1.57	0.52
1:B:303:CYS:SG	1:B:304:ASP:N	2.83	0.52
2:C:55:GLU:HA	2:C:61:HIS:H	1.75	0.52
2:E:209:ILE:HG23	2:E:230:LEU:HD22	1.92	0.52
1:J:303:CYS:SG	1:J:304:ASP:N	2.83	0.52
1:N:229:VAL:O	1:N:233:MET:HG3	2.09	0.52
1:P:21:TRP:HZ3	1:P:51:TYR:HE1	1.57	0.52
1:P:94:GLN:OE1	1:P:94:GLN:N	2.41	0.52
1:P:326:VAL:HA	1:P:329:GLN:NE2	2.24	0.52
2:O:187:SER:O	2:O:191:THR:HG22	2.09	0.52
1:B:58:LYS:NZ	1:B:59:TYR:O	2.41	0.52
2:A:209:ILE:HG23	2:A:230:LEU:HD22	1.92	0.52
1:D:72:THR:O	1:D:76:VAL:N	2.40	0.52
2:C:209:ILE:HG23	2:C:230:LEU:HD22	1.92	0.52

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:69:GLU:HB3	1:F:96:GLY:HA2	1.90	0.52
1:H:21:TRP:HZ3	1:H:51:TYR:HE1	1.57	0.52
1:H:229:VAL:O	1:H:233:MET:HG3	2.09	0.52
1:H:249:ASP:O	1:H:253:LEU:N	2.26	0.52
1:L:81:PHE:HA	1:L:84:LEU:HD23	1.91	0.52
1:L:303:CYS:SG	1:L:304:ASP:N	2.83	0.52
2:K:208:ALA:O	2:K:212:ILE:HG12	2.09	0.52
2:M:5:ILE:HG12	2:M:132:LEU:HD13	1.90	0.52
2:M:83:TYR:HA	2:M:86:LEU:HD13	1.92	0.52
1:B:103:LYS:NZ	1:B:143:THR:HG23	2.19	0.52
1:F:326:VAL:HA	1:F:329:GLN:NE2	2.24	0.52
1:H:103:LYS:NZ	1:H:143:THR:HG21	2.21	0.52
1:J:229:VAL:O	1:J:233:MET:HG3	2.09	0.52
1:N:253:LEU:O	1:N:257:MET:HB2	2.08	0.52
1:P:69:GLU:HB3	1:P:96:GLY:HA2	1.90	0.52
2:O:320:ARG:HG2	2:O:374:ALA:HB3	1.90	0.52
1:B:326:VAL:HA	1:B:329:GLN:NE2	2.24	0.52
1:D:58:LYS:NZ	1:D:59:TYR:O	2.41	0.52
1:H:58:LYS:NZ	1:H:59:TYR:O	2.41	0.52
1:H:303:CYS:SG	1:H:304:ASP:N	2.83	0.52
1:J:4:ILE:HG12	1:J:131:GLN:HB3	1.91	0.52
1:P:8:GLN:NE2	1:P:17:GLY:HA3	2.23	0.52
2:O:55:GLU:HA	2:O:61:HIS:H	1.75	0.52
1:F:265:PHE:HB3	1:F:374:ILE:HD13	1.92	0.52
1:H:265:PHE:HB3	1:H:374:ILE:HD13	1.92	0.52
2:G:208:ALA:O	2:G:212:ILE:HG12	2.09	0.52
1:J:101:TRP:HZ3	1:J:187:LEU:HB3	1.75	0.52
2:I:83:TYR:HA	2:I:86:LEU:HD13	1.92	0.52
1:N:21:TRP:HZ3	1:N:51:TYR:HE1	1.57	0.52
2:M:320:ARG:HG2	2:M:374:ALA:HB3	1.90	0.52
2:O:209:ILE:HG23	2:O:230:LEU:HD22	1.92	0.52
1:B:72:THR:O	1:B:76:VAL:N	2.40	0.52
1:F:72:THR:O	1:F:76:VAL:N	2.40	0.52
1:H:81:PHE:HA	1:H:84:LEU:HD23	1.91	0.52
2:K:187:SER:O	2:K:191:THR:HG22	2.09	0.52
1:P:58:LYS:NZ	1:P:59:TYR:O	2.41	0.52
2:M:208:ALA:O	2:M:212:ILE:HG12	2.09	0.52
1:B:229:VAL:O	1:B:233:MET:HG3	2.09	0.51
2:E:55:GLU:HA	2:E:61:HIS:H	1.74	0.51
2:G:55:GLU:HA	2:G:61:HIS:H	1.75	0.51
2:G:209:ILE:HG23	2:G:230:LEU:HD22	1.92	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:21:TRP:HZ3	1:J:51:TYR:HE1	1.57	0.51
1:J:265:PHE:HB3	1:J:374:ILE:HD13	1.92	0.51
2:I:229:ARG:HD2	2:I:363:VAL:HG11	1.93	0.51
1:L:21:TRP:HZ3	1:L:51:TYR:HE1	1.57	0.51
1:L:229:VAL:O	1:L:233:MET:HG3	2.09	0.51
1:L:326:VAL:HA	1:L:329:GLN:NE2	2.24	0.51
1:N:58:LYS:NZ	1:N:59:TYR:O	2.41	0.51
1:N:326:VAL:HA	1:N:329:GLN:NE2	2.24	0.51
2:M:229:ARG:HD2	2:M:363:VAL:HG11	1.93	0.51
1:P:4:ILE:HG12	1:P:131:GLN:HB3	1.91	0.51
1:P:303:CYS:SG	1:P:304:ASP:N	2.83	0.51
1:D:326:VAL:HA	1:D:329:GLN:NE2	2.24	0.51
2:G:141:PHE:O	2:G:147:SER:OG	2.26	0.51
2:I:47:ASP:OD1	2:I:48:SER:N	2.41	0.51
2:I:55:GLU:HA	2:I:61:HIS:H	1.74	0.51
1:D:101:TRP:HZ3	1:D:187:LEU:HB3	1.75	0.51
1:D:303:CYS:SG	1:D:304:ASP:N	2.83	0.51
1:F:4:ILE:HG12	1:F:131:GLN:HB3	1.91	0.51
1:F:101:TRP:HZ3	1:F:187:LEU:HB3	1.75	0.51
1:F:229:VAL:O	1:F:233:MET:HG3	2.09	0.51
2:I:208:ALA:O	2:I:212:ILE:HG12	2.09	0.51
2:M:209:ILE:HG23	2:M:230:LEU:HD22	1.92	0.51
2:E:141:PHE:O	2:E:147:SER:OG	2.26	0.51
1:L:249:ASP:O	1:L:253:LEU:N	2.26	0.51
2:K:55:GLU:HA	2:K:61:HIS:H	1.75	0.51
1:N:265:PHE:HB3	1:N:374:ILE:HD13	1.92	0.51
2:A:141:PHE:O	2:A:147:SER:OG	2.26	0.51
1:D:265:PHE:HB3	1:D:374:ILE:HD13	1.92	0.51
1:F:249:ASP:O	1:F:253:LEU:N	2.26	0.51
1:B:265:PHE:HB3	1:B:374:ILE:HD13	1.92	0.51
1:D:81:PHE:HA	1:D:84:LEU:HD23	1.91	0.51
2:E:229:ARG:HD2	2:E:363:VAL:HG11	1.93	0.51
1:H:313:VAL:HG21	1:H:341:PHE:HE1	1.76	0.51
1:N:4:ILE:HG12	1:N:131:GLN:HB3	1.91	0.51
1:N:8:GLN:NE2	1:N:17:GLY:HA3	2.23	0.51
1:P:313:VAL:HG21	1:P:341:PHE:HE1	1.76	0.51
2:A:83:TYR:HA	2:A:86:LEU:HD13	1.92	0.51
1:N:313:VAL:HG21	1:N:341:PHE:HE1	1.76	0.51
1:B:313:VAL:HG21	1:B:341:PHE:HE1	1.76	0.51
1:F:313:VAL:HG21	1:F:341:PHE:HE1	1.76	0.51
1:J:8:GLN:NE2	1:J:17:GLY:HA3	2.23	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:101:TRP:HZ3	1:H:187:LEU:HB3	1.75	0.51
2:G:229:ARG:HD2	2:G:363:VAL:HG11	1.93	0.51
1:L:265:PHE:HB3	1:L:374:ILE:HD13	1.92	0.51
2:K:83:TYR:HA	2:K:86:LEU:HD13	1.92	0.51
2:K:209:ILE:HG23	2:K:230:LEU:HD22	1.92	0.51
2:M:55:GLU:HA	2:M:61:HIS:H	1.74	0.51
2:M:136:LEU:HD13	2:M:167:LEU:HB3	1.93	0.51
1:P:72:THR:O	1:P:76:VAL:N	2.40	0.51
2:O:136:LEU:HD13	2:O:167:LEU:HB3	1.93	0.51
1:F:150:LEU:HG	1:F:154:LYS:HZ3	1.75	0.51
2:E:31:GLN:HB2	2:E:33:ASP:OD1	2.11	0.51
1:L:110:ALA:O	1:L:113:VAL:HG12	2.11	0.51
1:N:110:ALA:O	1:N:113:VAL:HG12	2.11	0.51
1:P:110:ALA:O	1:P:113:VAL:HG12	2.11	0.51
2:A:229:ARG:HD2	2:A:363:VAL:HG11	1.93	0.50
2:C:83:TYR:HA	2:C:86:LEU:HD13	1.92	0.50
2:E:198:SER:OG	2:E:266:HIS:NE2	2.31	0.50
2:G:168:GLU:O	2:G:202:PHE:N	2.33	0.50
2:I:209:ILE:HG23	2:I:230:LEU:HD22	1.92	0.50
2:K:31:GLN:HB2	2:K:33:ASP:OD1	2.11	0.50
2:K:47:ASP:OD1	2:K:48:SER:N	2.41	0.50
2:M:108:TYR:O	2:M:112:LYS:NZ	2.29	0.50
2:O:31:GLN:HB2	2:O:33:ASP:OD1	2.11	0.50
1:B:4:ILE:HG12	1:B:131:GLN:HB3	1.91	0.50
2:A:136:LEU:HD13	2:A:167:LEU:HB3	1.93	0.50
1:J:110:ALA:O	1:J:113:VAL:HG12	2.11	0.50
1:L:58:LYS:NZ	1:L:59:TYR:O	2.41	0.50
1:L:101:TRP:HZ3	1:L:187:LEU:HB3	1.75	0.50
1:L:313:VAL:HG21	1:L:341:PHE:HE1	1.76	0.50
2:K:136:LEU:HD13	2:K:167:LEU:HB3	1.93	0.50
1:P:103:LYS:NZ	1:P:143:THR:HG23	2.19	0.50
2:A:287:SER:HB3	2:A:290:GLU:HB2	1.94	0.50
2:C:31:GLN:HB2	2:C:33:ASP:OD1	2.11	0.50
1:H:215:LEU:HG	1:H:275:ALA:HB2	1.94	0.50
1:J:313:VAL:HG21	1:J:341:PHE:HE1	1.76	0.50
1:L:8:GLN:NE2	1:L:17:GLY:HA3	2.23	0.50
2:K:229:ARG:HD2	2:K:363:VAL:HG11	1.93	0.50
1:B:110:ALA:O	1:B:113:VAL:HG12	2.11	0.50
2:C:136:LEU:HD13	2:C:167:LEU:HB3	1.93	0.50
2:C:287:SER:HB3	2:C:290:GLU:HB2	1.94	0.50
2:E:83:TYR:HA	2:E:86:LEU:HD13	1.92	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:31:GLN:HB2	2:G:33:ASP:OD1	2.11	0.50
1:L:103:LYS:NZ	1:L:143:THR:HG21	2.21	0.50
1:L:215:LEU:HG	1:L:275:ALA:HB2	1.94	0.50
2:K:108:TYR:O	2:K:112:LYS:NZ	2.29	0.50
2:K:141:PHE:O	2:K:147:SER:OG	2.26	0.50
1:N:215:LEU:HG	1:N:275:ALA:HB2	1.94	0.50
2:M:70:LEU:HA	2:M:95:GLY:HA3	1.94	0.50
1:B:101:TRP:HZ3	1:B:187:LEU:HB3	1.75	0.50
1:D:313:VAL:HG21	1:D:341:PHE:HE1	1.76	0.50
1:L:70:PRO:HG3	1:L:94:GLN:HA	1.94	0.50
1:N:101:TRP:HZ3	1:N:187:LEU:HB3	1.75	0.50
1:P:7:ILE:HA	1:P:64:ILE:HG22	1.93	0.50
1:P:101:TRP:HZ3	1:P:187:LEU:HB3	1.75	0.50
1:B:7:ILE:HA	1:B:64:ILE:HG22	1.93	0.50
2:A:70:LEU:HA	2:A:95:GLY:HA3	1.94	0.50
1:D:103:LYS:NZ	1:D:143:THR:HG21	2.21	0.50
1:F:215:LEU:HG	1:F:275:ALA:HB2	1.94	0.50
1:H:70:PRO:HG3	1:H:94:GLN:HA	1.94	0.50
2:O:287:SER:HB3	2:O:290:GLU:HB2	1.94	0.50
1:D:110:ALA:O	1:D:113:VAL:HG12	2.11	0.50
2:C:160:ASP:OD1	2:C:161:TYR:N	2.45	0.50
2:E:108:TYR:O	2:E:112:LYS:NZ	2.29	0.50
2:G:160:ASP:OD1	2:G:161:TYR:N	2.45	0.50
1:J:215:LEU:HG	1:J:275:ALA:HB2	1.94	0.50
2:I:269:LEU:HD23	2:I:270:ALA:N	2.27	0.50
2:M:47:ASP:OD1	2:M:48:SER:N	2.41	0.50
2:O:83:TYR:HA	2:O:86:LEU:HD13	1.92	0.50
2:O:269:LEU:HD23	2:O:270:ALA:N	2.27	0.50
2:E:190:THR:O	2:E:194:THR:HG23	2.12	0.50
2:G:83:TYR:HA	2:G:86:LEU:HD13	1.92	0.50
2:G:344:VAL:HG12	2:G:346:TRP:H	1.77	0.50
2:I:344:VAL:HG12	2:I:346:TRP:H	1.77	0.50
2:K:70:LEU:HA	2:K:95:GLY:HA3	1.94	0.50
1:P:21:TRP:HA	1:P:24:ILE:HG12	1.94	0.50
1:P:265:PHE:HB3	1:P:374:ILE:HD13	1.92	0.50
2:A:160:ASP:OD1	2:A:161:TYR:N	2.45	0.50
2:A:190:THR:O	2:A:194:THR:HG23	2.12	0.50
2:C:229:ARG:HD2	2:C:363:VAL:HG11	1.93	0.50
2:E:160:ASP:OD1	2:E:161:TYR:N	2.45	0.50
2:E:269:LEU:HD23	2:E:270:ALA:N	2.27	0.50
2:E:344:VAL:HG12	2:E:346:TRP:H	1.77	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:105:ARG:CZ	1:J:251:ARG:HD3	2.42	0.50
1:J:21:TRP:HA	1:J:24:ILE:HG12	1.94	0.50
2:I:141:PHE:O	2:I:147:SER:OG	2.26	0.50
1:N:7:ILE:HA	1:N:64:ILE:HG22	1.93	0.50
1:P:215:LEU:HG	1:P:275:ALA:HB2	1.94	0.50
2:A:105:ARG:CZ	1:D:251:ARG:HD3	2.42	0.49
2:E:136:LEU:HD13	2:E:167:LEU:HB3	1.93	0.49
2:E:287:SER:HB3	2:E:290:GLU:HB2	1.94	0.49
1:H:110:ALA:O	1:H:113:VAL:HG12	2.11	0.49
2:I:70:LEU:HA	2:I:95:GLY:HA3	1.94	0.49
2:I:136:LEU:HD13	2:I:167:LEU:HB3	1.93	0.49
2:K:160:ASP:OD1	2:K:161:TYR:N	2.45	0.49
2:K:190:THR:O	2:K:194:THR:HG23	2.12	0.49
2:M:190:THR:O	2:M:194:THR:HG23	2.12	0.49
2:O:229:ARG:HD2	2:O:363:VAL:HG11	1.93	0.49
2:A:31:GLN:HB2	2:A:33:ASP:OD1	2.11	0.49
1:D:215:LEU:HG	1:D:275:ALA:HB2	1.94	0.49
2:G:102:ASN:ND2	2:G:411:GLU:OE2	2.44	0.49
1:L:21:TRP:HA	1:L:24:ILE:HG12	1.94	0.49
2:K:271:THR:HG22	2:K:301:GLN:HA	1.94	0.49
1:N:21:TRP:HA	1:N:24:ILE:HG12	1.94	0.49
2:M:31:GLN:HB2	2:M:33:ASP:OD1	2.11	0.49
1:P:103:LYS:NZ	1:P:143:THR:HG21	2.21	0.49
2:O:47:ASP:OD1	2:O:48:SER:N	2.41	0.49
2:O:160:ASP:OD1	2:O:161:TYR:N	2.45	0.49
2:E:271:THR:HG22	2:E:301:GLN:HA	1.94	0.49
2:G:70:LEU:HA	2:G:95:GLY:HA3	1.94	0.49
1:J:7:ILE:HA	1:J:64:ILE:HG22	1.93	0.49
1:P:97:ALA:HA	1:P:103:LYS:HZ1	1.78	0.49
1:B:215:LEU:HG	1:B:275:ALA:HB2	1.94	0.49
1:D:7:ILE:HA	1:D:64:ILE:HG22	1.93	0.49
2:C:105:ARG:CZ	1:F:251:ARG:HD3	2.42	0.49
2:C:190:THR:O	2:C:194:THR:HG23	2.12	0.49
2:C:344:VAL:HG12	2:C:346:TRP:H	1.77	0.49
2:E:70:LEU:HA	2:E:95:GLY:HA3	1.94	0.49
2:G:190:THR:O	2:G:194:THR:HG23	2.12	0.49
2:I:31:GLN:HB2	2:I:33:ASP:OD1	2.11	0.49
1:P:70:PRO:HG3	1:P:94:GLN:HA	1.94	0.49
2:O:190:THR:O	2:O:194:THR:HG23	2.12	0.49
2:A:168:GLU:O	2:A:202:PHE:N	2.33	0.49
2:C:271:THR:HG22	2:C:301:GLN:HA	1.94	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:7:ILE:HA	1:F:64:ILE:HG22	1.93	0.49
1:F:110:ALA:O	1:F:113:VAL:HG12	2.11	0.49
2:E:105:ARG:CZ	1:H:251:ARG:HD3	2.42	0.49
1:H:72:THR:O	1:H:76:VAL:N	2.40	0.49
2:I:105:ARG:CZ	1:L:251:ARG:HD3	2.42	0.49
2:K:269:LEU:HD23	2:K:270:ALA:N	2.27	0.49
1:B:21:TRP:HA	1:B:24:ILE:HG12	1.94	0.49
1:D:21:TRP:HA	1:D:24:ILE:HG12	1.94	0.49
1:D:70:PRO:HG3	1:D:94:GLN:HA	1.94	0.49
1:H:101:TRP:NE1	1:H:146:GLY:HA2	2.27	0.49
2:G:213:CYS:SG	2:G:227:LEU:HD23	2.53	0.49
2:I:192:HIS:ND1	2:I:424:ASP:OD2	2.45	0.49
2:K:105:ARG:CZ	1:N:251:ARG:HD3	2.42	0.49
1:N:197:ASP:HA	1:N:264:HIS:CD2	2.48	0.49
2:M:213:CYS:SG	2:M:227:LEU:HD23	2.53	0.49
2:M:287:SER:HB3	2:M:290:GLU:HB2	1.94	0.49
1:P:197:ASP:HA	1:P:264:HIS:CD2	2.48	0.49
2:O:213:CYS:SG	2:O:227:LEU:HD23	2.53	0.49
1:B:197:ASP:HA	1:B:264:HIS:CD2	2.48	0.49
2:A:47:ASP:OD1	2:A:48:SER:N	2.41	0.49
2:A:198:SER:OG	2:A:266:HIS:NE2	2.31	0.49
2:A:269:LEU:HD23	2:A:270:ALA:N	2.27	0.49
2:A:271:THR:HG22	2:A:301:GLN:HA	1.94	0.49
1:H:21:TRP:HA	1:H:24:ILE:HG12	1.94	0.49
2:G:136:LEU:HD13	2:G:167:LEU:HB3	1.93	0.49
1:J:197:ASP:HA	1:J:264:HIS:CD2	2.48	0.49
2:I:102:ASN:ND2	2:I:411:GLU:OE2	2.44	0.49
2:I:190:THR:O	2:I:194:THR:HG23	2.12	0.49
2:I:287:SER:HB3	2:I:290:GLU:HB2	1.94	0.49
1:L:7:ILE:HA	1:L:64:ILE:HG22	1.93	0.49
1:L:101:TRP:NE1	1:L:146:GLY:HA2	2.27	0.49
2:K:344:VAL:HG12	2:K:346:TRP:H	1.77	0.49
1:N:72:THR:O	1:N:76:VAL:N	2.40	0.49
2:M:40:LYS:O	2:M:41:THR:OG1	2.26	0.49
2:M:269:LEU:HD23	2:M:270:ALA:N	2.27	0.49
2:C:213:CYS:SG	2:C:227:LEU:HD23	2.53	0.49
2:E:102:ASN:ND2	2:E:411:GLU:OE2	2.44	0.49
2:I:198:SER:OG	2:I:266:HIS:NE2	2.31	0.49
2:M:102:ASN:ND2	2:M:411:GLU:OE2	2.44	0.49
2:O:70:LEU:HA	2:O:95:GLY:HA3	1.94	0.49
2:O:141:PHE:O	2:O:147:SER:OG	2.26	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:344:VAL:HG12	2:A:346:TRP:H	1.77	0.49
1:D:197:ASP:HA	1:D:264:HIS:CD2	2.48	0.49
1:F:21:TRP:HA	1:F:24:ILE:HG12	1.94	0.49
1:F:70:PRO:HG3	1:F:94:GLN:HA	1.94	0.49
1:F:197:ASP:HA	1:F:264:HIS:CD2	2.48	0.49
2:E:213:CYS:SG	2:E:227:LEU:HD23	2.53	0.49
1:H:197:ASP:HA	1:H:264:HIS:CD2	2.48	0.49
2:G:269:LEU:HD23	2:G:270:ALA:N	2.27	0.49
2:G:271:THR:HG22	2:G:301:GLN:HA	1.94	0.49
1:J:70:PRO:HG3	1:J:94:GLN:HA	1.94	0.49
2:K:213:CYS:SG	2:K:227:LEU:HD23	2.53	0.49
2:K:287:SER:HB3	2:K:290:GLU:HB2	1.94	0.49
1:N:101:TRP:NE1	1:N:146:GLY:HA2	2.27	0.49
2:M:105:ARG:CZ	1:P:251:ARG:HD3	2.42	0.49
2:I:108:TYR:O	2:I:112:LYS:NZ	2.29	0.49
2:I:160:ASP:OD1	2:I:161:TYR:N	2.45	0.49
2:O:108:TYR:O	2:O:112:LYS:NZ	2.29	0.49
1:B:251:ARG:HD3	2:O:105:ARG:CZ	2.42	0.48
2:C:269:LEU:HD23	2:C:270:ALA:N	2.27	0.48
2:I:213:CYS:SG	2:I:227:LEU:HD23	2.53	0.48
2:O:271:THR:HG22	2:O:301:GLN:HA	1.94	0.48
2:C:47:ASP:OD1	2:C:48:SER:N	2.41	0.48
1:H:166:THR:HG23	1:H:196:THR:HG21	1.95	0.48
2:G:287:SER:HB3	2:G:290:GLU:HB2	1.94	0.48
1:J:72:THR:O	1:J:76:VAL:N	2.40	0.48
1:J:166:THR:HG23	1:J:196:THR:HG21	1.95	0.48
1:L:117:LEU:HA	1:L:120:VAL:HG12	1.95	0.48
2:K:192:HIS:ND1	2:K:424:ASP:OD2	2.45	0.48
2:M:160:ASP:OD1	2:M:161:TYR:N	2.45	0.48
2:A:68:VAL:HG11	2:A:149:PHE:CE2	2.49	0.48
2:A:180:ALA:HA	1:D:256:ASN:ND2	2.29	0.48
2:A:213:CYS:SG	2:A:227:LEU:HD23	2.53	0.48
1:D:249:ASP:O	1:D:253:LEU:N	2.26	0.48
2:C:70:LEU:HA	2:C:95:GLY:HA3	1.94	0.48
2:C:180:ALA:HA	1:F:256:ASN:ND2	2.29	0.48
1:F:166:THR:HG23	1:F:196:THR:HG21	1.95	0.48
2:E:100:ALA:HB1	1:H:252:LYS:CB	2.44	0.48
2:I:68:VAL:HG11	2:I:149:PHE:CE2	2.49	0.48
2:K:66:VAL:HG23	2:K:91:GLN:O	2.14	0.48
2:M:68:VAL:HG11	2:M:149:PHE:CE2	2.49	0.48
2:M:344:VAL:HG12	2:M:346:TRP:H	1.77	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:68:VAL:HG11	2:O:149:PHE:CE2	2.49	0.48
2:O:192:HIS:ND1	2:O:424:ASP:OD2	2.45	0.48
2:C:100:ALA:HB1	1:F:252:LYS:CB	2.44	0.48
2:C:393:HIS:HA	2:C:396:ASP:OD1	2.14	0.48
2:E:68:VAL:HG11	2:E:149:PHE:CE2	2.49	0.48
2:G:7:ILE:HG22	2:G:137:VAL:HA	1.96	0.48
2:G:100:ALA:HB1	1:J:252:LYS:CB	2.44	0.48
1:J:6:HIS:HD1	1:J:21:TRP:HZ2	1.62	0.48
2:I:100:ALA:HB1	1:L:252:LYS:CB	2.44	0.48
1:L:166:THR:HG23	1:L:196:THR:HG21	1.95	0.48
2:K:16:ILE:HA	2:K:228:ASN:OD1	2.14	0.48
2:K:168:GLU:O	2:K:202:PHE:N	2.33	0.48
1:N:6:HIS:HD1	1:N:21:TRP:HZ2	1.62	0.48
2:C:192:HIS:ND1	2:C:424:ASP:OD2	2.45	0.48
1:F:322:SER:OG	1:F:325:GLU:HB3	2.13	0.48
1:H:7:ILE:HA	1:H:64:ILE:HG22	1.93	0.48
2:G:393:HIS:HA	2:G:396:ASP:OD1	2.14	0.48
1:J:101:TRP:NE1	1:J:146:GLY:HA2	2.27	0.48
2:I:7:ILE:HG22	2:I:137:VAL:HA	1.96	0.48
2:I:40:LYS:O	2:I:41:THR:OG1	2.26	0.48
2:I:91:GLN:O	2:I:92:LEU:HD23	2.14	0.48
1:L:142:GLY:C	1:L:144:GLY:H	2.17	0.48
1:L:322:SER:OG	1:L:325:GLU:HB3	2.14	0.48
1:N:70:PRO:HG3	1:N:94:GLN:HA	1.94	0.48
1:N:117:LEU:HA	1:N:120:VAL:HG12	1.95	0.48
1:N:322:SER:OG	1:N:325:GLU:HB3	2.13	0.48
2:M:7:ILE:HG22	2:M:137:VAL:HA	1.96	0.48
2:O:344:VAL:HG12	2:O:346:TRP:H	1.77	0.48
2:O:393:HIS:HA	2:O:396:ASP:OD1	2.14	0.48
1:B:256:ASN:ND2	2:O:180:ALA:HA	2.29	0.48
2:E:180:ALA:HA	1:H:256:ASN:ND2	2.29	0.48
2:K:407:TRP:CE3	1:N:255:VAL:HG12	2.49	0.48
2:A:66:VAL:HG23	2:A:91:GLN:O	2.14	0.48
1:D:149:THR:HG21	1:D:191:GLN:HG3	1.96	0.48
2:C:7:ILE:HG22	2:C:137:VAL:HA	1.96	0.48
1:F:181:GLU:O	1:F:184:ASN:N	2.47	0.48
1:H:6:HIS:HD1	1:H:21:TRP:HZ2	1.62	0.48
2:G:66:VAL:HG23	2:G:91:GLN:O	2.14	0.48
2:G:407:TRP:CE3	1:J:255:VAL:HG12	2.49	0.48
2:I:16:ILE:HA	2:I:228:ASN:OD1	2.14	0.48
2:K:180:ALA:HA	1:N:256:ASN:ND2	2.29	0.48

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:42:LEU:HD11	1:N:356:ILE:HD13	1.96	0.48
1:N:142:GLY:C	1:N:144:GLY:H	2.17	0.48
2:M:16:ILE:HA	2:M:228:ASN:OD1	2.14	0.48
2:M:271:THR:HG22	2:M:301:GLN:HA	1.94	0.48
1:P:6:HIS:HD1	1:P:21:TRP:HZ2	1.62	0.48
2:O:16:ILE:HA	2:O:228:ASN:OD1	2.14	0.48
1:B:181:GLU:O	1:B:184:ASN:N	2.47	0.48
1:D:117:LEU:HA	1:D:120:VAL:HG12	1.95	0.48
1:D:322:SER:OG	1:D:325:GLU:HB3	2.14	0.48
2:C:117:LEU:O	2:C:121:ARG:HG2	2.14	0.48
2:E:66:VAL:HG23	2:E:91:GLN:O	2.14	0.48
2:G:91:GLN:O	2:G:92:LEU:HD23	2.14	0.48
1:J:117:LEU:HA	1:J:120:VAL:HG12	1.95	0.48
1:J:142:GLY:C	1:J:144:GLY:H	2.17	0.48
2:K:91:GLN:O	2:K:92:LEU:HD23	2.14	0.48
2:K:100:ALA:HB1	1:N:252:LYS:CB	2.44	0.48
2:K:393:HIS:HA	2:K:396:ASP:OD1	2.14	0.48
2:M:192:HIS:ND1	2:M:424:ASP:OD2	2.45	0.48
2:M:393:HIS:HA	2:M:396:ASP:OD1	2.14	0.48
1:P:322:SER:OG	1:P:325:GLU:HB3	2.14	0.48
2:O:102:ASN:ND2	2:O:411:GLU:OE2	2.44	0.48
2:A:91:GLN:O	2:A:92:LEU:HD23	2.14	0.48
2:A:100:ALA:HB1	1:D:252:LYS:CB	2.44	0.48
2:C:16:ILE:HA	2:C:228:ASN:OD1	2.14	0.48
2:C:68:VAL:HG11	2:C:149:PHE:CE2	2.49	0.48
2:C:102:ASN:ND2	2:C:411:GLU:OE2	2.44	0.48
2:E:16:ILE:HA	2:E:228:ASN:OD1	2.14	0.48
1:H:150:LEU:HG	1:H:154:LYS:HZ3	1.78	0.48
2:G:16:ILE:HA	2:G:228:ASN:OD1	2.14	0.48
2:G:407:TRP:CD2	1:J:255:VAL:HG12	2.49	0.48
1:J:322:SER:OG	1:J:325:GLU:HB3	2.13	0.48
2:I:180:ALA:HA	1:L:256:ASN:ND2	2.29	0.48
1:L:197:ASP:HA	1:L:264:HIS:CD2	2.48	0.48
1:P:149:THR:HG21	1:P:191:GLN:HG3	1.96	0.48
1:B:166:THR:HG23	1:B:196:THR:HG21	1.95	0.48
2:A:7:ILE:HG22	2:A:137:VAL:HA	1.96	0.48
2:C:66:VAL:HG23	2:C:91:GLN:O	2.14	0.48
1:F:97:ALA:CA	1:F:143:THR:HG23	2.39	0.48
2:E:393:HIS:HA	2:E:396:ASP:OD1	2.14	0.48
2:E:407:TRP:CD2	1:H:255:VAL:HG12	2.49	0.48
1:H:12:CYS:SG	1:H:138:SER:OG	2.64	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:322:SER:OG	1:H:325:GLU:HB3	2.14	0.48
1:J:42:LEU:HD11	1:J:356:ILE:HD13	1.96	0.48
1:J:181:GLU:O	1:J:184:ASN:N	2.47	0.48
2:I:66:VAL:HG23	2:I:91:GLN:O	2.14	0.48
1:L:6:HIS:HD1	1:L:21:TRP:HZ2	1.62	0.48
1:L:72:THR:O	1:L:76:VAL:N	2.40	0.48
2:M:117:LEU:O	2:M:121:ARG:HG2	2.14	0.48
2:O:117:LEU:O	2:O:121:ARG:HG2	2.14	0.48
1:B:149:THR:HG21	1:B:191:GLN:HG3	1.96	0.47
1:B:322:SER:OG	1:B:325:GLU:HB3	2.13	0.47
2:A:393:HIS:HA	2:A:396:ASP:OD1	2.14	0.47
1:D:166:THR:HG23	1:D:196:THR:HG21	1.95	0.47
1:F:117:LEU:HA	1:F:120:VAL:HG12	1.95	0.47
1:F:149:THR:HG21	1:F:191:GLN:HG3	1.96	0.47
2:I:271:THR:HG22	2:I:301:GLN:HA	1.94	0.47
2:K:68:VAL:HG11	2:K:149:PHE:CE2	2.49	0.47
1:N:149:THR:HG21	1:N:191:GLN:HG3	1.96	0.47
1:P:142:GLY:C	1:P:144:GLY:H	2.17	0.47
2:O:7:ILE:HG22	2:O:137:VAL:HA	1.96	0.47
2:O:69:ASP:OD1	2:O:70:LEU:N	2.45	0.47
2:O:91:GLN:O	2:O:92:LEU:HD23	2.14	0.47
1:B:42:LEU:HD11	1:B:356:ILE:HD13	1.96	0.47
1:B:70:PRO:HG3	1:B:94:GLN:HA	1.94	0.47
2:E:407:TRP:CE3	1:H:255:VAL:HG12	2.49	0.47
2:G:192:HIS:ND1	2:G:424:ASP:OD2	2.45	0.47
2:G:213:CYS:HA	2:G:217:LEU:HB3	1.96	0.47
2:I:213:CYS:HA	2:I:217:LEU:HB3	1.96	0.47
2:I:329:ASN:HA	2:I:332:ILE:HD12	1.96	0.47
2:I:407:TRP:CE3	1:L:255:VAL:HG12	2.49	0.47
2:K:102:ASN:ND2	2:K:411:GLU:OE2	2.44	0.47
1:N:166:THR:HG23	1:N:196:THR:HG21	1.95	0.47
1:N:181:GLU:O	1:N:184:ASN:N	2.47	0.47
2:M:407:TRP:CE3	1:P:255:VAL:HG12	2.49	0.47
1:P:101:TRP:NE1	1:P:146:GLY:HA2	2.27	0.47
1:B:6:HIS:HD1	1:B:21:TRP:HZ2	1.62	0.47
1:B:255:VAL:HG12	2:O:407:TRP:CE3	2.49	0.47
1:B:255:VAL:HG12	2:O:407:TRP:CD2	2.49	0.47
2:A:117:LEU:O	2:A:121:ARG:HG2	2.14	0.47
1:D:42:LEU:HD11	1:D:356:ILE:HD13	1.96	0.47
2:G:117:LEU:O	2:G:121:ARG:HG2	2.14	0.47
2:K:7:ILE:HG22	2:K:137:VAL:HA	1.96	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:329:ASN:HA	2:M:332:ILE:HD12	1.96	0.47
2:C:69:ASP:OD1	2:C:70:LEU:N	2.45	0.47
2:C:407:TRP:CD2	1:F:255:VAL:HG12	2.49	0.47
1:F:6:HIS:HD1	1:F:21:TRP:HZ2	1.62	0.47
2:E:47:ASP:OD1	2:E:48:SER:N	2.41	0.47
1:H:181:GLU:O	1:H:184:ASN:N	2.47	0.47
2:G:180:ALA:HA	1:J:256:ASN:ND2	2.29	0.47
1:J:97:ALA:CA	1:J:143:THR:HG23	2.39	0.47
2:I:393:HIS:HA	2:I:396:ASP:OD1	2.14	0.47
1:L:181:GLU:O	1:L:184:ASN:N	2.47	0.47
2:K:117:LEU:O	2:K:121:ARG:HG2	2.14	0.47
1:P:42:LEU:HD11	1:P:356:ILE:HD13	1.96	0.47
2:O:66:VAL:HG23	2:O:91:GLN:O	2.14	0.47
1:B:117:LEU:HA	1:B:120:VAL:HG12	1.95	0.47
2:A:16:ILE:HA	2:A:228:ASN:OD1	2.14	0.47
2:A:102:ASN:ND2	2:A:411:GLU:OE2	2.44	0.47
2:C:91:GLN:O	2:C:92:LEU:HD23	2.14	0.47
2:C:407:TRP:CE3	1:F:255:VAL:HG12	2.49	0.47
1:F:189:ILE:HG23	1:F:415:MET:HE3	1.96	0.47
2:E:7:ILE:HG22	2:E:137:VAL:HA	1.96	0.47
1:H:142:GLY:C	1:H:144:GLY:H	2.17	0.47
2:G:240:ALA:HA	2:G:243:ARG:HG3	1.97	0.47
1:J:150:LEU:HG	1:J:154:LYS:HZ3	1.79	0.47
2:I:407:TRP:CD2	1:L:255:VAL:HG12	2.49	0.47
2:M:91:GLN:O	2:M:92:LEU:HD23	2.14	0.47
1:P:117:LEU:HA	1:P:120:VAL:HG12	1.95	0.47
2:A:8:HIS:O	2:A:68:VAL:N	2.47	0.47
2:A:329:ASN:HA	2:A:332:ILE:HD12	1.96	0.47
1:D:6:HIS:HD1	1:D:21:TRP:HZ2	1.62	0.47
1:D:7:ILE:HG22	1:D:135:LEU:HD13	1.97	0.47
1:F:42:LEU:HD11	1:F:356:ILE:HD13	1.96	0.47
1:F:182:PRO:HG3	1:F:384:GLN:OE1	2.15	0.47
2:E:240:ALA:HA	2:E:243:ARG:HG3	1.97	0.47
2:G:68:VAL:HG11	2:G:149:PHE:CE2	2.49	0.47
1:L:149:THR:HG21	1:L:191:GLN:HG3	1.96	0.47
1:L:282:ARG:HD3	1:L:282:ARG:HA	1.79	0.47
2:K:115:ILE:HD11	2:K:153:LEU:HD13	1.97	0.47
2:K:407:TRP:CD2	1:N:255:VAL:HG12	2.49	0.47
1:N:7:ILE:HG22	1:N:135:LEU:HD13	1.97	0.47
2:O:8:HIS:O	2:O:68:VAL:N	2.47	0.47
1:B:21:TRP:CZ3	1:B:61:PRO:HB3	2.50	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:GLY:C	1:B:144:GLY:H	2.17	0.47
2:A:240:ALA:HA	2:A:243:ARG:HG3	1.97	0.47
1:D:151:LEU:O	1:D:155:VAL:HG22	2.15	0.47
1:D:181:GLU:O	1:D:184:ASN:N	2.47	0.47
2:C:8:HIS:O	2:C:68:VAL:N	2.47	0.47
2:C:240:ALA:HA	2:C:243:ARG:HG3	1.97	0.47
1:F:101:TRP:NE1	1:F:146:GLY:HA2	2.27	0.47
1:F:150:LEU:HG	1:F:154:LYS:HZ1	1.76	0.47
2:E:8:HIS:O	2:E:68:VAL:N	2.47	0.47
2:E:91:GLN:O	2:E:92:LEU:HD23	2.14	0.47
2:E:117:LEU:O	2:E:121:ARG:HG2	2.14	0.47
1:H:117:LEU:HA	1:H:120:VAL:HG12	1.95	0.47
1:H:149:THR:HG21	1:H:191:GLN:HG3	1.96	0.47
1:H:151:LEU:O	1:H:155:VAL:HG22	2.15	0.47
2:G:8:HIS:O	2:G:68:VAL:N	2.47	0.47
2:G:33:ASP:OD1	2:G:34:GLY:N	2.48	0.47
2:G:172:TYR:HB3	2:G:205:ASP:HA	1.97	0.47
2:I:115:ILE:HD11	2:I:153:LEU:HD13	1.97	0.47
2:I:117:LEU:O	2:I:121:ARG:HG2	2.14	0.47
2:I:240:ALA:HA	2:I:243:ARG:HG3	1.97	0.47
2:K:213:CYS:HA	2:K:217:LEU:HB3	1.96	0.47
2:M:8:HIS:O	2:M:68:VAL:N	2.47	0.47
2:M:100:ALA:HB1	1:P:252:LYS:CB	2.44	0.47
2:M:180:ALA:HA	1:P:256:ASN:ND2	2.29	0.47
2:M:240:ALA:HA	2:M:243:ARG:HG3	1.97	0.47
2:M:407:TRP:CD2	1:P:255:VAL:HG12	2.49	0.47
1:P:181:GLU:O	1:P:184:ASN:N	2.47	0.47
2:O:33:ASP:OD1	2:O:34:GLY:N	2.48	0.47
2:O:40:LYS:O	2:O:41:THR:OG1	2.26	0.47
2:O:240:ALA:HA	2:O:243:ARG:HG3	1.97	0.47
1:B:252:LYS:CB	2:O:100:ALA:HB1	2.44	0.47
2:A:407:TRP:CD2	1:D:255:VAL:HG12	2.49	0.47
2:A:407:TRP:CE3	1:D:255:VAL:HG12	2.49	0.47
2:E:172:TYR:HB3	2:E:205:ASP:HA	1.97	0.47
2:E:213:CYS:HA	2:E:217:LEU:HB3	1.96	0.47
2:I:142:GLY:HA3	2:I:183:GLU:OE1	2.15	0.47
2:I:172:TYR:HB3	2:I:205:ASP:HA	1.97	0.47
2:K:240:ALA:HA	2:K:243:ARG:HG3	1.97	0.47
2:M:66:VAL:HG23	2:M:91:GLN:O	2.14	0.47
1:B:97:ALA:HB1	1:B:143:THR:HG1	1.79	0.47
1:B:216:LYS:HA	1:B:216:LYS:HD3	1.81	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:69:ASP:OD1	2:A:70:LEU:N	2.45	0.47
1:D:182:PRO:HG3	1:D:384:GLN:OE1	2.15	0.47
2:C:329:ASN:HA	2:C:332:ILE:HD12	1.96	0.47
1:F:142:GLY:C	1:F:144:GLY:H	2.17	0.47
2:E:329:ASN:HA	2:E:332:ILE:HD12	1.96	0.47
2:G:142:GLY:HA3	2:G:183:GLU:OE1	2.15	0.47
1:J:280:GLN:NE2	1:J:361:LEU:HA	2.30	0.47
1:L:42:LEU:HD11	1:L:356:ILE:HD13	1.96	0.47
1:L:151:LEU:O	1:L:155:VAL:HG22	2.15	0.47
2:K:8:HIS:O	2:K:68:VAL:N	2.47	0.47
1:N:21:TRP:CZ3	1:N:61:PRO:HB3	2.50	0.47
1:B:7:ILE:HG22	1:B:135:LEU:HD13	1.97	0.47
1:B:151:LEU:O	1:B:155:VAL:HG22	2.15	0.47
2:A:33:ASP:OD1	2:A:34:GLY:N	2.48	0.47
2:A:265:ILE:HG12	2:A:432:TYR:HE1	1.80	0.47
1:F:151:LEU:O	1:F:155:VAL:HG22	2.15	0.47
1:H:182:PRO:HG3	1:H:384:GLN:OE1	2.15	0.47
2:G:265:ILE:HG12	2:G:432:TYR:HE1	1.80	0.47
1:L:181:GLU:HA	1:L:184:ASN:ND2	2.24	0.47
1:N:40:SER:OG	1:N:41:ASP:N	2.48	0.47
1:N:280:GLN:NE2	1:N:361:LEU:HA	2.30	0.47
1:B:182:PRO:HG3	1:B:384:GLN:OE1	2.15	0.46
1:F:7:ILE:HG22	1:F:135:LEU:HD13	1.97	0.46
2:E:33:ASP:OD1	2:E:34:GLY:N	2.48	0.46
1:H:280:GLN:NE2	1:H:361:LEU:HA	2.30	0.46
1:J:21:TRP:CZ3	1:J:61:PRO:HB3	2.50	0.46
2:I:33:ASP:OD1	2:I:34:GLY:N	2.48	0.46
2:K:172:TYR:HB3	2:K:205:ASP:HA	1.97	0.46
2:K:272:TYR:CE1	2:K:274:PRO:HD2	2.51	0.46
2:M:172:TYR:HB3	2:M:205:ASP:HA	1.97	0.46
1:P:151:LEU:O	1:P:155:VAL:HG22	2.15	0.46
2:A:40:LYS:O	2:A:41:THR:OG1	2.26	0.46
1:D:21:TRP:CZ3	1:D:61:PRO:HB3	2.50	0.46
2:C:172:TYR:HB3	2:C:205:ASP:HA	1.97	0.46
2:C:265:ILE:HG12	2:C:432:TYR:HE1	1.80	0.46
2:G:115:ILE:HD11	2:G:153:LEU:HD13	1.97	0.46
1:J:149:THR:HG21	1:J:191:GLN:HG3	1.96	0.46
1:J:151:LEU:O	1:J:155:VAL:HG22	2.15	0.46
2:I:8:HIS:O	2:I:68:VAL:N	2.47	0.46
2:M:115:ILE:HD11	2:M:153:LEU:HD13	1.97	0.46
1:P:166:THR:HG23	1:P:196:THR:HG21	1.95	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:98:GLY:O	1:D:100:ASN:N	2.48	0.46
1:D:101:TRP:NE1	1:D:146:GLY:HA2	2.27	0.46
2:C:115:ILE:HD11	2:C:153:LEU:HD13	1.97	0.46
1:F:21:TRP:CZ3	1:F:61:PRO:HB3	2.50	0.46
2:E:142:GLY:HA3	2:E:183:GLU:OE1	2.15	0.46
2:E:272:TYR:CE1	2:E:274:PRO:HD2	2.51	0.46
1:H:7:ILE:HG22	1:H:135:LEU:HD13	1.97	0.46
1:J:7:ILE:HG22	1:J:135:LEU:HD13	1.97	0.46
1:L:280:GLN:NE2	1:L:361:LEU:HA	2.30	0.46
2:K:142:GLY:HA3	2:K:183:GLU:OE1	2.15	0.46
2:M:69:ASP:OD1	2:M:70:LEU:N	2.45	0.46
2:A:213:CYS:HA	2:A:217:LEU:HB3	1.96	0.46
1:D:142:GLY:C	1:D:144:GLY:H	2.17	0.46
2:C:142:GLY:HA3	2:C:183:GLU:OE1	2.15	0.46
2:E:265:ILE:HG12	2:E:432:TYR:HE1	1.80	0.46
1:H:21:TRP:CZ3	1:H:61:PRO:HB3	2.50	0.46
2:G:202:PHE:CE1	2:G:268:PRO:HG2	2.51	0.46
2:I:272:TYR:CE1	2:I:274:PRO:HD2	2.51	0.46
1:L:7:ILE:HG22	1:L:135:LEU:HD13	1.97	0.46
1:N:73:MET:HA	1:N:76:VAL:HB	1.98	0.46
2:M:33:ASP:OD1	2:M:34:GLY:N	2.48	0.46
2:M:142:GLY:HA3	2:M:183:GLU:OE1	2.15	0.46
1:P:7:ILE:HG22	1:P:135:LEU:HD13	1.97	0.46
1:P:182:PRO:HG3	1:P:384:GLN:OE1	2.15	0.46
2:O:172:TYR:HB3	2:O:205:ASP:HA	1.97	0.46
2:O:213:CYS:HA	2:O:217:LEU:HB3	1.96	0.46
2:A:115:ILE:HD11	2:A:153:LEU:HD13	1.97	0.46
2:A:142:GLY:HA3	2:A:183:GLU:OE1	2.15	0.46
1:D:150:LEU:HG	1:D:154:LYS:HZ3	1.79	0.46
1:J:40:SER:OG	1:J:41:ASP:N	2.48	0.46
1:J:181:GLU:HA	1:J:184:ASN:ND2	2.24	0.46
2:K:33:ASP:OD1	2:K:34:GLY:N	2.48	0.46
2:K:305:CYS:O	2:K:307:PRO:HD3	2.16	0.46
2:O:265:ILE:HG12	2:O:432:TYR:HE1	1.80	0.46
1:B:98:GLY:O	1:B:100:ASN:N	2.48	0.46
1:H:40:SER:OG	1:H:41:ASP:N	2.48	0.46
2:G:118:VAL:HG21	2:G:149:PHE:HZ	1.81	0.46
2:I:323:VAL:HG21	2:I:357:TYR:HE1	1.81	0.46
1:L:40:SER:OG	1:L:41:ASP:N	2.48	0.46
1:L:182:PRO:HG3	1:L:384:GLN:OE1	2.15	0.46
2:K:265:ILE:HG12	2:K:432:TYR:HE1	1.80	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:182:PRO:HG3	1:N:384:GLN:OE1	2.15	0.46
2:M:213:CYS:HA	2:M:217:LEU:HB3	1.96	0.46
2:M:231:ILE:HA	2:M:234:ILE:HG22	1.98	0.46
1:P:280:GLN:NE2	1:P:361:LEU:HA	2.30	0.46
2:O:231:ILE:HA	2:O:234:ILE:HG22	1.97	0.46
2:O:272:TYR:CE1	2:O:274:PRO:HD2	2.51	0.46
2:C:213:CYS:HA	2:C:217:LEU:HB3	1.96	0.46
1:F:280:GLN:NE2	1:F:361:LEU:HA	2.30	0.46
1:H:19:LYS:NZ	1:H:227:HIS:HA	2.31	0.46
1:H:73:MET:HA	1:H:76:VAL:HB	1.98	0.46
1:H:189:ILE:HG23	1:H:415:MET:HE3	1.98	0.46
1:H:318:ARG:NE	1:H:358:PRO:HG3	2.31	0.46
2:G:272:TYR:CE1	2:G:274:PRO:HD2	2.51	0.46
2:G:323:VAL:HG21	2:G:357:TYR:HE1	1.81	0.46
2:I:47:ASP:HB3	2:I:49:PHE:CE1	2.51	0.46
2:K:231:ILE:HA	2:K:234:ILE:HG22	1.97	0.46
2:K:329:ASN:HA	2:K:332:ILE:HD12	1.96	0.46
1:N:19:LYS:NZ	1:N:227:HIS:HA	2.31	0.46
2:M:305:CYS:O	2:M:307:PRO:HD3	2.16	0.46
2:O:142:GLY:HA3	2:O:183:GLU:OE1	2.15	0.46
2:O:329:ASN:HA	2:O:332:ILE:HD12	1.96	0.46
2:A:172:TYR:HB3	2:A:205:ASP:HA	1.97	0.46
1:D:40:SER:OG	1:D:41:ASP:N	2.48	0.46
2:E:202:PHE:CE1	2:E:268:PRO:HG2	2.51	0.46
1:H:42:LEU:HD11	1:H:356:ILE:HD13	1.96	0.46
1:J:19:LYS:NZ	1:J:227:HIS:HA	2.31	0.46
1:J:98:GLY:O	1:J:100:ASN:N	2.48	0.46
1:L:19:LYS:NZ	1:L:227:HIS:HA	2.31	0.46
2:K:47:ASP:HB3	2:K:49:PHE:CE1	2.51	0.46
2:M:139:HIS:O	2:M:170:SER:HA	2.16	0.46
2:M:236:SER:O	2:M:243:ARG:NH1	2.40	0.46
1:P:21:TRP:CZ3	1:P:61:PRO:HB3	2.50	0.46
1:P:318:ARG:NE	1:P:358:PRO:HG3	2.31	0.46
2:O:118:VAL:HG21	2:O:149:PHE:HZ	1.81	0.46
2:A:2:ARG:HD3	2:A:133:GLN:HG2	1.98	0.46
2:A:47:ASP:HB3	2:A:49:PHE:CE1	2.51	0.46
2:A:118:VAL:HG21	2:A:149:PHE:HZ	1.81	0.46
2:A:139:HIS:O	2:A:170:SER:HA	2.16	0.46
2:C:305:CYS:O	2:C:307:PRO:HD3	2.16	0.46
1:J:182:PRO:HG3	1:J:384:GLN:OE1	2.15	0.46
2:I:139:HIS:O	2:I:170:SER:HA	2.16	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:318:ARG:NE	1:L:358:PRO:HG3	2.31	0.46
1:N:181:GLU:HA	1:N:184:ASN:ND2	2.24	0.46
1:P:19:LYS:NZ	1:P:227:HIS:HA	2.31	0.46
2:O:139:HIS:O	2:O:170:SER:HA	2.16	0.46
1:B:40:SER:OG	1:B:41:ASP:N	2.48	0.46
2:C:47:ASP:HB3	2:C:49:PHE:CE1	2.51	0.46
2:C:118:VAL:HG21	2:C:149:PHE:HZ	1.81	0.46
1:F:40:SER:OG	1:F:41:ASP:N	2.48	0.46
1:F:73:MET:HA	1:F:76:VAL:HB	1.98	0.46
1:F:196:THR:HG22	1:F:198:GLU:H	1.82	0.46
2:E:2:ARG:HD3	2:E:133:GLN:HG2	1.98	0.46
2:E:115:ILE:HD11	2:E:153:LEU:HD13	1.97	0.46
2:E:202:PHE:HE1	2:E:268:PRO:HG2	1.81	0.46
2:E:305:CYS:O	2:E:307:PRO:HD3	2.16	0.46
2:G:47:ASP:HB3	2:G:49:PHE:CE1	2.51	0.46
2:G:329:ASN:HA	2:G:332:ILE:HD12	1.96	0.46
1:J:8:GLN:NE2	1:J:14:ASN:HA	2.31	0.46
1:J:73:MET:HA	1:J:76:VAL:HB	1.98	0.46
1:L:36:TYR:OH	1:L:40:SER:O	2.24	0.46
2:K:139:HIS:O	2:K:170:SER:HA	2.16	0.46
1:N:151:LEU:O	1:N:155:VAL:HG22	2.15	0.46
2:M:118:VAL:HG21	2:M:149:PHE:HZ	1.81	0.46
1:P:73:MET:HA	1:P:76:VAL:HB	1.98	0.46
2:O:115:ILE:HD11	2:O:153:LEU:HD13	1.97	0.46
1:D:8:GLN:NE2	1:D:14:ASN:HA	2.31	0.45
1:D:73:MET:HA	1:D:76:VAL:HB	1.98	0.45
1:D:190:HIS:ND1	1:D:411:ALA:HA	2.31	0.45
1:D:196:THR:HG22	1:D:198:GLU:H	1.82	0.45
1:F:190:HIS:ND1	1:F:411:ALA:HA	2.31	0.45
1:F:318:ARG:NE	1:F:358:PRO:HG3	2.31	0.45
1:J:282:ARG:HA	1:J:282:ARG:HD3	1.79	0.45
1:L:21:TRP:CZ3	1:L:61:PRO:HB3	2.50	0.45
2:K:323:VAL:HG21	2:K:357:TYR:HE1	1.81	0.45
2:M:2:ARG:NH1	2:M:132:LEU:O	2.49	0.45
2:M:265:ILE:HG12	2:M:432:TYR:HE1	1.80	0.45
1:P:8:GLN:NE2	1:P:14:ASN:HA	2.31	0.45
2:O:47:ASP:HB3	2:O:49:PHE:CE1	2.51	0.45
2:A:272:TYR:CE1	2:A:274:PRO:HD2	2.51	0.45
2:E:323:VAL:HG21	2:E:357:TYR:HE1	1.81	0.45
2:G:108:TYR:O	2:G:112:LYS:NZ	2.29	0.45
2:G:202:PHE:HE1	2:G:268:PRO:HG2	1.81	0.45

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2:ARG:NH1	2:I:132:LEU:O	2.49	0.45
2:I:91:GLN:HA	2:I:121:ARG:NH2	2.32	0.45
2:I:118:VAL:HG21	2:I:149:PHE:HZ	1.81	0.45
2:I:231:ILE:HA	2:I:234:ILE:HG22	1.98	0.45
1:L:190:HIS:ND1	1:L:411:ALA:HA	2.31	0.45
2:K:2:ARG:NH1	2:K:132:LEU:O	2.49	0.45
2:K:202:PHE:CE1	2:K:268:PRO:HG2	2.51	0.45
2:M:47:ASP:HB3	2:M:49:PHE:CE1	2.51	0.45
2:M:272:TYR:CE1	2:M:274:PRO:HD2	2.51	0.45
2:O:2:ARG:NH1	2:O:132:LEU:O	2.49	0.45
2:O:305:CYS:O	2:O:307:PRO:HD3	2.16	0.45
2:A:108:TYR:O	2:A:112:LYS:NZ	2.29	0.45
2:A:305:CYS:O	2:A:307:PRO:HD3	2.16	0.45
2:C:33:ASP:OD1	2:C:34:GLY:N	2.48	0.45
2:E:47:ASP:HB3	2:E:49:PHE:CE1	2.51	0.45
2:G:2:ARG:HD3	2:G:133:GLN:HG2	1.98	0.45
2:G:139:HIS:ND1	2:G:146:GLY:O	2.50	0.45
2:G:305:CYS:O	2:G:307:PRO:HD3	2.16	0.45
2:I:202:PHE:CE1	2:I:268:PRO:HG2	2.51	0.45
1:L:73:MET:HA	1:L:76:VAL:HB	1.98	0.45
1:L:329:GLN:HG2	1:L:330:MET:HE3	1.98	0.45
1:N:8:GLN:NE2	1:N:14:ASN:HA	2.31	0.45
1:N:190:HIS:ND1	1:N:411:ALA:HA	2.31	0.45
1:P:40:SER:OG	1:P:41:ASP:N	2.48	0.45
1:B:73:MET:HA	1:B:76:VAL:HB	1.98	0.45
2:A:231:ILE:HA	2:A:234:ILE:HG22	1.98	0.45
2:C:272:TYR:CE1	2:C:274:PRO:HD2	2.51	0.45
2:E:118:VAL:HG21	2:E:149:PHE:HZ	1.81	0.45
2:E:139:HIS:ND1	2:E:146:GLY:O	2.50	0.45
2:E:231:ILE:HA	2:E:234:ILE:HG22	1.98	0.45
1:H:187:LEU:HD11	1:H:408:PHE:CZ	2.52	0.45
1:H:190:HIS:ND1	1:H:411:ALA:HA	2.31	0.45
1:H:196:THR:HG22	1:H:198:GLU:H	1.82	0.45
2:G:139:HIS:O	2:G:170:SER:HA	2.16	0.45
2:K:118:VAL:HG21	2:K:149:PHE:HZ	1.81	0.45
2:O:2:ARG:HD3	2:O:133:GLN:HG2	1.98	0.45
1:B:101:TRP:NE1	1:B:146:GLY:HA2	2.27	0.45
1:B:187:LEU:HD11	1:B:408:PHE:CZ	2.52	0.45
1:D:187:LEU:HD11	1:D:408:PHE:CZ	2.52	0.45
1:D:318:ARG:NE	1:D:358:PRO:HG3	2.31	0.45
2:C:139:HIS:O	2:C:170:SER:HA	2.16	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:231:ILE:HA	2:C:234:ILE:HG22	1.97	0.45
1:F:8:GLN:NE2	1:F:14:ASN:HA	2.31	0.45
1:F:187:LEU:HD11	1:F:408:PHE:CZ	2.52	0.45
2:E:91:GLN:HA	2:E:121:ARG:NH2	2.32	0.45
2:G:2:ARG:NH1	2:G:132:LEU:O	2.49	0.45
2:G:91:GLN:HA	2:G:121:ARG:NH2	2.32	0.45
2:G:231:ILE:HA	2:G:234:ILE:HG22	1.97	0.45
1:L:8:GLN:NE2	1:L:14:ASN:HA	2.31	0.45
1:L:98:GLY:O	1:L:100:ASN:N	2.48	0.45
2:K:91:GLN:HA	2:K:121:ARG:NH2	2.32	0.45
1:N:187:LEU:HD11	1:N:408:PHE:CZ	2.52	0.45
2:A:139:HIS:ND1	2:A:146:GLY:O	2.50	0.45
1:D:280:GLN:NE2	1:D:361:LEU:HA	2.30	0.45
2:C:91:GLN:HA	2:C:121:ARG:NH2	2.32	0.45
2:C:139:HIS:ND1	2:C:146:GLY:O	2.50	0.45
2:C:236:SER:O	2:C:243:ARG:NH1	2.40	0.45
1:F:19:LYS:NZ	1:F:227:HIS:HA	2.31	0.45
1:J:318:ARG:NE	1:J:358:PRO:HG3	2.31	0.45
2:I:139:HIS:ND1	2:I:146:GLY:O	2.50	0.45
1:L:293:MET:HG3	1:L:294:PHE:CD1	2.52	0.45
1:N:150:LEU:HG	1:N:154:LYS:HZ3	1.79	0.45
1:N:196:THR:HG22	1:N:198:GLU:H	1.82	0.45
2:M:202:PHE:HE1	2:M:268:PRO:HG2	1.81	0.45
1:P:190:HIS:ND1	1:P:411:ALA:HA	2.31	0.45
2:O:202:PHE:HE1	2:O:268:PRO:HG2	1.81	0.45
1:B:137:HIS:O	1:B:168:SER:HA	2.17	0.45
1:B:280:GLN:NE2	1:B:361:LEU:HA	2.30	0.45
1:B:332:ALA:O	1:B:336:LYS:HG2	2.17	0.45
1:D:332:ALA:O	1:D:336:LYS:HG2	2.17	0.45
1:F:332:ALA:O	1:F:336:LYS:HG2	2.17	0.45
2:E:168:GLU:O	2:E:202:PHE:N	2.33	0.45
1:J:187:LEU:HD11	1:J:408:PHE:CZ	2.52	0.45
1:J:293:MET:HG3	1:J:294:PHE:CD1	2.52	0.45
2:I:265:ILE:HG12	2:I:432:TYR:HE1	1.80	0.45
1:N:293:MET:HG3	1:N:294:PHE:CD1	2.52	0.45
1:N:329:GLN:HG2	1:N:330:MET:HE3	1.98	0.45
2:M:139:HIS:ND1	2:M:146:GLY:O	2.50	0.45
1:P:98:GLY:O	1:P:100:ASN:N	2.48	0.45
2:O:323:VAL:HG21	2:O:357:TYR:HE1	1.81	0.45
2:A:202:PHE:CE1	2:A:268:PRO:HG2	2.51	0.45
2:A:213:CYS:O	2:A:217:LEU:HB3	2.17	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:ALA:HB1	1:D:143:THR:HG1	1.81	0.45
2:C:313:MET:HA	2:C:344:VAL:HG23	1.99	0.45
2:E:213:CYS:O	2:E:217:LEU:HB3	2.17	0.45
1:J:190:HIS:ND1	1:J:411:ALA:HA	2.31	0.45
1:J:280:GLN:HE21	1:J:361:LEU:HD12	1.82	0.45
2:I:202:PHE:HE1	2:I:268:PRO:HG2	1.81	0.45
1:L:254:ALA:O	1:L:258:VAL:HG12	2.17	0.45
2:K:69:ASP:OD1	2:K:70:LEU:N	2.45	0.45
2:K:139:HIS:ND1	2:K:146:GLY:O	2.50	0.45
2:K:213:CYS:O	2:K:217:LEU:HB3	2.17	0.45
2:K:236:SER:O	2:K:243:ARG:NH1	2.40	0.45
1:N:137:HIS:O	1:N:168:SER:HA	2.17	0.45
1:N:282:ARG:HA	1:N:282:ARG:HD3	1.79	0.45
2:M:213:CYS:O	2:M:217:LEU:HB3	2.17	0.45
2:M:323:VAL:HG21	2:M:357:TYR:HE1	1.81	0.45
1:P:332:ALA:O	1:P:336:LYS:HG2	2.17	0.45
2:O:202:PHE:CE1	2:O:268:PRO:HG2	2.51	0.45
1:B:318:ARG:NE	1:B:358:PRO:HG3	2.31	0.45
2:C:323:VAL:HG21	2:C:357:TYR:HE1	1.81	0.45
1:H:332:ALA:O	1:H:336:LYS:HG2	2.17	0.45
2:I:305:CYS:O	2:I:307:PRO:HD3	2.16	0.45
1:N:318:ARG:NE	1:N:358:PRO:HG3	2.31	0.45
1:B:19:LYS:NZ	1:B:227:HIS:HA	2.31	0.45
2:A:323:VAL:HG21	2:A:357:TYR:HE1	1.81	0.45
1:D:113:VAL:HA	1:D:116:VAL:HB	1.99	0.45
2:C:202:PHE:HE1	2:C:268:PRO:HG2	1.81	0.45
1:F:98:GLY:O	1:F:100:ASN:N	2.48	0.45
1:H:98:GLY:O	1:H:100:ASN:N	2.48	0.45
1:H:293:MET:HG3	1:H:294:PHE:CD1	2.52	0.45
1:J:196:THR:HG22	1:J:198:GLU:H	1.82	0.45
1:L:189:ILE:HG23	1:L:415:MET:HE3	1.99	0.45
1:P:196:THR:HG22	1:P:198:GLU:H	1.82	0.45
1:B:113:VAL:HA	1:B:116:VAL:HB	1.99	0.44
1:B:190:HIS:ND1	1:B:411:ALA:HA	2.31	0.44
1:B:196:THR:HG22	1:B:198:GLU:H	1.82	0.44
2:A:202:PHE:HE1	2:A:268:PRO:HG2	1.81	0.44
2:E:2:ARG:NH1	2:E:132:LEU:O	2.49	0.44
2:E:40:LYS:O	2:E:41:THR:OG1	2.26	0.44
2:G:69:ASP:OD1	2:G:70:LEU:N	2.45	0.44
2:I:213:CYS:O	2:I:217:LEU:HB3	2.17	0.44
2:I:236:SER:O	2:I:243:ARG:NH1	2.40	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:100:ASN:HB3	1:L:103:LYS:HD3	1.99	0.44
1:L:187:LEU:HD11	1:L:408:PHE:CZ	2.52	0.44
2:K:313:MET:HA	2:K:344:VAL:HG23	1.99	0.44
1:N:98:GLY:O	1:N:100:ASN:N	2.48	0.44
2:O:139:HIS:ND1	2:O:146:GLY:O	2.50	0.44
2:O:192:HIS:NE2	2:O:420:GLU:OE1	2.51	0.44
1:B:103:LYS:HA	1:B:401:GLU:OE2	2.17	0.44
2:A:91:GLN:HA	2:A:121:ARG:NH2	2.32	0.44
1:F:254:ALA:O	1:F:258:VAL:HG12	2.17	0.44
2:E:313:MET:HA	2:E:344:VAL:HG23	1.99	0.44
1:H:8:GLN:NE2	1:H:14:ASN:HA	2.31	0.44
1:H:181:GLU:HA	1:H:184:ASN:ND2	2.24	0.44
2:M:202:PHE:CE1	2:M:268:PRO:HG2	2.51	0.44
1:B:8:GLN:NE2	1:B:14:ASN:HA	2.31	0.44
1:B:100:ASN:HB3	1:B:103:LYS:HD3	1.99	0.44
2:A:313:MET:HA	2:A:344:VAL:HG23	1.99	0.44
1:D:103:LYS:HA	1:D:401:GLU:OE2	2.17	0.44
1:F:113:VAL:HA	1:F:116:VAL:HB	1.99	0.44
1:F:293:MET:HG3	1:F:294:PHE:CD1	2.52	0.44
2:E:69:ASP:OD1	2:E:70:LEU:N	2.45	0.44
1:H:100:ASN:HB3	1:H:103:LYS:HD3	1.99	0.44
1:J:103:LYS:HA	1:J:401:GLU:OE2	2.17	0.44
1:J:329:GLN:HG2	1:J:330:MET:HE3	1.99	0.44
1:L:196:THR:HG22	1:L:198:GLU:H	1.82	0.44
1:P:97:ALA:CA	1:P:143:THR:HG23	2.39	0.44
2:O:91:GLN:HA	2:O:121:ARG:NH2	2.32	0.44
2:A:2:ARG:NH1	2:A:132:LEU:O	2.49	0.44
2:A:192:HIS:NE2	2:A:420:GLU:OE1	2.51	0.44
1:D:19:LYS:NZ	1:D:227:HIS:HA	2.31	0.44
2:C:2:ARG:HD3	2:C:133:GLN:HG2	1.98	0.44
2:C:202:PHE:CE1	2:C:268:PRO:HG2	2.51	0.44
2:C:213:CYS:O	2:C:217:LEU:HB3	2.17	0.44
1:F:137:HIS:O	1:F:168:SER:HA	2.17	0.44
1:F:280:GLN:HE21	1:F:361:LEU:HD12	1.82	0.44
2:E:139:HIS:O	2:E:170:SER:HA	2.16	0.44
1:H:113:VAL:HA	1:H:116:VAL:HB	1.99	0.44
1:J:332:ALA:O	1:J:336:LYS:HG2	2.17	0.44
1:N:254:ALA:O	1:N:258:VAL:HG12	2.17	0.44
2:M:192:HIS:NE2	2:M:420:GLU:OE1	2.51	0.44
1:P:187:LEU:HD11	1:P:408:PHE:CZ	2.52	0.44
1:P:254:ALA:O	1:P:258:VAL:HG12	2.17	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:147:SER:HB3	2:A:190:THR:HB	2.00	0.44
2:A:192:HIS:ND1	2:A:424:ASP:OD2	2.45	0.44
1:D:280:GLN:HE21	1:D:361:LEU:HD12	1.82	0.44
2:C:31:GLN:N	2:C:31:GLN:OE1	2.51	0.44
2:I:2:ARG:HD3	2:I:133:GLN:HG2	1.98	0.44
1:L:22:GLU:HG3	1:L:81:PHE:HE1	1.83	0.44
1:L:172:SER:CB	1:L:205:GLU:HB2	2.48	0.44
1:N:103:LYS:HA	1:N:401:GLU:OE2	2.17	0.44
1:N:280:GLN:HE21	1:N:361:LEU:HD12	1.82	0.44
2:M:271:THR:OG1	2:M:377:MET:HB3	2.17	0.44
1:P:100:ASN:HB3	1:P:103:LYS:HD3	1.99	0.44
1:P:103:LYS:HA	1:P:401:GLU:OE2	2.17	0.44
1:P:293:MET:HG3	1:P:294:PHE:CD1	2.52	0.44
2:O:147:SER:HB3	2:O:190:THR:HB	2.00	0.44
2:O:213:CYS:O	2:O:217:LEU:HB3	2.17	0.44
2:A:31:GLN:OE1	2:A:31:GLN:N	2.51	0.44
1:D:254:ALA:O	1:D:258:VAL:HG12	2.17	0.44
2:G:271:THR:OG1	2:G:377:MET:HB3	2.17	0.44
2:I:313:MET:HA	2:I:344:VAL:HG23	1.99	0.44
1:L:332:ALA:O	1:L:336:LYS:HG2	2.17	0.44
2:K:31:GLN:OE1	2:K:31:GLN:N	2.51	0.44
1:N:172:SER:CB	1:N:205:GLU:HB2	2.48	0.44
1:N:332:ALA:O	1:N:336:LYS:HG2	2.17	0.44
2:M:2:ARG:HD3	2:M:133:GLN:HG2	1.98	0.44
2:M:80:THR:HA	2:M:84:ARG:HG2	1.99	0.44
1:P:280:GLN:HE21	1:P:361:LEU:HD12	1.82	0.44
1:B:172:SER:CB	1:B:205:GLU:HB2	2.48	0.44
1:B:280:GLN:HE21	1:B:361:LEU:HD12	1.82	0.44
1:D:91:ILE:H	1:D:91:ILE:HD12	1.83	0.44
1:D:100:ASN:HB3	1:D:103:LYS:HD3	1.99	0.44
1:D:172:SER:CB	1:D:205:GLU:HB2	2.48	0.44
2:C:80:THR:HA	2:C:84:ARG:HG2	1.99	0.44
2:C:192:HIS:NE2	2:C:420:GLU:OE1	2.51	0.44
1:F:103:LYS:HA	1:F:401:GLU:OE2	2.17	0.44
2:E:80:THR:HA	2:E:84:ARG:HG2	1.99	0.44
1:H:254:ALA:O	1:H:258:VAL:HG12	2.17	0.44
1:H:280:GLN:HE21	1:H:361:LEU:HD12	1.82	0.44
2:I:80:THR:HA	2:I:84:ARG:HG2	1.99	0.44
1:N:91:ILE:H	1:N:91:ILE:HD12	1.83	0.44
2:M:147:SER:HB3	2:M:190:THR:HB	2.00	0.44
2:M:313:MET:HA	2:M:344:VAL:HG23	1.99	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:MET:HG3	1:B:294:PHE:CD1	2.52	0.44
1:D:67:ASP:OD1	1:D:67:ASP:N	2.51	0.44
1:D:137:HIS:O	1:D:168:SER:HA	2.17	0.44
2:C:2:ARG:NH1	2:C:132:LEU:O	2.49	0.44
1:F:97:ALA:HB1	1:F:143:THR:HG1	1.83	0.44
1:F:100:ASN:HB3	1:F:103:LYS:HD3	1.99	0.44
1:F:172:SER:CB	1:F:205:GLU:HB2	2.48	0.44
1:H:172:SER:CB	1:H:205:GLU:HB2	2.48	0.44
2:G:155:GLU:O	2:G:159:VAL:HG23	2.18	0.44
2:G:213:CYS:O	2:G:217:LEU:HB3	2.17	0.44
1:J:100:ASN:HB3	1:J:103:LYS:HD3	1.99	0.44
1:J:137:HIS:O	1:J:168:SER:HA	2.17	0.44
1:J:254:ALA:O	1:J:258:VAL:HG12	2.17	0.44
2:I:168:GLU:O	2:I:202:PHE:N	2.33	0.44
2:I:192:HIS:NE2	2:I:420:GLU:OE1	2.51	0.44
2:K:155:GLU:O	2:K:159:VAL:HG23	2.18	0.44
2:K:271:THR:OG1	2:K:377:MET:HB3	2.17	0.44
1:N:22:GLU:HG3	1:N:81:PHE:HE1	1.83	0.44
2:M:91:GLN:HA	2:M:121:ARG:NH2	2.32	0.44
1:P:67:ASP:N	1:P:67:ASP:OD1	2.51	0.44
1:P:181:GLU:HA	1:P:184:ASN:ND2	2.24	0.44
2:A:80:THR:HA	2:A:84:ARG:HG2	1.99	0.44
1:F:67:ASP:N	1:F:67:ASP:OD1	2.51	0.44
2:E:192:HIS:NE2	2:E:420:GLU:OE1	2.51	0.44
2:E:192:HIS:ND1	2:E:424:ASP:OD2	2.45	0.44
2:G:31:GLN:OE1	2:G:31:GLN:N	2.51	0.44
2:G:313:MET:HA	2:G:344:VAL:HG23	1.99	0.44
1:J:22:GLU:HG3	1:J:81:PHE:HE1	1.83	0.44
2:I:182:VAL:HG23	2:I:186:ASN:HD21	1.83	0.44
2:K:147:SER:HB3	2:K:190:THR:HB	2.00	0.44
2:K:182:VAL:HG23	2:K:186:ASN:HD21	1.83	0.44
2:K:251:ASP:N	2:K:254:GLU:OE1	2.50	0.44
2:O:173:PRO:HA	2:O:206:ASN:OD1	2.18	0.44
2:O:182:VAL:HG23	2:O:186:ASN:HD21	1.83	0.44
1:B:67:ASP:OD1	1:B:67:ASP:N	2.51	0.43
2:A:251:ASP:N	2:A:254:GLU:OE1	2.50	0.43
1:D:329:GLN:HG2	1:D:330:MET:HE3	2.00	0.43
2:C:147:SER:HB3	2:C:190:THR:HB	2.00	0.43
2:C:173:PRO:HA	2:C:206:ASN:OD1	2.18	0.43
2:G:192:HIS:NE2	2:G:420:GLU:OE1	2.51	0.43
1:J:102:ALA:HB2	1:J:403:MET:HE2	2.00	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:113:VAL:HA	1:J:116:VAL:HB	1.99	0.43
2:I:155:GLU:O	2:I:159:VAL:HG23	2.18	0.43
1:N:326:VAL:O	1:N:330:MET:HG2	2.18	0.43
2:M:182:VAL:HG23	2:M:186:ASN:HD21	1.83	0.43
1:P:113:VAL:HA	1:P:116:VAL:HB	1.99	0.43
1:P:326:VAL:O	1:P:330:MET:HG2	2.18	0.43
2:O:271:THR:OG1	2:O:377:MET:HB3	2.17	0.43
1:B:326:VAL:O	1:B:330:MET:HG2	2.18	0.43
2:A:271:THR:OG1	2:A:377:MET:HB3	2.17	0.43
2:C:182:VAL:HG23	2:C:186:ASN:HD21	1.83	0.43
2:C:271:THR:OG1	2:C:377:MET:HB3	2.17	0.43
2:E:155:GLU:O	2:E:159:VAL:HG23	2.18	0.43
1:H:91:ILE:H	1:H:91:ILE:HD12	1.83	0.43
2:I:147:SER:HB3	2:I:190:THR:HB	2.00	0.43
1:L:91:ILE:H	1:L:91:ILE:HD12	1.83	0.43
1:L:280:GLN:HE21	1:L:361:LEU:HD12	1.82	0.43
2:K:192:HIS:NE2	2:K:420:GLU:OE1	2.51	0.43
2:K:202:PHE:HE1	2:K:268:PRO:HG2	1.81	0.43
1:N:100:ASN:HB3	1:N:103:LYS:HD3	1.99	0.43
2:M:265:ILE:HG12	2:M:432:TYR:CE1	2.54	0.43
1:P:137:HIS:O	1:P:168:SER:HA	2.17	0.43
2:O:352:LYS:H	2:O:352:LYS:HD2	1.83	0.43
1:B:254:ALA:O	1:B:258:VAL:HG12	2.17	0.43
1:D:355:ASP:N	1:D:355:ASP:OD1	2.51	0.43
2:C:155:GLU:O	2:C:159:VAL:HG23	2.18	0.43
1:F:282:ARG:HA	1:F:282:ARG:HD3	1.79	0.43
2:E:31:GLN:OE1	2:E:31:GLN:N	2.51	0.43
2:E:271:THR:OG1	2:E:377:MET:HB3	2.17	0.43
1:H:67:ASP:N	1:H:67:ASP:OD1	2.51	0.43
2:G:137:VAL:O	2:G:169:PHE:N	2.34	0.43
1:J:67:ASP:OD1	1:J:67:ASP:N	2.51	0.43
1:J:237:THR:O	1:J:241:ARG:HG3	2.19	0.43
1:L:67:ASP:OD1	1:L:67:ASP:N	2.51	0.43
1:L:355:ASP:N	1:L:355:ASP:OD1	2.51	0.43
1:N:113:VAL:HA	1:N:116:VAL:HB	1.99	0.43
2:M:31:GLN:OE1	2:M:31:GLN:N	2.51	0.43
1:B:91:ILE:HD12	1:B:91:ILE:H	1.83	0.43
1:D:211:CYS:O	1:D:215:LEU:HB3	2.19	0.43
2:E:265:ILE:HG12	2:E:432:TYR:CE1	2.54	0.43
2:G:80:THR:HA	2:G:84:ARG:HG2	1.99	0.43
1:J:172:SER:CB	1:J:205:GLU:HB2	2.48	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:355:ASP:N	1:J:355:ASP:OD1	2.51	0.43
2:I:31:GLN:N	2:I:31:GLN:OE1	2.51	0.43
1:L:326:VAL:O	1:L:330:MET:HG2	2.18	0.43
2:K:265:ILE:HG12	2:K:432:TYR:CE1	2.53	0.43
1:P:22:GLU:HG3	1:P:81:PHE:HE1	1.83	0.43
2:O:31:GLN:OE1	2:O:31:GLN:N	2.51	0.43
2:O:251:ASP:N	2:O:254:GLU:OE1	2.50	0.43
1:B:211:CYS:O	1:B:215:LEU:HB3	2.19	0.43
2:C:227:LEU:O	2:C:231:ILE:HG23	2.19	0.43
2:C:229:ARG:HD3	2:C:229:ARG:HA	1.89	0.43
1:F:237:THR:O	1:F:241:ARG:HG3	2.19	0.43
2:G:167:LEU:HD21	2:G:202:PHE:CE2	2.54	0.43
2:G:182:VAL:HG23	2:G:186:ASN:HD21	1.83	0.43
2:I:265:ILE:HG12	2:I:432:TYR:CE1	2.54	0.43
1:L:103:LYS:HA	1:L:401:GLU:OE2	2.17	0.43
1:L:237:THR:O	1:L:241:ARG:HG3	2.19	0.43
2:K:2:ARG:HD3	2:K:133:GLN:HG2	1.98	0.43
2:K:227:LEU:O	2:K:231:ILE:HG23	2.19	0.43
2:M:167:LEU:HD21	2:M:202:PHE:CE2	2.54	0.43
2:M:251:ASP:N	2:M:254:GLU:OE1	2.50	0.43
1:P:355:ASP:OD1	1:P:355:ASP:N	2.51	0.43
2:O:227:LEU:O	2:O:231:ILE:HG23	2.19	0.43
2:A:182:VAL:HG23	2:A:186:ASN:HD21	1.83	0.43
1:D:97:ALA:CA	1:D:143:THR:HG23	2.39	0.43
1:D:293:MET:HG3	1:D:294:PHE:CD1	2.52	0.43
2:C:40:LYS:O	2:C:41:THR:OG1	2.26	0.43
2:C:251:ASP:N	2:C:254:GLU:OE1	2.50	0.43
1:H:22:GLU:HG3	1:H:81:PHE:HE1	1.83	0.43
1:J:91:ILE:HD12	1:J:91:ILE:H	1.83	0.43
1:J:326:VAL:O	1:J:330:MET:HG2	2.18	0.43
2:I:69:ASP:OD1	2:I:70:LEU:N	2.45	0.43
2:I:271:THR:OG1	2:I:377:MET:HB3	2.17	0.43
1:L:97:ALA:CA	1:L:143:THR:HG23	2.39	0.43
2:K:173:PRO:HA	2:K:206:ASN:OD1	2.18	0.43
1:P:172:SER:CB	1:P:205:GLU:HB2	2.48	0.43
1:P:329:GLN:HG2	1:P:330:MET:HE3	2.00	0.43
1:D:326:VAL:O	1:D:330:MET:HG2	2.18	0.43
1:F:355:ASP:OD1	1:F:355:ASP:N	2.51	0.43
1:J:342:VAL:HG13	1:J:345:ILE:H	1.84	0.43
2:K:91:GLN:HA	2:K:121:ARG:HH22	1.84	0.43
2:K:352:LYS:H	2:K:352:LYS:HD2	1.83	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:67:ASP:N	1:N:67:ASP:OD1	2.51	0.43
2:M:352:LYS:H	2:M:352:LYS:HD2	1.83	0.43
1:P:150:LEU:HG	1:P:154:LYS:HZ1	1.83	0.43
2:O:80:THR:HA	2:O:84:ARG:HG2	1.99	0.43
2:O:155:GLU:O	2:O:159:VAL:HG23	2.18	0.43
2:O:265:ILE:HG12	2:O:432:TYR:CE1	2.53	0.43
1:B:97:ALA:CA	1:B:143:THR:HG23	2.39	0.43
1:B:355:ASP:N	1:B:355:ASP:OD1	2.51	0.43
2:A:173:PRO:HA	2:A:206:ASN:OD1	2.18	0.43
2:A:352:LYS:H	2:A:352:LYS:HD2	1.83	0.43
1:D:237:THR:O	1:D:241:ARG:HG3	2.19	0.43
2:C:21:TRP:CZ3	2:C:63:PRO:HB3	2.54	0.43
1:F:211:CYS:O	1:F:215:LEU:HB3	2.19	0.43
1:F:342:VAL:HG13	1:F:345:ILE:H	1.84	0.43
2:E:91:GLN:HA	2:E:121:ARG:HH22	1.84	0.43
2:E:173:PRO:HA	2:E:206:ASN:OD1	2.18	0.43
2:E:182:VAL:HG23	2:E:186:ASN:HD21	1.83	0.43
1:H:137:HIS:O	1:H:168:SER:HA	2.17	0.43
1:H:326:VAL:O	1:H:330:MET:HG2	2.18	0.43
1:H:342:VAL:HG13	1:H:345:ILE:H	1.84	0.43
2:G:147:SER:HB3	2:G:190:THR:HB	2.00	0.43
1:J:72:THR:O	1:J:76:VAL:HG23	2.19	0.43
2:I:167:LEU:HD21	2:I:202:PHE:CE2	2.54	0.43
1:L:137:HIS:O	1:L:168:SER:HA	2.17	0.43
1:L:416:ASN:HA	1:L:419:VAL:HG12	2.01	0.43
2:A:39:ASP:O	2:A:41:THR:HG23	2.19	0.43
2:A:155:GLU:O	2:A:159:VAL:HG23	2.18	0.43
1:D:342:VAL:HG13	1:D:345:ILE:H	1.84	0.43
2:C:352:LYS:H	2:C:352:LYS:HD2	1.83	0.43
1:F:22:GLU:HG3	1:F:81:PHE:HE1	1.83	0.43
1:F:326:VAL:O	1:F:330:MET:HG2	2.18	0.43
1:H:72:THR:O	1:H:76:VAL:HG23	2.19	0.43
1:H:103:LYS:HA	1:H:401:GLU:OE2	2.17	0.43
2:G:173:PRO:HA	2:G:206:ASN:OD1	2.18	0.43
1:J:203:ASP:OD2	1:J:302:ALA:HB2	2.19	0.43
1:J:416:ASN:HA	1:J:419:VAL:HG12	2.01	0.43
1:L:342:VAL:HG13	1:L:345:ILE:H	1.84	0.43
1:P:91:ILE:H	1:P:91:ILE:HD12	1.83	0.43
1:P:416:ASN:HA	1:P:419:VAL:HG12	2.01	0.43
1:B:22:GLU:HG3	1:B:81:PHE:HE1	1.83	0.43
2:A:91:GLN:HA	2:A:121:ARG:HH22	1.84	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:39:ASP:O	2:C:41:THR:HG23	2.19	0.43
1:F:72:THR:O	1:F:76:VAL:HG23	2.19	0.43
1:F:203:ASP:OD2	1:F:302:ALA:HB2	2.19	0.43
2:E:147:SER:HB3	2:E:190:THR:HB	2.00	0.43
1:H:211:CYS:O	1:H:215:LEU:HB3	2.19	0.43
2:G:227:LEU:O	2:G:231:ILE:HG23	2.19	0.43
2:I:21:TRP:CZ3	2:I:63:PRO:HB3	2.54	0.43
1:L:113:VAL:HA	1:L:116:VAL:HB	1.99	0.43
1:L:136:THR:HA	1:L:167:PHE:HB2	2.01	0.43
2:K:39:ASP:O	2:K:41:THR:HG23	2.19	0.43
2:K:80:THR:HA	2:K:84:ARG:HG2	1.99	0.43
2:K:213:CYS:SG	2:K:230:LEU:HD13	2.59	0.43
1:N:216:LYS:HA	1:N:216:LYS:HD3	1.81	0.43
1:N:416:ASN:HA	1:N:419:VAL:HG12	2.01	0.43
2:M:39:ASP:O	2:M:41:THR:HG23	2.19	0.43
2:O:91:GLN:HA	2:O:121:ARG:HH22	1.84	0.43
2:O:155:GLU:HA	2:O:197:HIS:CD2	2.54	0.43
2:O:213:CYS:SG	2:O:230:LEU:HD13	2.59	0.43
1:B:203:ASP:OD2	1:B:302:ALA:HB2	2.19	0.42
1:B:342:VAL:HG13	1:B:345:ILE:H	1.84	0.42
2:A:167:LEU:HD21	2:A:202:PHE:CE2	2.54	0.42
1:D:282:ARG:HD3	1:D:282:ARG:HA	1.79	0.42
1:F:91:ILE:H	1:F:91:ILE:HD12	1.83	0.42
2:E:236:SER:O	2:E:243:ARG:NH1	2.40	0.42
1:H:237:THR:O	1:H:241:ARG:HG3	2.19	0.42
2:G:319:TYR:HB2	2:G:355:ILE:HG23	2.01	0.42
1:J:77:ARG:HG3	1:J:82:GLY:HA3	2.01	0.42
2:I:210:TYR:CE2	2:I:222:PRO:HG2	2.54	0.42
1:L:64:ILE:O	1:L:65:LEU:HD23	2.19	0.42
1:L:203:ASP:OD2	1:L:302:ALA:HB2	2.19	0.42
1:L:216:LYS:HA	1:L:216:LYS:HD3	1.81	0.42
2:M:155:GLU:O	2:M:159:VAL:HG23	2.18	0.42
1:P:203:ASP:OD2	1:P:302:ALA:HB2	2.19	0.42
2:A:213:CYS:SG	2:A:230:LEU:HD13	2.59	0.42
1:D:77:ARG:HG3	1:D:82:GLY:HA3	2.01	0.42
2:C:265:ILE:HG12	2:C:432:TYR:CE1	2.53	0.42
1:F:77:ARG:HG3	1:F:82:GLY:HA3	2.01	0.42
2:E:319:TYR:HB2	2:E:355:ILE:HG23	2.01	0.42
1:H:64:ILE:O	1:H:65:LEU:HD23	2.19	0.42
1:H:416:ASN:HA	1:H:419:VAL:HG12	2.01	0.42
2:G:40:LYS:O	2:G:41:THR:OG1	2.26	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:155:GLU:HA	2:G:197:HIS:CD2	2.54	0.42
2:G:236:SER:O	2:G:243:ARG:NH1	2.40	0.42
2:G:352:LYS:H	2:G:352:LYS:HD2	1.83	0.42
2:I:155:GLU:HA	2:I:197:HIS:CD2	2.54	0.42
2:I:213:CYS:SG	2:I:230:LEU:HD13	2.59	0.42
2:K:167:LEU:HD21	2:K:202:PHE:CE2	2.54	0.42
1:N:342:VAL:HG13	1:N:345:ILE:H	1.84	0.42
2:M:155:GLU:HA	2:M:197:HIS:CD2	2.54	0.42
1:P:211:CYS:O	1:P:215:LEU:HB3	2.19	0.42
2:O:21:TRP:CZ3	2:O:63:PRO:HB3	2.54	0.42
2:O:319:TYR:HB2	2:O:355:ILE:HG23	2.01	0.42
1:B:237:THR:O	1:B:241:ARG:HG3	2.19	0.42
2:A:265:ILE:HG12	2:A:432:TYR:CE1	2.54	0.42
2:A:319:TYR:HB2	2:A:355:ILE:HG23	2.01	0.42
2:C:167:LEU:HD21	2:C:202:PHE:CE2	2.54	0.42
2:E:21:TRP:CZ3	2:E:63:PRO:HB3	2.54	0.42
2:E:39:ASP:O	2:E:41:THR:HG23	2.19	0.42
2:E:155:GLU:HA	2:E:197:HIS:CD2	2.54	0.42
2:E:210:TYR:CE2	2:E:222:PRO:HG2	2.54	0.42
2:E:213:CYS:SG	2:E:230:LEU:HD13	2.59	0.42
1:H:77:ARG:HG3	1:H:82:GLY:HA3	2.01	0.42
1:H:203:ASP:OD2	1:H:302:ALA:HB2	2.19	0.42
1:J:64:ILE:O	1:J:65:LEU:HD23	2.19	0.42
2:I:136:LEU:HD12	2:I:169:PHE:HE2	1.85	0.42
2:I:352:LYS:H	2:I:352:LYS:HD2	1.83	0.42
2:K:40:LYS:O	2:K:41:THR:OG1	2.26	0.42
1:N:72:THR:O	1:N:76:VAL:HG23	2.19	0.42
2:M:21:TRP:CZ3	2:M:63:PRO:HB3	2.54	0.42
2:M:210:TYR:CE2	2:M:222:PRO:HG2	2.54	0.42
1:P:237:THR:O	1:P:241:ARG:HG3	2.19	0.42
2:O:39:ASP:O	2:O:41:THR:HG23	2.19	0.42
2:O:313:MET:HA	2:O:344:VAL:HG23	1.99	0.42
2:A:27:GLU:OE2	2:A:244:PHE:HZ	2.02	0.42
1:D:22:GLU:HG3	1:D:81:PHE:HE1	1.83	0.42
1:D:203:ASP:OD2	1:D:302:ALA:HB2	2.19	0.42
2:C:136:LEU:HD12	2:C:169:PHE:HE2	1.85	0.42
2:C:155:GLU:HA	2:C:197:HIS:CD2	2.54	0.42
2:C:319:TYR:HB2	2:C:355:ILE:HG23	2.01	0.42
1:F:317:PHE:HB2	1:F:353:VAL:HG22	2.01	0.42
2:E:167:LEU:HD21	2:E:202:PHE:CE2	2.54	0.42
1:H:317:PHE:HB2	1:H:353:VAL:HG22	2.01	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:91:GLN:HA	2:G:121:ARG:HH22	1.84	0.42
2:I:227:LEU:O	2:I:231:ILE:HG23	2.19	0.42
1:N:317:PHE:HB2	1:N:353:VAL:HG22	2.01	0.42
1:N:355:ASP:OD1	1:N:355:ASP:N	2.51	0.42
2:M:136:LEU:HD12	2:M:169:PHE:HE2	1.85	0.42
2:M:173:PRO:HA	2:M:206:ASN:OD1	2.18	0.42
2:M:227:LEU:O	2:M:231:ILE:HG23	2.19	0.42
1:P:317:PHE:HB2	1:P:353:VAL:HG22	2.01	0.42
1:P:342:VAL:HG13	1:P:345:ILE:H	1.84	0.42
1:B:64:ILE:O	1:B:65:LEU:HD23	2.19	0.42
1:B:136:THR:HA	1:B:167:PHE:HB2	2.01	0.42
1:B:139:LEU:HG	1:B:168:SER:OG	2.20	0.42
1:B:416:ASN:HA	1:B:419:VAL:HG12	2.01	0.42
1:D:416:ASN:HA	1:D:419:VAL:HG12	2.01	0.42
2:C:27:GLU:OE2	2:C:244:PHE:HZ	2.02	0.42
1:F:64:ILE:O	1:F:65:LEU:HD23	2.19	0.42
1:H:139:LEU:HG	1:H:168:SER:OG	2.20	0.42
2:G:27:GLU:HG2	2:G:361:THR:OG1	2.20	0.42
2:I:39:ASP:O	2:I:41:THR:HG23	2.19	0.42
2:I:173:PRO:HA	2:I:206:ASN:OD1	2.18	0.42
2:I:319:TYR:HB2	2:I:355:ILE:HG23	2.01	0.42
2:K:27:GLU:HG2	2:K:361:THR:OG1	2.20	0.42
2:M:27:GLU:OE2	2:M:244:PHE:HZ	2.02	0.42
2:M:319:TYR:HB2	2:M:355:ILE:HG23	2.01	0.42
2:A:210:TYR:CE2	2:A:222:PRO:HG2	2.54	0.42
1:D:139:LEU:HG	1:D:168:SER:OG	2.20	0.42
2:C:91:GLN:HA	2:C:121:ARG:HH22	1.84	0.42
2:C:210:TYR:CE2	2:C:222:PRO:HG2	2.55	0.42
2:C:213:CYS:SG	2:C:230:LEU:HD13	2.59	0.42
1:F:139:LEU:HG	1:F:168:SER:OG	2.20	0.42
1:F:181:GLU:HA	1:F:184:ASN:ND2	2.24	0.42
1:F:187:LEU:O	1:F:190:HIS:HB3	2.20	0.42
2:E:229:ARG:HH11	2:E:363:VAL:HG21	1.85	0.42
2:E:352:LYS:H	2:E:352:LYS:HD2	1.83	0.42
2:G:265:ILE:HG12	2:G:432:TYR:CE1	2.53	0.42
1:J:216:LYS:HA	1:J:216:LYS:HD3	1.81	0.42
2:I:27:GLU:HG2	2:I:361:THR:OG1	2.20	0.42
1:L:72:THR:O	1:L:76:VAL:HG23	2.19	0.42
2:K:27:GLU:OE2	2:K:244:PHE:HZ	2.02	0.42
1:N:97:ALA:CA	1:N:143:THR:HG23	2.39	0.42
1:N:203:ASP:OD2	1:N:302:ALA:HB2	2.19	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:211:CYS:O	1:N:215:LEU:HB3	2.19	0.42
1:N:318:ARG:HA	1:N:354:CYS:O	2.20	0.42
2:M:168:GLU:O	2:M:202:PHE:N	2.33	0.42
2:M:213:CYS:SG	2:M:230:LEU:HD13	2.59	0.42
1:P:136:THR:HA	1:P:167:PHE:HB2	2.01	0.42
1:P:139:LEU:HG	1:P:168:SER:OG	2.20	0.42
1:P:187:LEU:O	1:P:190:HIS:HB3	2.20	0.42
1:P:216:LYS:HA	1:P:216:LYS:HD3	1.81	0.42
1:P:221:THR:HG23	1:P:224:ASP:H	1.85	0.42
2:O:27:GLU:OE2	2:O:244:PHE:HZ	2.02	0.42
1:B:72:THR:O	1:B:76:VAL:HG23	2.19	0.42
2:A:227:LEU:O	2:A:231:ILE:HG23	2.19	0.42
1:F:329:GLN:HG2	1:F:330:MET:HE3	2.01	0.42
2:E:27:GLU:HG2	2:E:361:THR:OG1	2.20	0.42
2:E:251:ASP:N	2:E:254:GLU:OE1	2.50	0.42
1:H:355:ASP:OD1	1:H:355:ASP:N	2.51	0.42
2:G:213:CYS:SG	2:G:230:LEU:HD13	2.59	0.42
2:I:91:GLN:HA	2:I:121:ARG:HH22	1.84	0.42
2:K:155:GLU:HA	2:K:197:HIS:CD2	2.54	0.42
1:N:136:THR:HA	1:N:167:PHE:HB2	2.01	0.42
1:N:139:LEU:HG	1:N:168:SER:OG	2.20	0.42
1:N:237:THR:O	1:N:241:ARG:HG3	2.19	0.42
2:M:229:ARG:HD3	2:M:229:ARG:HA	1.89	0.42
1:P:64:ILE:O	1:P:65:LEU:HD23	2.19	0.42
1:B:187:LEU:O	1:B:190:HIS:HB3	2.20	0.42
1:B:318:ARG:HA	1:B:354:CYS:O	2.20	0.42
1:B:329:GLN:HG2	1:B:330:MET:HE3	2.01	0.42
1:D:187:LEU:O	1:D:190:HIS:HB3	2.20	0.42
2:C:163:LYS:HA	2:C:163:LYS:HD2	1.92	0.42
2:C:319:TYR:HB2	2:C:355:ILE:HD12	2.02	0.42
2:G:229:ARG:HH11	2:G:363:VAL:HG21	1.85	0.42
1:J:139:LEU:HG	1:J:168:SER:OG	2.20	0.42
1:L:221:THR:HG23	1:L:224:ASP:H	1.85	0.42
2:O:167:LEU:HD21	2:O:202:PHE:CE2	2.54	0.42
1:B:77:ARG:HG3	1:B:82:GLY:HA3	2.01	0.42
2:A:155:GLU:HA	2:A:197:HIS:CD2	2.54	0.42
1:D:64:ILE:O	1:D:65:LEU:HD23	2.19	0.42
2:C:229:ARG:HH11	2:C:363:VAL:HG21	1.85	0.42
1:F:416:ASN:HA	1:F:419:VAL:HG12	2.01	0.42
2:E:135:PHE:CE2	2:E:157:LEU:HD23	2.55	0.42
2:E:136:LEU:HD12	2:E:169:PHE:HE2	1.85	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:187:LEU:O	1:H:190:HIS:HB3	2.20	0.42
2:G:136:LEU:HD12	2:G:169:PHE:HE2	1.85	0.42
2:G:319:TYR:HB2	2:G:355:ILE:HD12	2.02	0.42
2:I:135:PHE:CE2	2:I:157:LEU:HD23	2.55	0.42
1:L:77:ARG:HG3	1:L:82:GLY:HA3	2.01	0.42
1:B:181:GLU:HA	1:B:184:ASN:ND2	2.24	0.42
1:B:221:THR:HG23	1:B:224:ASP:H	1.85	0.42
1:B:317:PHE:HB2	1:B:353:VAL:HG22	2.01	0.42
2:A:136:LEU:HD12	2:A:169:PHE:HE2	1.85	0.42
2:C:27:GLU:HG2	2:C:361:THR:OG1	2.20	0.42
2:C:135:PHE:CE2	2:C:157:LEU:HD23	2.55	0.42
2:E:27:GLU:OE2	2:E:244:PHE:HZ	2.02	0.42
1:H:97:ALA:CA	1:H:143:THR:HG23	2.39	0.42
2:G:21:TRP:CZ3	2:G:63:PRO:HB3	2.54	0.42
2:G:39:ASP:O	2:G:41:THR:HG23	2.19	0.42
1:J:136:THR:HA	1:J:167:PHE:HB2	2.01	0.42
1:J:211:CYS:O	1:J:215:LEU:HB3	2.19	0.42
1:J:318:ARG:HA	1:J:354:CYS:O	2.20	0.42
2:K:21:TRP:CZ3	2:K:63:PRO:HB3	2.54	0.42
1:N:77:ARG:HG3	1:N:82:GLY:HA3	2.01	0.42
1:N:187:LEU:O	1:N:190:HIS:HB3	2.20	0.42
2:M:91:GLN:HA	2:M:121:ARG:HH22	1.84	0.42
2:O:183:GLU:HB3	2:O:184:PRO:HD3	2.02	0.42
2:O:236:SER:O	2:O:243:ARG:NH1	2.40	0.42
1:D:72:THR:O	1:D:76:VAL:HG23	2.19	0.41
2:E:227:LEU:O	2:E:231:ILE:HG23	2.19	0.41
2:E:229:ARG:HD3	2:E:229:ARG:HA	1.89	0.41
1:J:317:PHE:HB2	1:J:353:VAL:HG22	2.01	0.41
2:I:229:ARG:HH11	2:I:363:VAL:HG21	1.85	0.41
1:L:317:PHE:HB2	1:L:353:VAL:HG22	2.01	0.41
2:K:319:TYR:HB2	2:K:355:ILE:HG23	2.01	0.41
2:K:399:TYR:OH	2:K:415:GLU:O	2.39	0.41
2:M:27:GLU:HG2	2:M:361:THR:OG1	2.20	0.41
2:M:135:PHE:CE2	2:M:157:LEU:HD23	2.55	0.41
1:P:270:PHE:CZ	1:P:272:PRO:HG2	2.55	0.41
2:O:210:TYR:CE2	2:O:222:PRO:HG2	2.55	0.41
2:A:406:HIS:HE1	1:D:260:PHE:CA	2.31	0.41
1:D:317:PHE:HB2	1:D:353:VAL:HG22	2.01	0.41
2:C:247:ALA:O	2:C:250:VAL:HG23	2.21	0.41
1:F:102:ALA:HB2	1:F:403:MET:HE2	2.01	0.41
2:G:210:TYR:CE2	2:G:222:PRO:HG2	2.55	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:189:ILE:HG23	1:J:415:MET:HE3	2.02	0.41
1:J:221:THR:HG23	1:J:224:ASP:H	1.85	0.41
2:I:27:GLU:OE2	2:I:244:PHE:HZ	2.02	0.41
2:I:247:ALA:O	2:I:250:VAL:HG23	2.21	0.41
2:A:135:PHE:CE2	2:A:157:LEU:HD23	2.55	0.41
1:F:3:GLU:HA	1:F:49:VAL:HG23	2.03	0.41
1:F:105:HIS:ND1	1:F:150:LEU:HB2	2.36	0.41
1:F:221:THR:HG23	1:F:224:ASP:H	1.85	0.41
1:H:270:PHE:CZ	1:H:272:PRO:HG2	2.55	0.41
1:L:211:CYS:O	1:L:215:LEU:HB3	2.19	0.41
1:L:258:VAL:HG13	1:L:258:VAL:O	2.21	0.41
2:K:135:PHE:CE2	2:K:157:LEU:HD23	2.55	0.41
2:K:247:ALA:O	2:K:250:VAL:HG23	2.21	0.41
1:N:64:ILE:O	1:N:65:LEU:HD23	2.19	0.41
2:M:229:ARG:HH11	2:M:363:VAL:HG21	1.85	0.41
2:M:247:ALA:O	2:M:250:VAL:HG23	2.21	0.41
1:P:77:ARG:HG3	1:P:82:GLY:HA3	2.01	0.41
2:O:135:PHE:CE2	2:O:157:LEU:HD23	2.55	0.41
2:O:247:ALA:O	2:O:250:VAL:HG23	2.21	0.41
2:O:319:TYR:HB2	2:O:355:ILE:HD12	2.02	0.41
1:B:258:VAL:HG13	1:B:258:VAL:O	2.21	0.41
1:D:105:HIS:ND1	1:D:150:LEU:HB2	2.36	0.41
1:D:221:THR:HG23	1:D:224:ASP:H	1.85	0.41
1:D:273:LEU:HD23	1:D:298:ASN:HD22	1.86	0.41
1:F:258:VAL:HG13	1:F:258:VAL:O	2.21	0.41
1:F:270:PHE:CZ	1:F:272:PRO:HG2	2.55	0.41
2:G:27:GLU:OE2	2:G:244:PHE:HZ	2.02	0.41
2:G:135:PHE:CE2	2:G:157:LEU:HD23	2.55	0.41
1:J:187:LEU:O	1:J:190:HIS:HB3	2.20	0.41
1:J:321:MET:O	1:J:323:MET:HE3	2.21	0.41
1:L:3:GLU:HA	1:L:49:VAL:HG23	2.03	0.41
1:L:37:VAL:O	1:L:37:VAL:HG12	2.21	0.41
1:L:225:LEU:HD22	4:L:502:GDP:HN1	1.86	0.41
1:L:270:PHE:CZ	1:L:272:PRO:HG2	2.55	0.41
2:K:229:ARG:HH11	2:K:363:VAL:HG21	1.85	0.41
1:N:221:THR:HG23	1:N:224:ASP:H	1.85	0.41
1:N:258:VAL:HG13	1:N:258:VAL:O	2.21	0.41
1:P:258:VAL:HG13	1:P:258:VAL:O	2.21	0.41
1:B:21:TRP:CZ3	1:B:51:TYR:HE1	2.38	0.41
2:A:399:TYR:OH	2:A:415:GLU:O	2.39	0.41
1:D:136:THR:HA	1:D:167:PHE:HB2	2.01	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:399:TYR:OH	2:E:418:PHE:HB2	2.21	0.41
1:H:221:THR:HG23	1:H:224:ASP:H	1.85	0.41
1:H:318:ARG:HA	1:H:354:CYS:O	2.20	0.41
2:G:247:ALA:O	2:G:250:VAL:HG23	2.21	0.41
1:J:258:VAL:HG13	1:J:258:VAL:O	2.21	0.41
2:I:399:TYR:OH	2:I:415:GLU:O	2.39	0.41
1:L:139:LEU:HG	1:L:168:SER:OG	2.20	0.41
2:K:210:TYR:CE2	2:K:222:PRO:HG2	2.55	0.41
2:K:319:TYR:HB2	2:K:355:ILE:HD12	2.02	0.41
2:M:399:TYR:OH	2:M:415:GLU:O	2.39	0.41
1:P:72:THR:O	1:P:76:VAL:HG23	2.19	0.41
2:O:27:GLU:HG2	2:O:361:THR:OG1	2.20	0.41
2:O:399:TYR:OH	2:O:418:PHE:HB2	2.21	0.41
2:A:21:TRP:CZ3	2:A:63:PRO:HB3	2.54	0.41
2:A:183:GLU:HB3	2:A:184:PRO:HD3	2.02	0.41
2:A:247:ALA:O	2:A:250:VAL:HG23	2.21	0.41
1:D:270:PHE:CZ	1:D:272:PRO:HG2	2.55	0.41
2:C:3:GLU:HG2	2:C:64:ARG:HD2	2.03	0.41
2:C:399:TYR:OH	2:C:418:PHE:HB2	2.21	0.41
1:F:37:VAL:O	1:F:37:VAL:HG12	2.21	0.41
1:F:136:THR:HA	1:F:167:PHE:HB2	2.01	0.41
2:E:319:TYR:HB2	2:E:355:ILE:HD12	2.02	0.41
1:H:3:GLU:HA	1:H:49:VAL:HG23	2.03	0.41
2:G:399:TYR:OH	2:G:418:PHE:HB2	2.21	0.41
2:I:319:TYR:HB2	2:I:355:ILE:HD12	2.02	0.41
1:L:187:LEU:O	1:L:190:HIS:HB3	2.20	0.41
1:N:37:VAL:O	1:N:37:VAL:HG12	2.21	0.41
1:N:270:PHE:CZ	1:N:272:PRO:HG2	2.55	0.41
1:P:210:ILE:HG21	1:P:297:LYS:O	2.21	0.41
1:P:273:LEU:HD23	1:P:298:ASN:HD22	1.86	0.41
2:A:3:GLU:HG2	2:A:64:ARG:HD2	2.03	0.41
2:A:166:LYS:HB3	2:A:166:LYS:HE3	1.95	0.41
2:A:229:ARG:HH11	2:A:363:VAL:HG21	1.85	0.41
1:D:318:ARG:HA	1:D:354:CYS:O	2.20	0.41
1:F:225:LEU:HD22	4:F:502:GDP:HN1	1.86	0.41
1:H:273:LEU:HD23	1:H:298:ASN:HD22	1.86	0.41
1:J:37:VAL:O	1:J:37:VAL:HG12	2.21	0.41
1:J:270:PHE:CZ	1:J:272:PRO:HG2	2.55	0.41
2:I:3:GLU:HG2	2:I:64:ARG:HD2	2.03	0.41
1:N:98:GLY:O	1:N:142:GLY:CA	2.62	0.41
1:P:282:ARG:HA	1:P:282:ARG:HD3	1.79	0.41

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:318:ARG:HA	1:P:354:CYS:O	2.20	0.41
1:P:407:GLU:HA	1:P:410:GLU:HG2	2.03	0.41
1:B:273:LEU:HD23	1:B:298:ASN:HD22	1.86	0.41
2:A:27:GLU:HG2	2:A:361:THR:OG1	2.20	0.41
2:A:399:TYR:OH	2:A:418:PHE:HB2	2.21	0.41
2:A:403:ALA:HB1	2:A:404:PHE:HD1	1.86	0.41
1:D:258:VAL:HG13	1:D:258:VAL:O	2.21	0.41
2:C:399:TYR:OH	2:C:415:GLU:O	2.39	0.41
1:F:210:ILE:HG21	1:F:297:LYS:O	2.21	0.41
2:E:3:GLU:HG2	2:E:64:ARG:HD2	2.03	0.41
1:H:37:VAL:O	1:H:37:VAL:HG12	2.21	0.41
1:H:210:ILE:HG21	1:H:297:LYS:O	2.21	0.41
1:H:216:LYS:HA	1:H:216:LYS:HD3	1.81	0.41
2:G:3:GLU:HG2	2:G:64:ARG:HD2	2.03	0.41
2:G:399:TYR:OH	2:G:415:GLU:O	2.39	0.41
2:K:136:LEU:HD12	2:K:169:PHE:HE2	1.85	0.41
2:K:403:ALA:HB1	2:K:404:PHE:HD1	1.86	0.41
1:N:3:GLU:HA	1:N:49:VAL:HG23	2.03	0.41
1:N:86:ARG:NE	1:N:89:ASN:OD1	2.53	0.41
1:N:273:LEU:HD23	1:N:298:ASN:HD22	1.86	0.41
1:P:225:LEU:HD22	4:P:502:GDP:HN1	1.86	0.41
2:O:136:LEU:HD12	2:O:169:PHE:HE2	1.85	0.41
1:B:105:HIS:ND1	1:B:150:LEU:HB2	2.36	0.41
1:B:212:PHE:HD2	1:B:213:ARG:HE	1.69	0.41
1:D:3:GLU:HA	1:D:49:VAL:HG23	2.03	0.41
1:D:37:VAL:O	1:D:37:VAL:HG12	2.21	0.41
1:D:212:PHE:HD2	1:D:213:ARG:HE	1.69	0.41
1:D:225:LEU:HD22	4:D:502:GDP:HN1	1.86	0.41
1:D:280:GLN:O	1:D:281:TYR:CG	2.74	0.41
2:C:403:ALA:HB1	2:C:404:PHE:HD1	1.86	0.41
1:F:212:PHE:HD2	1:F:213:ARG:HE	1.69	0.41
2:E:105:ARG:O	2:E:109:THR:OG1	2.30	0.41
2:E:403:ALA:HB1	2:E:404:PHE:HD1	1.86	0.41
1:H:52:ASN:OD1	1:H:62:ARG:NH1	2.54	0.41
1:H:136:THR:HA	1:H:167:PHE:HB2	2.01	0.41
1:H:225:LEU:HD22	4:H:502:GDP:HN1	1.86	0.41
1:H:280:GLN:O	1:H:281:TYR:CG	2.74	0.41
1:J:52:ASN:OD1	1:J:62:ARG:NH1	2.54	0.41
2:I:229:ARG:HD3	2:I:229:ARG:HA	1.89	0.41
1:L:210:ILE:HG21	1:L:297:LYS:O	2.21	0.41
1:L:273:LEU:HD23	1:L:298:ASN:HD22	1.86	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:318:ARG:HA	1:L:354:CYS:O	2.20	0.41
1:N:105:HIS:ND1	1:N:150:LEU:HB2	2.36	0.41
2:M:191:THR:HG23	2:M:425:MET:HE3	2.02	0.41
2:M:399:TYR:OH	2:M:418:PHE:HB2	2.21	0.41
2:M:403:ALA:HB1	2:M:404:PHE:HD1	1.86	0.41
1:P:189:ILE:HG23	1:P:415:MET:HE3	2.02	0.41
1:P:212:PHE:HD2	1:P:213:ARG:HE	1.69	0.41
2:O:166:LYS:HB3	2:O:166:LYS:HE3	1.95	0.41
2:O:191:THR:HG23	2:O:425:MET:CE	2.51	0.41
2:O:229:ARG:HH11	2:O:363:VAL:HG21	1.85	0.41
2:A:319:TYR:HB2	2:A:355:ILE:HD12	2.02	0.41
1:D:21:TRP:CZ3	1:D:51:TYR:HE1	2.37	0.41
1:F:273:LEU:HD23	1:F:298:ASN:ND2	2.36	0.41
2:E:399:TYR:OH	2:E:415:GLU:O	2.39	0.41
1:H:258:VAL:HG13	1:H:258:VAL:O	2.21	0.41
1:H:329:GLN:HG2	1:H:330:MET:HE3	2.01	0.41
1:J:210:ILE:HG21	1:J:297:LYS:O	2.21	0.41
1:J:407:GLU:HA	1:J:410:GLU:HG2	2.03	0.41
1:L:52:ASN:OD1	1:L:62:ARG:NH1	2.54	0.41
2:K:191:THR:HG23	2:K:425:MET:CE	2.51	0.41
2:M:183:GLU:HB3	2:M:184:PRO:HD3	2.02	0.41
2:M:217:LEU:HD12	2:M:277:SER:HA	2.04	0.41
1:P:285:THR:OG1	1:P:287:PRO:HD2	2.21	0.41
2:A:81:GLY:O	2:A:84:ARG:HG3	2.21	0.40
1:D:138:SER:C	1:D:140:GLY:H	2.25	0.40
2:E:406:HIS:HE1	1:H:260:PHE:CA	2.31	0.40
1:H:105:HIS:ND1	1:H:150:LEU:HB2	2.36	0.40
1:H:321:MET:O	1:H:323:MET:HE3	2.21	0.40
2:G:229:ARG:HD3	2:G:229:ARG:HA	1.89	0.40
2:G:406:HIS:CE1	1:J:259:PRO:C	2.61	0.40
1:J:273:LEU:HD23	1:J:298:ASN:ND2	2.36	0.40
2:I:217:LEU:HD12	2:I:277:SER:HA	2.04	0.40
2:I:403:ALA:HB1	2:I:404:PHE:HD1	1.86	0.40
1:L:407:GLU:HA	1:L:410:GLU:HG2	2.03	0.40
2:K:3:GLU:HG2	2:K:64:ARG:HD2	2.03	0.40
2:K:137:VAL:O	2:K:169:PHE:N	2.34	0.40
2:K:217:LEU:HD12	2:K:277:SER:HA	2.04	0.40
1:N:68:LEU:HD12	1:N:143:THR:HG22	2.03	0.40
2:M:191:THR:HG23	2:M:425:MET:CE	2.51	0.40
1:P:52:ASN:OD1	1:P:62:ARG:NH1	2.54	0.40
1:P:290:THR:O	1:P:293:MET:HB3	2.21	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:403:ALA:HB1	2:O:404:PHE:HD1	1.86	0.40
1:B:270:PHE:CZ	1:B:272:PRO:HG2	2.55	0.40
1:B:282:ARG:HA	1:B:282:ARG:HD3	1.79	0.40
1:B:407:GLU:HA	1:B:410:GLU:HG2	2.03	0.40
1:D:210:ILE:HG21	1:D:297:LYS:O	2.21	0.40
2:C:183:GLU:HB3	2:C:184:PRO:HD3	2.02	0.40
1:F:52:ASN:OD1	1:F:62:ARG:NH1	2.54	0.40
1:F:138:SER:C	1:F:140:GLY:H	2.25	0.40
1:F:318:ARG:HA	1:F:354:CYS:O	2.20	0.40
1:H:280:GLN:NE2	1:H:362:LYS:H	2.19	0.40
1:J:86:ARG:NE	1:J:89:ASN:OD1	2.53	0.40
1:J:280:GLN:O	1:J:281:TYR:CG	2.74	0.40
2:I:163:LYS:HA	2:I:163:LYS:HD2	1.92	0.40
2:I:399:TYR:OH	2:I:418:PHE:HB2	2.21	0.40
1:L:86:ARG:NE	1:L:89:ASN:OD1	2.53	0.40
2:K:183:GLU:HB3	2:K:184:PRO:HD3	2.02	0.40
1:N:85:PHE:HB2	1:N:90:PHE:HZ	1.86	0.40
1:N:210:ILE:HG21	1:N:297:LYS:O	2.21	0.40
2:O:217:LEU:HD12	2:O:277:SER:HA	2.04	0.40
2:O:399:TYR:OH	2:O:415:GLU:O	2.39	0.40
1:B:3:GLU:HA	1:B:49:VAL:HG23	2.03	0.40
1:B:280:GLN:O	1:B:281:TYR:CG	2.74	0.40
1:D:52:ASN:OD1	1:D:62:ARG:NH1	2.54	0.40
1:D:181:GLU:HA	1:D:184:ASN:ND2	2.24	0.40
1:D:285:THR:OG1	1:D:287:PRO:HD2	2.21	0.40
1:F:273:LEU:HD23	1:F:298:ASN:HD22	1.86	0.40
1:F:285:THR:OG1	1:F:287:PRO:HD2	2.22	0.40
2:E:183:GLU:HB3	2:E:184:PRO:HD3	2.02	0.40
2:E:247:ALA:O	2:E:250:VAL:HG23	2.21	0.40
1:H:58:LYS:HE2	1:H:58:LYS:HB2	1.95	0.40
2:G:183:GLU:HB3	2:G:184:PRO:HD3	2.02	0.40
2:G:251:ASP:N	2:G:254:GLU:OE1	2.50	0.40
2:G:403:ALA:HB1	2:G:404:PHE:HD1	1.86	0.40
1:J:44:LEU:HD22	1:J:59:TYR:CZ	2.57	0.40
1:J:170:VAL:HG22	1:J:203:ASP:HA	2.04	0.40
1:L:321:MET:O	1:L:323:MET:HE3	2.22	0.40
1:N:285:THR:OG1	1:N:287:PRO:HD2	2.22	0.40
2:M:3:GLU:HG2	2:M:64:ARG:HD2	2.03	0.40
1:P:37:VAL:O	1:P:37:VAL:HG12	2.21	0.40
1:P:44:LEU:HD22	1:P:59:TYR:CZ	2.57	0.40
2:O:3:GLU:HG2	2:O:64:ARG:HD2	2.03	0.40

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:163:LYS:HA	2:O:163:LYS:HD2	1.92	0.40
1:B:273:LEU:HD23	1:B:298:ASN:ND2	2.36	0.40
1:B:290:THR:O	1:B:293:MET:HB3	2.21	0.40
2:A:191:THR:HG23	2:A:425:MET:CE	2.51	0.40
2:A:406:HIS:CE1	1:D:259:PRO:C	2.61	0.40
1:H:44:LEU:HD22	1:H:59:TYR:CZ	2.57	0.40
2:G:217:LEU:HD12	2:G:277:SER:HA	2.04	0.40
1:J:285:THR:OG1	1:J:287:PRO:HD2	2.22	0.40
2:I:183:GLU:HB3	2:I:184:PRO:HD3	2.02	0.40
1:L:98:GLY:O	1:L:142:GLY:CA	2.62	0.40
1:L:170:VAL:HG22	1:L:203:ASP:HA	2.04	0.40
2:K:95:GLY:O	2:K:96:LYS:HD2	2.22	0.40
1:N:212:PHE:HD2	1:N:213:ARG:HE	1.69	0.40
1:N:273:LEU:HD23	1:N:298:ASN:ND2	2.36	0.40
2:M:319:TYR:HB2	2:M:355:ILE:HD12	2.02	0.40
1:P:105:HIS:ND1	1:P:150:LEU:HB2	2.36	0.40
1:B:225:LEU:HD22	4:B:502:GDP:HN1	1.86	0.40
2:C:95:GLY:O	2:C:96:LYS:HD2	2.22	0.40
1:F:44:LEU:HD22	1:F:59:TYR:CZ	2.57	0.40
2:E:95:GLY:O	2:E:96:LYS:HD2	2.22	0.40
1:H:170:VAL:HG22	1:H:203:ASP:HA	2.04	0.40
1:H:212:PHE:HD2	1:H:213:ARG:HE	1.69	0.40
1:H:285:THR:OG1	1:H:287:PRO:HD2	2.21	0.40
1:H:407:GLU:HA	1:H:410:GLU:HG2	2.03	0.40
1:J:273:LEU:HD23	1:J:298:ASN:HD22	1.86	0.40
2:I:81:GLY:O	2:I:84:ARG:HG3	2.21	0.40
1:L:105:HIS:ND1	1:L:150:LEU:HB2	2.36	0.40
1:L:273:LEU:HD23	1:L:298:ASN:ND2	2.36	0.40
1:N:290:THR:O	1:N:293:MET:HB3	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	D	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	F	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	H	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	J	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	L	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	N	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
1	P	426/450 (95%)	382 (90%)	42 (10%)	2 (0%)	29	63
2	A	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	C	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	E	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	G	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	I	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	K	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	M	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
2	O	434/451 (96%)	386 (89%)	47 (11%)	1 (0%)	47	78
All	All	6880/7208 (95%)	6144 (89%)	712 (10%)	24 (0%)	44	73

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	143	THR
2	A	37	PRO
1	D	143	THR
2	C	37	PRO
1	F	143	THR
2	E	37	PRO
1	H	143	THR
2	G	37	PRO
1	J	143	THR
2	I	37	PRO
1	L	143	THR
2	K	37	PRO
1	N	143	THR
2	M	37	PRO
1	P	143	THR
2	O	37	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	281	TYR
1	D	281	TYR
1	F	281	TYR
1	H	281	TYR
1	J	281	TYR
1	L	281	TYR
1	N	281	TYR
1	P	281	TYR

### 5.3.2 Protein sidechains [i](#)

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	B	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	D	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	F	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	H	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	J	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	L	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	N	358/386 (93%)	352 (98%)	6 (2%)	60	80
1	P	358/386 (93%)	352 (98%)	6 (2%)	60	80
2	A	351/379 (93%)	351 (100%)	0	100	100
2	C	351/379 (93%)	351 (100%)	0	100	100
2	E	351/379 (93%)	351 (100%)	0	100	100
2	G	351/379 (93%)	351 (100%)	0	100	100
2	I	351/379 (93%)	351 (100%)	0	100	100
2	K	351/379 (93%)	351 (100%)	0	100	100
2	M	351/379 (93%)	351 (100%)	0	100	100
2	O	351/379 (93%)	351 (100%)	0	100	100
All	All	5672/6120 (93%)	5624 (99%)	48 (1%)	82	91

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	77	ARG
1	B	86	ARG
1	B	321	MET
1	B	347	ASN
1	B	349	VAL
1	B	363	MET
1	D	77	ARG
1	D	86	ARG
1	D	321	MET
1	D	347	ASN
1	D	349	VAL
1	D	363	MET
1	F	77	ARG
1	F	86	ARG
1	F	321	MET
1	F	347	ASN
1	F	349	VAL
1	F	363	MET
1	H	77	ARG
1	H	86	ARG
1	H	321	MET
1	H	347	ASN
1	H	349	VAL
1	H	363	MET
1	J	77	ARG
1	J	86	ARG
1	J	321	MET
1	J	347	ASN
1	J	349	VAL
1	J	363	MET
1	L	77	ARG
1	L	86	ARG
1	L	321	MET
1	L	347	ASN
1	L	349	VAL
1	L	363	MET
1	N	77	ARG
1	N	86	ARG
1	N	321	MET
1	N	347	ASN
1	N	349	VAL
1	N	363	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	P	77	ARG
1	P	86	ARG
1	P	321	MET
1	P	347	ASN
1	P	349	VAL
1	P	363	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	8	GLN
1	B	99	ASN
1	B	134	GLN
1	B	256	ASN
2	A	28	HIS
2	A	133	GLN
2	A	406	HIS
1	D	8	GLN
1	D	99	ASN
1	D	134	GLN
1	D	256	ASN
2	C	28	HIS
2	C	133	GLN
2	C	186	ASN
2	C	406	HIS
1	F	8	GLN
1	F	99	ASN
1	F	134	GLN
1	F	256	ASN
2	E	28	HIS
2	E	133	GLN
2	E	186	ASN
2	E	406	HIS
1	H	8	GLN
1	H	99	ASN
1	H	134	GLN
1	H	256	ASN
2	G	28	HIS
2	G	133	GLN
2	G	406	HIS
1	J	8	GLN
1	J	99	ASN

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	J	134	GLN
1	J	256	ASN
2	I	28	HIS
2	I	133	GLN
2	I	186	ASN
2	I	406	HIS
1	L	8	GLN
1	L	99	ASN
1	L	134	GLN
1	L	256	ASN
2	K	28	HIS
2	K	133	GLN
2	K	186	ASN
2	K	406	HIS
1	N	8	GLN
1	N	99	ASN
1	N	134	GLN
1	N	256	ASN
2	M	28	HIS
2	M	133	GLN
2	M	186	ASN
2	M	406	HIS
1	P	8	GLN
1	P	99	ASN
1	P	134	GLN
1	P	256	ASN
2	O	28	HIS
2	O	133	GLN
2	O	186	ASN
2	O	406	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

24 ligands are modelled in this entry.

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
4	GDP	P	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
3	YNP	D	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.47	18 (30%)
3	YNP	J	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.48	19 (32%)
5	GTP	I	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
3	YNP	B	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.48	19 (32%)
4	GDP	H	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
5	GTP	G	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
5	GTP	O	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
4	GDP	D	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
4	GDP	F	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
4	GDP	L	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
5	GTP	E	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
5	GTP	C	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
3	YNP	L	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.47	18 (30%)
5	GTP	K	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
5	GTP	A	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
3	YNP	P	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.47	18 (30%)
4	GDP	B	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
4	GDP	J	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
3	YNP	N	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.48	19 (32%)
4	GDP	N	502	-	24,30,30	0.96	1 (4%)	30,47,47	1.29	3 (10%)
3	YNP	F	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.48	19 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GTP	M	501	-	26,34,34	0.95	2 (7%)	32,54,54	0.69	0
3	YNP	H	501	-	49,49,49	2.72	14 (28%)	59,68,68	3.47	18 (30%)

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
4	GDP	P	502	-	-	3/12/32/32	0/3/3/3
3	YNP	D	501	-	-	38/57/62/62	0/3/4/4
3	YNP	J	501	-	-	38/57/62/62	0/3/4/4
5	GTP	I	501	-	-	6/18/38/38	0/3/3/3
3	YNP	B	501	-	-	38/57/62/62	0/3/4/4
4	GDP	H	502	-	-	3/12/32/32	0/3/3/3
5	GTP	G	501	-	-	6/18/38/38	0/3/3/3
5	GTP	O	501	-	-	6/18/38/38	0/3/3/3
4	GDP	D	502	-	-	3/12/32/32	0/3/3/3
4	GDP	F	502	-	-	3/12/32/32	0/3/3/3
4	GDP	L	502	-	-	3/12/32/32	0/3/3/3
5	GTP	E	501	-	-	6/18/38/38	0/3/3/3
5	GTP	C	501	-	-	6/18/38/38	0/3/3/3
3	YNP	L	501	-	-	38/57/62/62	0/3/4/4
5	GTP	K	501	-	-	6/18/38/38	0/3/3/3
5	GTP	A	501	-	-	6/18/38/38	0/3/3/3
3	YNP	P	501	-	-	38/57/62/62	0/3/4/4
4	GDP	B	502	-	-	3/12/32/32	0/3/3/3
4	GDP	J	502	-	-	3/12/32/32	0/3/3/3
3	YNP	N	501	-	-	38/57/62/62	0/3/4/4
4	GDP	N	502	-	-	3/12/32/32	0/3/3/3
3	YNP	F	501	-	-	38/57/62/62	0/3/4/4
5	GTP	M	501	-	-	6/18/38/38	0/3/3/3
3	YNP	H	501	-	-	38/57/62/62	0/3/4/4

All (136) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	YNP	O1-C4	8.72	1.40	1.23
3	F	501	YNP	O1-C4	8.72	1.40	1.23
3	J	501	YNP	O1-C4	8.72	1.40	1.23
3	N	501	YNP	O1-C4	8.72	1.40	1.23
3	D	501	YNP	O1-C4	8.70	1.40	1.23
3	H	501	YNP	O1-C4	8.70	1.40	1.23
3	L	501	YNP	O1-C4	8.70	1.40	1.23
3	P	501	YNP	O1-C4	8.70	1.40	1.23
3	D	501	YNP	C20-C21	8.25	1.59	1.46
3	H	501	YNP	C20-C21	8.25	1.59	1.46
3	L	501	YNP	C20-C21	8.25	1.59	1.46
3	P	501	YNP	C20-C21	8.25	1.59	1.46
3	B	501	YNP	C20-C21	8.23	1.59	1.46
3	F	501	YNP	C20-C21	8.23	1.59	1.46
3	J	501	YNP	C20-C21	8.23	1.59	1.46
3	N	501	YNP	C20-C21	8.23	1.59	1.46
3	B	501	YNP	O2-C6	7.94	1.39	1.24
3	F	501	YNP	O2-C6	7.94	1.39	1.24
3	J	501	YNP	O2-C6	7.94	1.39	1.24
3	N	501	YNP	O2-C6	7.94	1.39	1.24
3	D	501	YNP	O2-C6	7.91	1.39	1.24
3	H	501	YNP	O2-C6	7.91	1.39	1.24
3	L	501	YNP	O2-C6	7.91	1.39	1.24
3	P	501	YNP	O2-C6	7.91	1.39	1.24
3	B	501	YNP	O7-C20	-5.97	1.34	1.44
3	F	501	YNP	O7-C20	-5.97	1.34	1.44
3	J	501	YNP	O7-C20	-5.97	1.34	1.44
3	N	501	YNP	O7-C20	-5.97	1.34	1.44
3	D	501	YNP	O7-C20	-5.97	1.34	1.44
3	H	501	YNP	O7-C20	-5.97	1.34	1.44
3	L	501	YNP	O7-C20	-5.97	1.34	1.44
3	P	501	YNP	O7-C20	-5.97	1.34	1.44
3	B	501	YNP	C4-N1	5.68	1.46	1.33
3	F	501	YNP	C4-N1	5.68	1.46	1.33
3	J	501	YNP	C4-N1	5.68	1.46	1.33
3	N	501	YNP	C4-N1	5.68	1.46	1.33
3	D	501	YNP	C4-N1	5.67	1.46	1.33
3	H	501	YNP	C4-N1	5.67	1.46	1.33
3	L	501	YNP	C4-N1	5.67	1.46	1.33
3	P	501	YNP	C4-N1	5.67	1.46	1.33
3	D	501	YNP	C6-N2	4.77	1.45	1.34
3	H	501	YNP	C6-N2	4.77	1.45	1.34
3	L	501	YNP	C6-N2	4.77	1.45	1.34

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	501	YNP	C6-N2	4.77	1.45	1.34
3	B	501	YNP	C6-N2	4.75	1.45	1.34
3	F	501	YNP	C6-N2	4.75	1.45	1.34
3	J	501	YNP	C6-N2	4.75	1.45	1.34
3	N	501	YNP	C6-N2	4.75	1.45	1.34
3	D	501	YNP	O3-C10	-3.37	1.40	1.46
3	H	501	YNP	O3-C10	-3.37	1.40	1.46
3	L	501	YNP	O3-C10	-3.37	1.40	1.46
3	P	501	YNP	O3-C10	-3.37	1.40	1.46
3	B	501	YNP	O3-C10	-3.36	1.40	1.46
3	F	501	YNP	O3-C10	-3.36	1.40	1.46
3	J	501	YNP	O3-C10	-3.36	1.40	1.46
3	N	501	YNP	O3-C10	-3.36	1.40	1.46
3	B	501	YNP	O7-C21	-2.83	1.38	1.45
3	F	501	YNP	O7-C21	-2.83	1.38	1.45
3	J	501	YNP	O7-C21	-2.83	1.38	1.45
3	N	501	YNP	O7-C21	-2.83	1.38	1.45
3	D	501	YNP	O7-C21	-2.79	1.38	1.45
3	H	501	YNP	O7-C21	-2.79	1.38	1.45
3	L	501	YNP	O7-C21	-2.79	1.38	1.45
3	P	501	YNP	O7-C21	-2.79	1.38	1.45
3	B	501	YNP	O5-C13	2.77	1.40	1.34
3	F	501	YNP	O5-C13	2.77	1.40	1.34
3	J	501	YNP	O5-C13	2.77	1.40	1.34
3	N	501	YNP	O5-C13	2.77	1.40	1.34
3	D	501	YNP	O5-C13	2.77	1.40	1.34
3	H	501	YNP	O5-C13	2.77	1.40	1.34
3	L	501	YNP	O5-C13	2.77	1.40	1.34
3	P	501	YNP	O5-C13	2.77	1.40	1.34
5	C	501	GTP	C5-C6	-2.68	1.42	1.47
5	G	501	GTP	C5-C6	-2.68	1.42	1.47
5	K	501	GTP	C5-C6	-2.68	1.42	1.47
5	O	501	GTP	C5-C6	-2.68	1.42	1.47
5	A	501	GTP	C5-C6	-2.65	1.42	1.47
5	E	501	GTP	C5-C6	-2.65	1.42	1.47
5	I	501	GTP	C5-C6	-2.65	1.42	1.47
5	M	501	GTP	C5-C6	-2.65	1.42	1.47
3	B	501	YNP	O3-C11	2.60	1.40	1.34
3	F	501	YNP	O3-C11	2.60	1.40	1.34
3	J	501	YNP	O3-C11	2.60	1.40	1.34
3	N	501	YNP	O3-C11	2.60	1.40	1.34
3	D	501	YNP	O3-C11	2.57	1.40	1.34

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	501	YNP	O3-C11	2.57	1.40	1.34
3	L	501	YNP	O3-C11	2.57	1.40	1.34
3	P	501	YNP	O3-C11	2.57	1.40	1.34
3	B	501	YNP	O5-C12	-2.41	1.41	1.45
3	F	501	YNP	O5-C12	-2.41	1.41	1.45
3	J	501	YNP	O5-C12	-2.41	1.41	1.45
3	N	501	YNP	O5-C12	-2.41	1.41	1.45
3	D	501	YNP	O5-C12	-2.40	1.41	1.45
3	H	501	YNP	O5-C12	-2.40	1.41	1.45
3	L	501	YNP	O5-C12	-2.40	1.41	1.45
3	P	501	YNP	O5-C12	-2.40	1.41	1.45
4	B	502	GDP	C6-N1	-2.35	1.34	1.37
4	F	502	GDP	C6-N1	-2.35	1.34	1.37
4	J	502	GDP	C6-N1	-2.35	1.34	1.37
4	N	502	GDP	C6-N1	-2.35	1.34	1.37
4	D	502	GDP	C6-N1	-2.35	1.34	1.37
4	H	502	GDP	C6-N1	-2.35	1.34	1.37
4	L	502	GDP	C6-N1	-2.35	1.34	1.37
4	P	502	GDP	C6-N1	-2.35	1.34	1.37
3	D	501	YNP	C7-C6	2.34	1.53	1.48
3	H	501	YNP	C7-C6	2.34	1.53	1.48
3	L	501	YNP	C7-C6	2.34	1.53	1.48
3	P	501	YNP	C7-C6	2.34	1.53	1.48
3	B	501	YNP	C7-C6	2.34	1.53	1.48
3	F	501	YNP	C7-C6	2.34	1.53	1.48
3	J	501	YNP	C7-C6	2.34	1.53	1.48
3	N	501	YNP	C7-C6	2.34	1.53	1.48
3	D	501	YNP	O8-C32	2.32	1.40	1.37
3	H	501	YNP	O8-C32	2.32	1.40	1.37
3	L	501	YNP	O8-C32	2.32	1.40	1.37
3	P	501	YNP	O8-C32	2.32	1.40	1.37
3	D	501	YNP	C31-CL1	2.28	1.79	1.73
3	H	501	YNP	C31-CL1	2.28	1.79	1.73
3	L	501	YNP	C31-CL1	2.28	1.79	1.73
3	P	501	YNP	C31-CL1	2.28	1.79	1.73
3	B	501	YNP	O8-C32	2.28	1.40	1.37
3	F	501	YNP	O8-C32	2.28	1.40	1.37
3	J	501	YNP	O8-C32	2.28	1.40	1.37
3	N	501	YNP	O8-C32	2.28	1.40	1.37
3	B	501	YNP	C31-CL1	2.27	1.79	1.73
3	F	501	YNP	C31-CL1	2.27	1.79	1.73
3	J	501	YNP	C31-CL1	2.27	1.79	1.73

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	501	YNP	C31-CL1	2.27	1.79	1.73
5	C	501	GTP	C8-N7	-2.09	1.31	1.35
5	G	501	GTP	C8-N7	-2.09	1.31	1.35
5	K	501	GTP	C8-N7	-2.09	1.31	1.35
5	O	501	GTP	C8-N7	-2.09	1.31	1.35
5	A	501	GTP	C8-N7	-2.06	1.31	1.35
5	E	501	GTP	C8-N7	-2.06	1.31	1.35
5	I	501	GTP	C8-N7	-2.06	1.31	1.35
5	M	501	GTP	C8-N7	-2.06	1.31	1.35

All (172) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	YNP	C20-O7-C21	14.49	71.20	60.78
3	F	501	YNP	C20-O7-C21	14.49	71.20	60.78
3	J	501	YNP	C20-O7-C21	14.49	71.20	60.78
3	N	501	YNP	C20-O7-C21	14.49	71.20	60.78
3	D	501	YNP	C20-O7-C21	14.46	71.18	60.78
3	H	501	YNP	C20-O7-C21	14.46	71.18	60.78
3	L	501	YNP	C20-O7-C21	14.46	71.18	60.78
3	P	501	YNP	C20-O7-C21	14.46	71.18	60.78
3	D	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	H	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	L	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	P	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	B	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	F	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	J	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	N	501	YNP	C3-N1-C4	12.09	145.75	122.67
3	D	501	YNP	O7-C21-C20	-8.30	53.18	59.13
3	H	501	YNP	O7-C21-C20	-8.30	53.18	59.13
3	L	501	YNP	O7-C21-C20	-8.30	53.18	59.13
3	P	501	YNP	O7-C21-C20	-8.30	53.18	59.13
3	B	501	YNP	O7-C21-C20	-8.28	53.20	59.13
3	F	501	YNP	O7-C21-C20	-8.28	53.20	59.13
3	J	501	YNP	O7-C21-C20	-8.28	53.20	59.13
3	N	501	YNP	O7-C21-C20	-8.28	53.20	59.13
3	B	501	YNP	O7-C21-C22	7.63	125.66	117.26
3	F	501	YNP	O7-C21-C22	7.63	125.66	117.26
3	J	501	YNP	O7-C21-C22	7.63	125.66	117.26
3	N	501	YNP	O7-C21-C22	7.63	125.66	117.26
3	D	501	YNP	O7-C21-C22	7.60	125.63	117.26

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	501	YNP	O7-C21-C22	7.60	125.63	117.26
3	L	501	YNP	O7-C21-C22	7.60	125.63	117.26
3	P	501	YNP	O7-C21-C22	7.60	125.63	117.26
3	B	501	YNP	O7-C20-C21	-6.80	55.60	60.09
3	F	501	YNP	O7-C20-C21	-6.80	55.60	60.09
3	J	501	YNP	O7-C20-C21	-6.80	55.60	60.09
3	N	501	YNP	O7-C20-C21	-6.80	55.60	60.09
3	D	501	YNP	O7-C20-C21	-6.74	55.64	60.09
3	H	501	YNP	O7-C20-C21	-6.74	55.64	60.09
3	L	501	YNP	O7-C20-C21	-6.74	55.64	60.09
3	P	501	YNP	O7-C20-C21	-6.74	55.64	60.09
3	B	501	YNP	O5-C13-C2	4.82	118.99	111.24
3	F	501	YNP	O5-C13-C2	4.82	118.99	111.24
3	J	501	YNP	O5-C13-C2	4.82	118.99	111.24
3	N	501	YNP	O5-C13-C2	4.82	118.99	111.24
3	D	501	YNP	O5-C13-C2	4.80	118.96	111.24
3	H	501	YNP	O5-C13-C2	4.80	118.96	111.24
3	L	501	YNP	O5-C13-C2	4.80	118.96	111.24
3	P	501	YNP	O5-C13-C2	4.80	118.96	111.24
3	B	501	YNP	C7-C6-N2	4.74	123.67	114.56
3	F	501	YNP	C7-C6-N2	4.74	123.67	114.56
3	J	501	YNP	C7-C6-N2	4.74	123.67	114.56
3	N	501	YNP	C7-C6-N2	4.74	123.67	114.56
3	D	501	YNP	C7-C6-N2	4.72	123.63	114.56
3	H	501	YNP	C7-C6-N2	4.72	123.63	114.56
3	L	501	YNP	C7-C6-N2	4.72	123.63	114.56
3	P	501	YNP	C7-C6-N2	4.72	123.63	114.56
3	D	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	H	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	L	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	P	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	B	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	F	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	J	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	N	501	YNP	O3-C11-C12	3.99	116.83	110.02
3	D	501	YNP	O8-C32-C31	3.99	120.48	116.60
3	H	501	YNP	O8-C32-C31	3.99	120.48	116.60
3	L	501	YNP	O8-C32-C31	3.99	120.48	116.60
3	P	501	YNP	O8-C32-C31	3.99	120.48	116.60
3	B	501	YNP	O8-C32-C31	3.98	120.47	116.60
3	F	501	YNP	O8-C32-C31	3.98	120.47	116.60
3	J	501	YNP	O8-C32-C31	3.98	120.47	116.60

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	501	YNP	O8-C32-C31	3.98	120.47	116.60
4	B	502	GDP	PA-O3A-PB	-3.47	120.93	132.83
4	F	502	GDP	PA-O3A-PB	-3.47	120.93	132.83
4	J	502	GDP	PA-O3A-PB	-3.47	120.93	132.83
4	N	502	GDP	PA-O3A-PB	-3.47	120.93	132.83
4	D	502	GDP	PA-O3A-PB	-3.46	120.95	132.83
4	H	502	GDP	PA-O3A-PB	-3.46	120.95	132.83
4	L	502	GDP	PA-O3A-PB	-3.46	120.95	132.83
4	P	502	GDP	PA-O3A-PB	-3.46	120.95	132.83
3	B	501	YNP	C9-C8-C7	-3.44	118.31	126.00
3	F	501	YNP	C9-C8-C7	-3.44	118.31	126.00
3	J	501	YNP	C9-C8-C7	-3.44	118.31	126.00
3	N	501	YNP	C9-C8-C7	-3.44	118.31	126.00
3	B	501	YNP	O2-C6-N2	-3.43	117.81	122.35
3	F	501	YNP	O2-C6-N2	-3.43	117.81	122.35
3	J	501	YNP	O2-C6-N2	-3.43	117.81	122.35
3	N	501	YNP	O2-C6-N2	-3.43	117.81	122.35
3	D	501	YNP	O2-C6-N2	-3.42	117.83	122.35
3	H	501	YNP	O2-C6-N2	-3.42	117.83	122.35
3	L	501	YNP	O2-C6-N2	-3.42	117.83	122.35
3	P	501	YNP	O2-C6-N2	-3.42	117.83	122.35
3	D	501	YNP	C9-C8-C7	-3.42	118.36	126.00
3	H	501	YNP	C9-C8-C7	-3.42	118.36	126.00
3	L	501	YNP	C9-C8-C7	-3.42	118.36	126.00
3	P	501	YNP	C9-C8-C7	-3.42	118.36	126.00
3	B	501	YNP	O5-C12-C14	3.27	113.86	106.64
3	F	501	YNP	O5-C12-C14	3.27	113.86	106.64
3	J	501	YNP	O5-C12-C14	3.27	113.86	106.64
3	N	501	YNP	O5-C12-C14	3.27	113.86	106.64
3	D	501	YNP	O5-C12-C14	3.26	113.85	106.64
3	H	501	YNP	O5-C12-C14	3.26	113.85	106.64
3	L	501	YNP	O5-C12-C14	3.26	113.85	106.64
3	P	501	YNP	O5-C12-C14	3.26	113.85	106.64
3	D	501	YNP	O8-C32-C33	-2.79	119.59	124.37
3	H	501	YNP	O8-C32-C33	-2.79	119.59	124.37
3	L	501	YNP	O8-C32-C33	-2.79	119.59	124.37
3	P	501	YNP	O8-C32-C33	-2.79	119.59	124.37
3	B	501	YNP	O8-C32-C33	-2.78	119.60	124.37
3	F	501	YNP	O8-C32-C33	-2.78	119.60	124.37
3	J	501	YNP	O8-C32-C33	-2.78	119.60	124.37
3	N	501	YNP	O8-C32-C33	-2.78	119.60	124.37
3	D	501	YNP	C5-C4-N1	2.78	122.14	116.54

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	501	YNP	C5-C4-N1	2.78	122.14	116.54
3	L	501	YNP	C5-C4-N1	2.78	122.14	116.54
3	P	501	YNP	C5-C4-N1	2.78	122.14	116.54
3	B	501	YNP	C5-C4-N1	2.77	122.12	116.54
3	F	501	YNP	C5-C4-N1	2.77	122.12	116.54
3	J	501	YNP	C5-C4-N1	2.77	122.12	116.54
3	N	501	YNP	C5-C4-N1	2.77	122.12	116.54
3	D	501	YNP	C15-C14-C12	-2.74	110.95	115.25
3	H	501	YNP	C15-C14-C12	-2.74	110.95	115.25
3	L	501	YNP	C15-C14-C12	-2.74	110.95	115.25
3	P	501	YNP	C15-C14-C12	-2.74	110.95	115.25
3	B	501	YNP	C15-C14-C12	-2.74	110.96	115.25
3	F	501	YNP	C15-C14-C12	-2.74	110.96	115.25
3	J	501	YNP	C15-C14-C12	-2.74	110.96	115.25
3	N	501	YNP	C15-C14-C12	-2.74	110.96	115.25
4	D	502	GDP	C3'-C2'-C1'	2.68	105.02	100.98
4	H	502	GDP	C3'-C2'-C1'	2.68	105.02	100.98
4	L	502	GDP	C3'-C2'-C1'	2.68	105.02	100.98
4	P	502	GDP	C3'-C2'-C1'	2.68	105.02	100.98
4	B	502	GDP	C3'-C2'-C1'	2.64	104.96	100.98
4	F	502	GDP	C3'-C2'-C1'	2.64	104.96	100.98
4	J	502	GDP	C3'-C2'-C1'	2.64	104.96	100.98
4	N	502	GDP	C3'-C2'-C1'	2.64	104.96	100.98
3	D	501	YNP	C35-O8-C32	-2.41	113.88	117.53
3	H	501	YNP	C35-O8-C32	-2.41	113.88	117.53
3	L	501	YNP	C35-O8-C32	-2.41	113.88	117.53
3	P	501	YNP	C35-O8-C32	-2.41	113.88	117.53
3	B	501	YNP	C35-O8-C32	-2.39	113.92	117.53
3	F	501	YNP	C35-O8-C32	-2.39	113.92	117.53
3	J	501	YNP	C35-O8-C32	-2.39	113.92	117.53
3	N	501	YNP	C35-O8-C32	-2.39	113.92	117.53
4	B	502	GDP	C8-N7-C5	2.38	107.53	102.99
4	F	502	GDP	C8-N7-C5	2.38	107.53	102.99
4	J	502	GDP	C8-N7-C5	2.38	107.53	102.99
4	N	502	GDP	C8-N7-C5	2.38	107.53	102.99
4	D	502	GDP	C8-N7-C5	2.38	107.52	102.99
4	H	502	GDP	C8-N7-C5	2.38	107.52	102.99
4	L	502	GDP	C8-N7-C5	2.38	107.52	102.99
4	P	502	GDP	C8-N7-C5	2.38	107.52	102.99
3	B	501	YNP	C10-O3-C11	-2.20	114.59	117.89
3	F	501	YNP	C10-O3-C11	-2.20	114.59	117.89
3	J	501	YNP	C10-O3-C11	-2.20	114.59	117.89

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	501	YNP	C10-O3-C11	-2.20	114.59	117.89
3	D	501	YNP	C10-O3-C11	-2.19	114.60	117.89
3	H	501	YNP	C10-O3-C11	-2.19	114.60	117.89
3	L	501	YNP	C10-O3-C11	-2.19	114.60	117.89
3	P	501	YNP	C10-O3-C11	-2.19	114.60	117.89
3	B	501	YNP	O1-C4-N1	-2.05	118.59	122.99
3	F	501	YNP	O1-C4-N1	-2.05	118.59	122.99
3	J	501	YNP	O1-C4-N1	-2.05	118.59	122.99
3	N	501	YNP	O1-C4-N1	-2.05	118.59	122.99
3	D	501	YNP	O1-C4-N1	-2.04	118.61	122.99
3	H	501	YNP	O1-C4-N1	-2.04	118.61	122.99
3	L	501	YNP	O1-C4-N1	-2.04	118.61	122.99
3	P	501	YNP	O1-C4-N1	-2.04	118.61	122.99
3	B	501	YNP	O2-C6-C7	-2.00	118.47	123.03
3	F	501	YNP	O2-C6-C7	-2.00	118.47	123.03
3	J	501	YNP	O2-C6-C7	-2.00	118.47	123.03
3	N	501	YNP	O2-C6-C7	-2.00	118.47	123.03

There are no chirality outliers.

All (376) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	YNP	C5-C4-N1-C3
3	B	501	YNP	O1-C4-N1-C3
3	B	501	YNP	C13-C2-C3-N1
3	B	501	YNP	C28-C5-N2-C6
3	B	501	YNP	O2-C6-N2-C5
3	B	501	YNP	C7-C6-N2-C5
3	B	501	YNP	O3-C10-C18-C19
3	B	501	YNP	C11-C12-C14-C15
3	B	501	YNP	C14-C12-O5-C13
3	B	501	YNP	C2-C13-O5-C12
3	B	501	YNP	O6-C13-O5-C12
3	B	501	YNP	C12-C14-C15-C17
3	B	501	YNP	C31-C32-O8-C35
3	D	501	YNP	C5-C4-N1-C3
3	D	501	YNP	O1-C4-N1-C3
3	D	501	YNP	C13-C2-C3-N1
3	D	501	YNP	C28-C5-N2-C6
3	D	501	YNP	O2-C6-N2-C5
3	D	501	YNP	C7-C6-N2-C5
3	D	501	YNP	O3-C10-C18-C19

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	D	501	YNP	C11-C12-C14-C15
3	D	501	YNP	C14-C12-O5-C13
3	D	501	YNP	C2-C13-O5-C12
3	D	501	YNP	O6-C13-O5-C12
3	D	501	YNP	C12-C14-C15-C17
3	D	501	YNP	C31-C32-O8-C35
3	F	501	YNP	C5-C4-N1-C3
3	F	501	YNP	O1-C4-N1-C3
3	F	501	YNP	C13-C2-C3-N1
3	F	501	YNP	C28-C5-N2-C6
3	F	501	YNP	O2-C6-N2-C5
3	F	501	YNP	C7-C6-N2-C5
3	F	501	YNP	O3-C10-C18-C19
3	F	501	YNP	C11-C12-C14-C15
3	F	501	YNP	C14-C12-O5-C13
3	F	501	YNP	C2-C13-O5-C12
3	F	501	YNP	O6-C13-O5-C12
3	F	501	YNP	C12-C14-C15-C17
3	F	501	YNP	C31-C32-O8-C35
3	H	501	YNP	C5-C4-N1-C3
3	H	501	YNP	O1-C4-N1-C3
3	H	501	YNP	C13-C2-C3-N1
3	H	501	YNP	C28-C5-N2-C6
3	H	501	YNP	O2-C6-N2-C5
3	H	501	YNP	C7-C6-N2-C5
3	H	501	YNP	O3-C10-C18-C19
3	H	501	YNP	C11-C12-C14-C15
3	H	501	YNP	C14-C12-O5-C13
3	H	501	YNP	C2-C13-O5-C12
3	H	501	YNP	O6-C13-O5-C12
3	H	501	YNP	C12-C14-C15-C17
3	H	501	YNP	C31-C32-O8-C35
3	J	501	YNP	C5-C4-N1-C3
3	J	501	YNP	O1-C4-N1-C3
3	J	501	YNP	C13-C2-C3-N1
3	J	501	YNP	C28-C5-N2-C6
3	J	501	YNP	O2-C6-N2-C5
3	J	501	YNP	C7-C6-N2-C5
3	J	501	YNP	O3-C10-C18-C19
3	J	501	YNP	C11-C12-C14-C15
3	J	501	YNP	C14-C12-O5-C13
3	J	501	YNP	C2-C13-O5-C12

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	J	501	YNP	O6-C13-O5-C12
3	J	501	YNP	C12-C14-C15-C17
3	J	501	YNP	C31-C32-O8-C35
3	L	501	YNP	C5-C4-N1-C3
3	L	501	YNP	O1-C4-N1-C3
3	L	501	YNP	C13-C2-C3-N1
3	L	501	YNP	C28-C5-N2-C6
3	L	501	YNP	O2-C6-N2-C5
3	L	501	YNP	C7-C6-N2-C5
3	L	501	YNP	O3-C10-C18-C19
3	L	501	YNP	C11-C12-C14-C15
3	L	501	YNP	C14-C12-O5-C13
3	L	501	YNP	C2-C13-O5-C12
3	L	501	YNP	O6-C13-O5-C12
3	L	501	YNP	C12-C14-C15-C17
3	L	501	YNP	C31-C32-O8-C35
3	N	501	YNP	C5-C4-N1-C3
3	N	501	YNP	O1-C4-N1-C3
3	N	501	YNP	C13-C2-C3-N1
3	N	501	YNP	C28-C5-N2-C6
3	N	501	YNP	O2-C6-N2-C5
3	N	501	YNP	C7-C6-N2-C5
3	N	501	YNP	O3-C10-C18-C19
3	N	501	YNP	C11-C12-C14-C15
3	N	501	YNP	C14-C12-O5-C13
3	N	501	YNP	C2-C13-O5-C12
3	N	501	YNP	O6-C13-O5-C12
3	N	501	YNP	C12-C14-C15-C17
3	N	501	YNP	C31-C32-O8-C35
3	P	501	YNP	C5-C4-N1-C3
3	P	501	YNP	O1-C4-N1-C3
3	P	501	YNP	C13-C2-C3-N1
3	P	501	YNP	C28-C5-N2-C6
3	P	501	YNP	O2-C6-N2-C5
3	P	501	YNP	C7-C6-N2-C5
3	P	501	YNP	O3-C10-C18-C19
3	P	501	YNP	C11-C12-C14-C15
3	P	501	YNP	C14-C12-O5-C13
3	P	501	YNP	C2-C13-O5-C12
3	P	501	YNP	O6-C13-O5-C12
3	P	501	YNP	C12-C14-C15-C17
3	P	501	YNP	C31-C32-O8-C35

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	O4'-C4'-C5'-O5'
5	A	501	GTP	C3'-C4'-C5'-O5'
5	C	501	GTP	O4'-C4'-C5'-O5'
5	C	501	GTP	C3'-C4'-C5'-O5'
5	E	501	GTP	O4'-C4'-C5'-O5'
5	E	501	GTP	C3'-C4'-C5'-O5'
5	G	501	GTP	O4'-C4'-C5'-O5'
5	G	501	GTP	C3'-C4'-C5'-O5'
5	I	501	GTP	O4'-C4'-C5'-O5'
5	I	501	GTP	C3'-C4'-C5'-O5'
5	K	501	GTP	O4'-C4'-C5'-O5'
5	K	501	GTP	C3'-C4'-C5'-O5'
5	M	501	GTP	O4'-C4'-C5'-O5'
5	M	501	GTP	C3'-C4'-C5'-O5'
5	O	501	GTP	O4'-C4'-C5'-O5'
5	O	501	GTP	C3'-C4'-C5'-O5'
3	B	501	YNP	C33-C32-O8-C35
3	D	501	YNP	C33-C32-O8-C35
3	F	501	YNP	C33-C32-O8-C35
3	H	501	YNP	C33-C32-O8-C35
3	J	501	YNP	C33-C32-O8-C35
3	L	501	YNP	C33-C32-O8-C35
3	N	501	YNP	C33-C32-O8-C35
3	P	501	YNP	C33-C32-O8-C35
4	B	502	GDP	O4'-C4'-C5'-O5'
4	B	502	GDP	C3'-C4'-C5'-O5'
4	D	502	GDP	O4'-C4'-C5'-O5'
4	D	502	GDP	C3'-C4'-C5'-O5'
4	F	502	GDP	O4'-C4'-C5'-O5'
4	F	502	GDP	C3'-C4'-C5'-O5'
4	H	502	GDP	O4'-C4'-C5'-O5'
4	H	502	GDP	C3'-C4'-C5'-O5'
4	J	502	GDP	O4'-C4'-C5'-O5'
4	J	502	GDP	C3'-C4'-C5'-O5'
4	L	502	GDP	O4'-C4'-C5'-O5'
4	L	502	GDP	C3'-C4'-C5'-O5'
4	N	502	GDP	O4'-C4'-C5'-O5'
4	N	502	GDP	C3'-C4'-C5'-O5'
4	P	502	GDP	O4'-C4'-C5'-O5'
4	P	502	GDP	C3'-C4'-C5'-O5'
3	B	501	YNP	O2-C6-C7-C8
3	D	501	YNP	O2-C6-C7-C8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	F	501	YNP	O2-C6-C7-C8
3	H	501	YNP	O2-C6-C7-C8
3	J	501	YNP	O2-C6-C7-C8
3	L	501	YNP	O2-C6-C7-C8
3	N	501	YNP	O2-C6-C7-C8
3	P	501	YNP	O2-C6-C7-C8
3	B	501	YNP	N2-C6-C7-C8
3	D	501	YNP	N2-C6-C7-C8
3	F	501	YNP	N2-C6-C7-C8
3	H	501	YNP	N2-C6-C7-C8
3	J	501	YNP	N2-C6-C7-C8
3	L	501	YNP	N2-C6-C7-C8
3	N	501	YNP	N2-C6-C7-C8
3	P	501	YNP	N2-C6-C7-C8
3	B	501	YNP	C12-C14-C15-C16
3	D	501	YNP	C12-C14-C15-C16
3	F	501	YNP	C12-C14-C15-C16
3	H	501	YNP	C12-C14-C15-C16
3	J	501	YNP	C12-C14-C15-C16
3	L	501	YNP	C12-C14-C15-C16
3	N	501	YNP	C12-C14-C15-C16
3	P	501	YNP	C12-C14-C15-C16
3	B	501	YNP	O7-C21-C22-C23
3	D	501	YNP	O7-C21-C22-C23
3	F	501	YNP	O7-C21-C22-C23
3	H	501	YNP	O7-C21-C22-C23
3	J	501	YNP	O7-C21-C22-C23
3	L	501	YNP	O7-C21-C22-C23
3	N	501	YNP	O7-C21-C22-C23
3	P	501	YNP	O7-C21-C22-C23
3	B	501	YNP	O4-C11-O3-C10
3	D	501	YNP	O4-C11-O3-C10
3	F	501	YNP	O4-C11-O3-C10
3	H	501	YNP	O4-C11-O3-C10
3	J	501	YNP	O4-C11-O3-C10
3	L	501	YNP	O4-C11-O3-C10
3	N	501	YNP	O4-C11-O3-C10
3	P	501	YNP	O4-C11-O3-C10
3	B	501	YNP	C12-C11-O3-C10
3	D	501	YNP	C12-C11-O3-C10
3	F	501	YNP	C12-C11-O3-C10
3	H	501	YNP	C12-C11-O3-C10

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	J	501	YNP	C12-C11-O3-C10
3	L	501	YNP	C12-C11-O3-C10
3	N	501	YNP	C12-C11-O3-C10
3	P	501	YNP	C12-C11-O3-C10
3	B	501	YNP	C2-C3-N1-C4
3	D	501	YNP	C2-C3-N1-C4
3	F	501	YNP	C2-C3-N1-C4
3	H	501	YNP	C2-C3-N1-C4
3	J	501	YNP	C2-C3-N1-C4
3	L	501	YNP	C2-C3-N1-C4
3	N	501	YNP	C2-C3-N1-C4
3	P	501	YNP	C2-C3-N1-C4
3	B	501	YNP	C49-C2-C3-N1
3	D	501	YNP	C49-C2-C3-N1
3	F	501	YNP	C49-C2-C3-N1
3	H	501	YNP	C49-C2-C3-N1
3	J	501	YNP	C49-C2-C3-N1
3	L	501	YNP	C49-C2-C3-N1
3	N	501	YNP	C49-C2-C3-N1
3	P	501	YNP	C49-C2-C3-N1
3	B	501	YNP	O5-C12-C14-C15
3	D	501	YNP	O5-C12-C14-C15
3	F	501	YNP	O5-C12-C14-C15
3	H	501	YNP	O5-C12-C14-C15
3	J	501	YNP	O5-C12-C14-C15
3	L	501	YNP	O5-C12-C14-C15
3	N	501	YNP	O5-C12-C14-C15
3	P	501	YNP	O5-C12-C14-C15
3	B	501	YNP	O1-C4-C5-N2
3	D	501	YNP	O1-C4-C5-N2
3	F	501	YNP	O1-C4-C5-N2
3	H	501	YNP	O1-C4-C5-N2
3	J	501	YNP	O1-C4-C5-N2
3	L	501	YNP	O1-C4-C5-N2
3	N	501	YNP	O1-C4-C5-N2
3	P	501	YNP	O1-C4-C5-N2
3	D	501	YNP	N1-C4-C5-N2
3	H	501	YNP	N1-C4-C5-N2
3	L	501	YNP	N1-C4-C5-N2
3	P	501	YNP	N1-C4-C5-N2
3	B	501	YNP	N1-C4-C5-N2
3	F	501	YNP	N1-C4-C5-N2

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	J	501	YNP	N1-C4-C5-N2
3	N	501	YNP	N1-C4-C5-N2
3	B	501	YNP	O4-C11-C12-O5
3	D	501	YNP	O4-C11-C12-O5
3	F	501	YNP	O4-C11-C12-O5
3	H	501	YNP	O4-C11-C12-O5
3	J	501	YNP	O4-C11-C12-O5
3	L	501	YNP	O4-C11-C12-O5
3	N	501	YNP	O4-C11-C12-O5
3	P	501	YNP	O4-C11-C12-O5
3	B	501	YNP	O7-C21-C22-C27
3	D	501	YNP	O7-C21-C22-C27
3	F	501	YNP	O7-C21-C22-C27
3	H	501	YNP	O7-C21-C22-C27
3	J	501	YNP	O7-C21-C22-C27
3	L	501	YNP	O7-C21-C22-C27
3	N	501	YNP	O7-C21-C22-C27
3	P	501	YNP	O7-C21-C22-C27
4	B	502	GDP	C4'-C5'-O5'-PA
4	D	502	GDP	C4'-C5'-O5'-PA
4	F	502	GDP	C4'-C5'-O5'-PA
4	H	502	GDP	C4'-C5'-O5'-PA
4	J	502	GDP	C4'-C5'-O5'-PA
4	L	502	GDP	C4'-C5'-O5'-PA
4	N	502	GDP	C4'-C5'-O5'-PA
4	P	502	GDP	C4'-C5'-O5'-PA
3	B	501	YNP	O4-C11-C12-C14
3	D	501	YNP	O4-C11-C12-C14
3	F	501	YNP	O4-C11-C12-C14
3	H	501	YNP	O4-C11-C12-C14
3	J	501	YNP	O4-C11-C12-C14
3	L	501	YNP	O4-C11-C12-C14
3	N	501	YNP	O4-C11-C12-C14
3	P	501	YNP	O4-C11-C12-C14
5	A	501	GTP	PG-O3B-PB-O1B
5	A	501	GTP	PB-O3A-PA-O2A
5	C	501	GTP	PG-O3B-PB-O1B
5	C	501	GTP	PB-O3A-PA-O2A
5	E	501	GTP	PG-O3B-PB-O1B
5	E	501	GTP	PB-O3A-PA-O2A
5	G	501	GTP	PG-O3B-PB-O1B
5	G	501	GTP	PB-O3A-PA-O2A

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
5	I	501	GTP	PG-O3B-PB-O1B
5	I	501	GTP	PB-O3A-PA-O2A
5	K	501	GTP	PG-O3B-PB-O1B
5	K	501	GTP	PB-O3A-PA-O2A
5	M	501	GTP	PG-O3B-PB-O1B
5	M	501	GTP	PB-O3A-PA-O2A
5	O	501	GTP	PG-O3B-PB-O1B
5	O	501	GTP	PB-O3A-PA-O2A
3	B	501	YNP	O6-C13-C2-C49
3	D	501	YNP	O6-C13-C2-C49
3	F	501	YNP	O6-C13-C2-C49
3	H	501	YNP	O6-C13-C2-C49
3	J	501	YNP	O6-C13-C2-C49
3	L	501	YNP	O6-C13-C2-C49
3	N	501	YNP	O6-C13-C2-C49
3	P	501	YNP	O6-C13-C2-C49
3	B	501	YNP	O3-C11-C12-C14
3	B	501	YNP	C10-C18-C20-O7
3	D	501	YNP	O3-C11-C12-C14
3	D	501	YNP	C10-C18-C20-O7
3	F	501	YNP	O3-C11-C12-C14
3	F	501	YNP	C10-C18-C20-O7
3	H	501	YNP	O3-C11-C12-C14
3	H	501	YNP	C10-C18-C20-O7
3	J	501	YNP	O3-C11-C12-C14
3	J	501	YNP	C10-C18-C20-O7
3	L	501	YNP	O3-C11-C12-C14
3	L	501	YNP	C10-C18-C20-O7
3	N	501	YNP	O3-C11-C12-C14
3	N	501	YNP	C10-C18-C20-O7
3	P	501	YNP	O3-C11-C12-C14
3	P	501	YNP	C10-C18-C20-O7
3	B	501	YNP	O5-C13-C2-C49
3	D	501	YNP	O5-C13-C2-C49
3	F	501	YNP	O5-C13-C2-C49
3	H	501	YNP	O5-C13-C2-C49
3	J	501	YNP	O5-C13-C2-C49
3	L	501	YNP	O5-C13-C2-C49
3	N	501	YNP	O5-C13-C2-C49
3	P	501	YNP	O5-C13-C2-C49
3	B	501	YNP	O3-C10-C9-C8
3	D	501	YNP	O3-C10-C9-C8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	F	501	YNP	O3-C10-C9-C8
3	H	501	YNP	O3-C10-C9-C8
3	J	501	YNP	O3-C10-C9-C8
3	L	501	YNP	O3-C10-C9-C8
3	N	501	YNP	O3-C10-C9-C8
3	P	501	YNP	O3-C10-C9-C8
3	B	501	YNP	C19-C18-C20-O7
3	D	501	YNP	C19-C18-C20-O7
3	F	501	YNP	C19-C18-C20-O7
3	H	501	YNP	C19-C18-C20-O7
3	J	501	YNP	C19-C18-C20-O7
3	L	501	YNP	C19-C18-C20-O7
3	N	501	YNP	C19-C18-C20-O7
3	P	501	YNP	C19-C18-C20-O7
5	A	501	GTP	PG-O3B-PB-O2B
5	A	501	GTP	PB-O3A-PA-O1A
5	C	501	GTP	PG-O3B-PB-O2B
5	C	501	GTP	PB-O3A-PA-O1A
5	E	501	GTP	PG-O3B-PB-O2B
5	E	501	GTP	PB-O3A-PA-O1A
5	G	501	GTP	PG-O3B-PB-O2B
5	G	501	GTP	PB-O3A-PA-O1A
5	I	501	GTP	PG-O3B-PB-O2B
5	I	501	GTP	PB-O3A-PA-O1A
5	K	501	GTP	PG-O3B-PB-O2B
5	K	501	GTP	PB-O3A-PA-O1A
5	M	501	GTP	PG-O3B-PB-O2B
5	M	501	GTP	PB-O3A-PA-O1A
5	O	501	GTP	PG-O3B-PB-O2B
5	O	501	GTP	PB-O3A-PA-O1A
3	B	501	YNP	C9-C10-C18-C19
3	D	501	YNP	C9-C10-C18-C19
3	F	501	YNP	C9-C10-C18-C19
3	H	501	YNP	C9-C10-C18-C19
3	J	501	YNP	C9-C10-C18-C19
3	L	501	YNP	C9-C10-C18-C19
3	N	501	YNP	C9-C10-C18-C19
3	P	501	YNP	C9-C10-C18-C19
3	B	501	YNP	O3-C11-C12-O5
3	D	501	YNP	O3-C11-C12-O5
3	F	501	YNP	O3-C11-C12-O5
3	H	501	YNP	O3-C11-C12-O5

*Continued on next page...*

*Continued from previous page...*

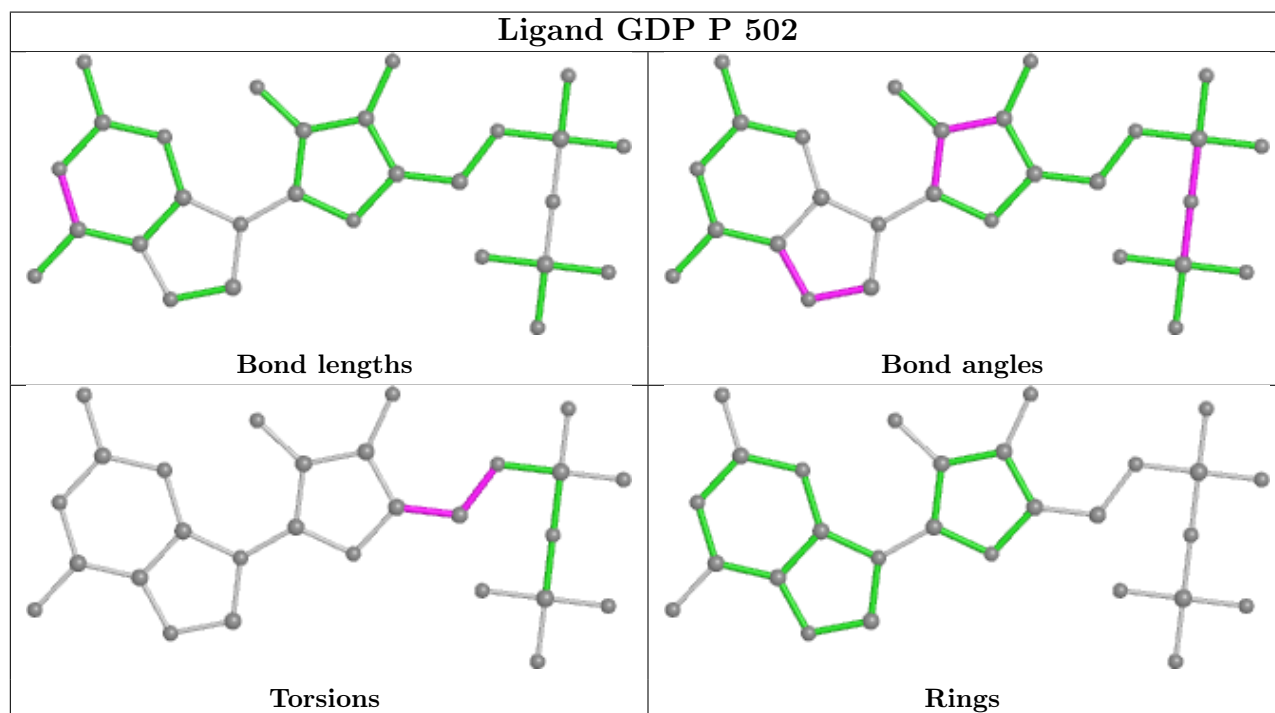
Mol	Chain	Res	Type	Atoms
3	J	501	YNP	O3-C11-C12-O5
3	L	501	YNP	O3-C11-C12-O5
3	N	501	YNP	O3-C11-C12-O5
3	P	501	YNP	O3-C11-C12-O5
3	B	501	YNP	C5-C28-C29-C34
3	D	501	YNP	C5-C28-C29-C34
3	F	501	YNP	C5-C28-C29-C34
3	H	501	YNP	C5-C28-C29-C34
3	J	501	YNP	C5-C28-C29-C34
3	L	501	YNP	C5-C28-C29-C34
3	N	501	YNP	C5-C28-C29-C34
3	P	501	YNP	C5-C28-C29-C34
3	B	501	YNP	C5-C28-C29-C30
3	F	501	YNP	C5-C28-C29-C30
3	J	501	YNP	C5-C28-C29-C30
3	N	501	YNP	C5-C28-C29-C30
3	D	501	YNP	C5-C28-C29-C30
3	H	501	YNP	C5-C28-C29-C30
3	L	501	YNP	C5-C28-C29-C30
3	P	501	YNP	C5-C28-C29-C30

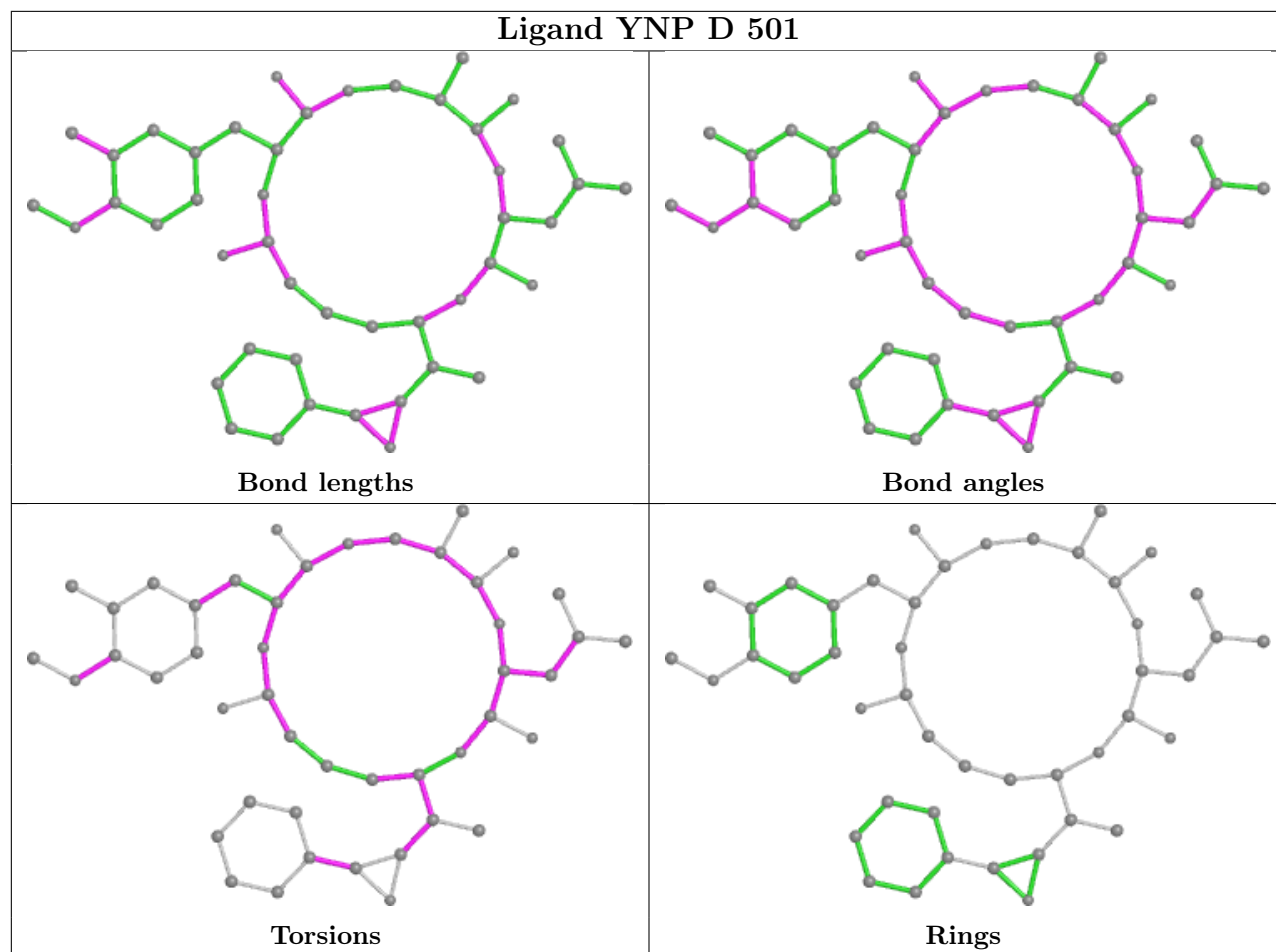
There are no ring outliers.

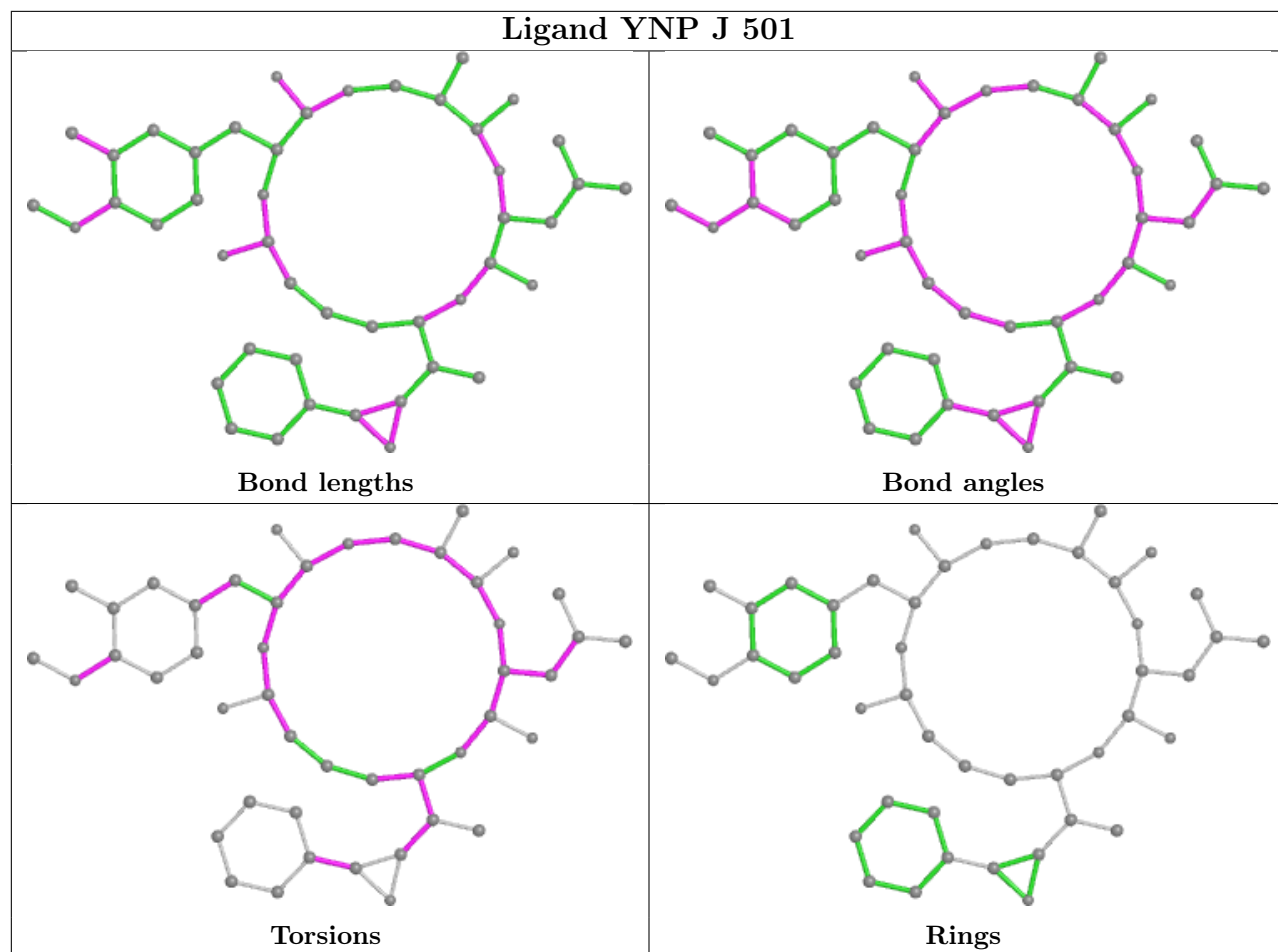
16 monomers are involved in 38 short contacts:

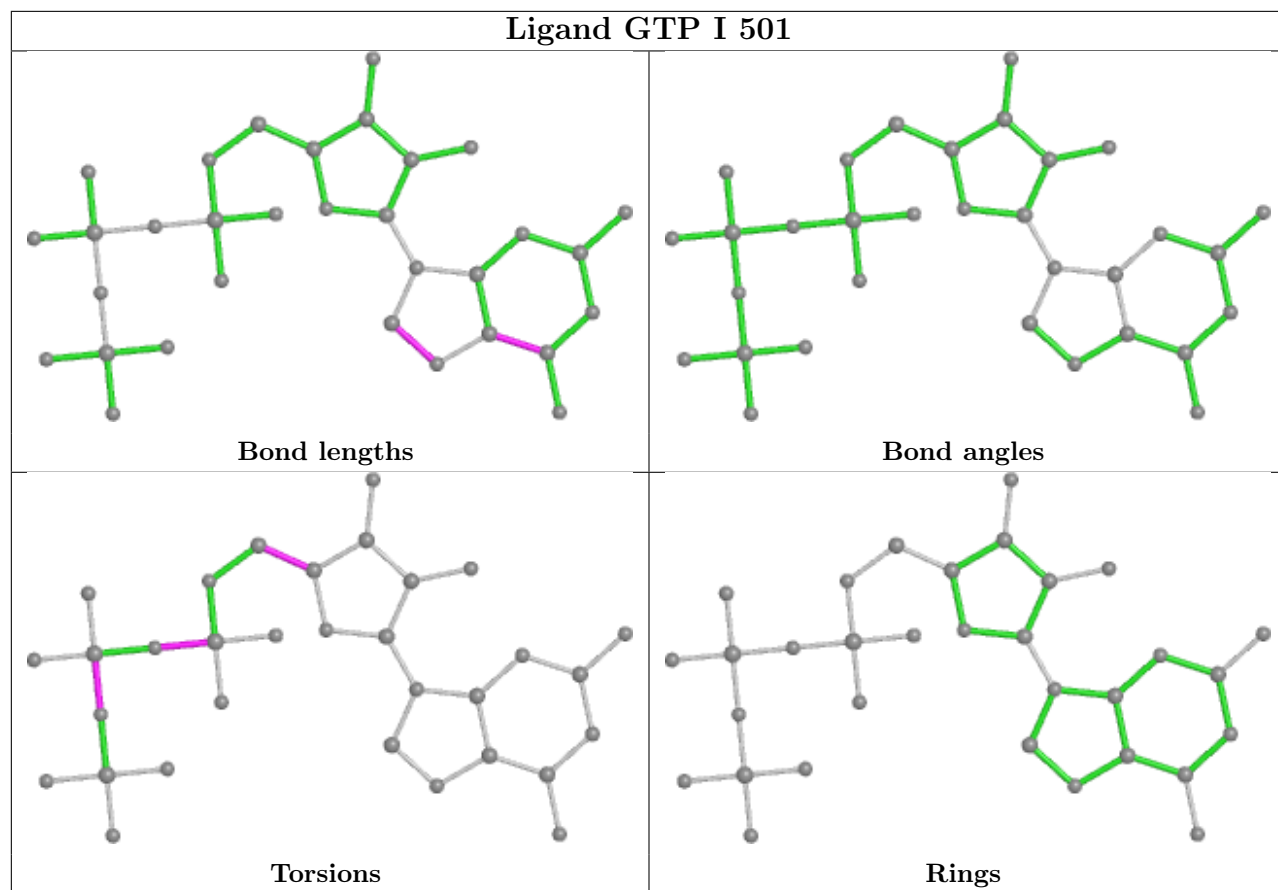
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	P	502	GDP	4	0
3	D	501	YNP	1	0
3	J	501	YNP	1	0
3	B	501	YNP	1	0
4	H	502	GDP	4	0
4	D	502	GDP	4	0
4	F	502	GDP	4	0
4	L	502	GDP	4	0
3	L	501	YNP	1	0
3	P	501	YNP	1	0
4	B	502	GDP	4	0
4	J	502	GDP	3	0
3	N	501	YNP	1	0
4	N	502	GDP	3	0
3	F	501	YNP	1	0
3	H	501	YNP	1	0

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.

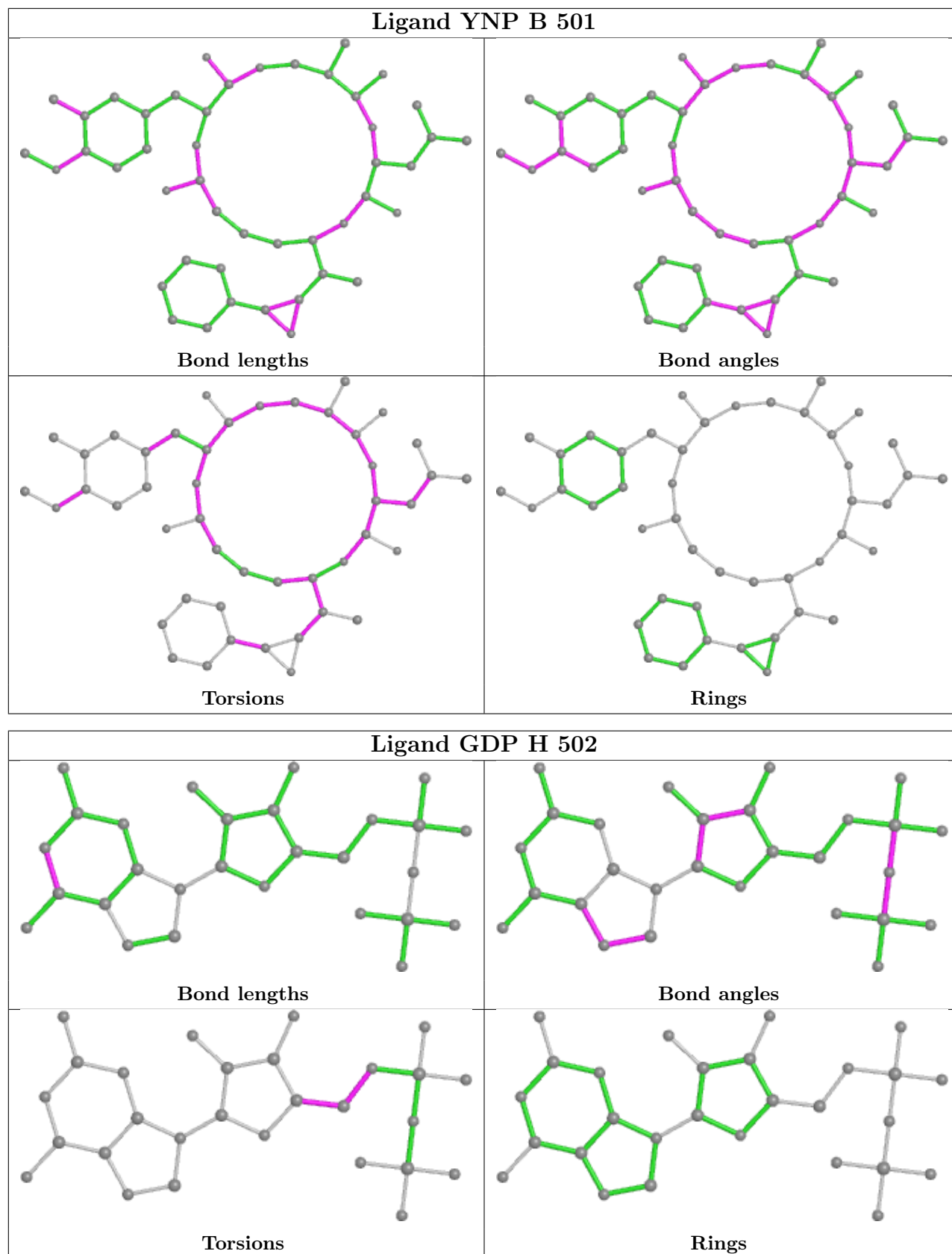


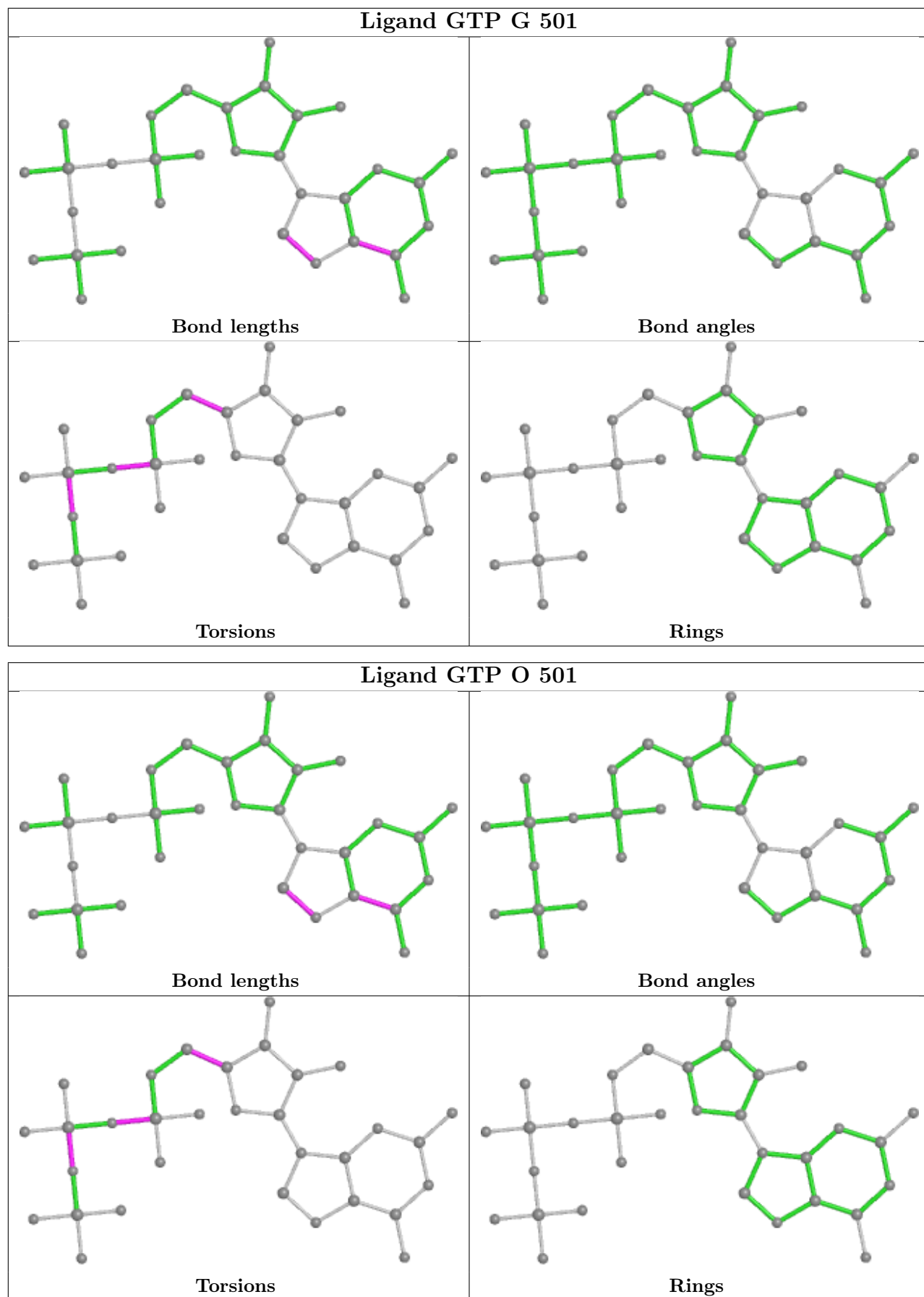


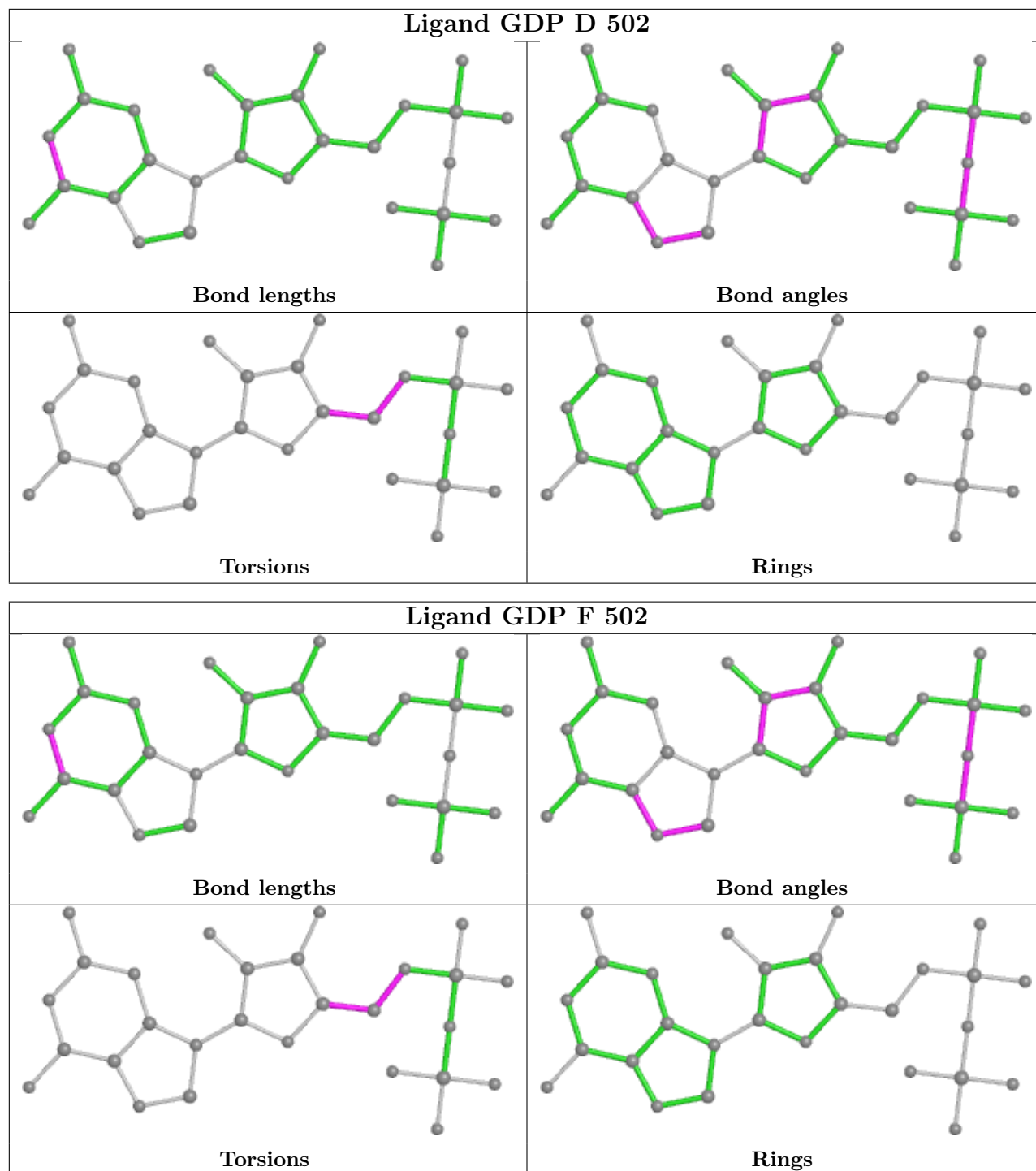


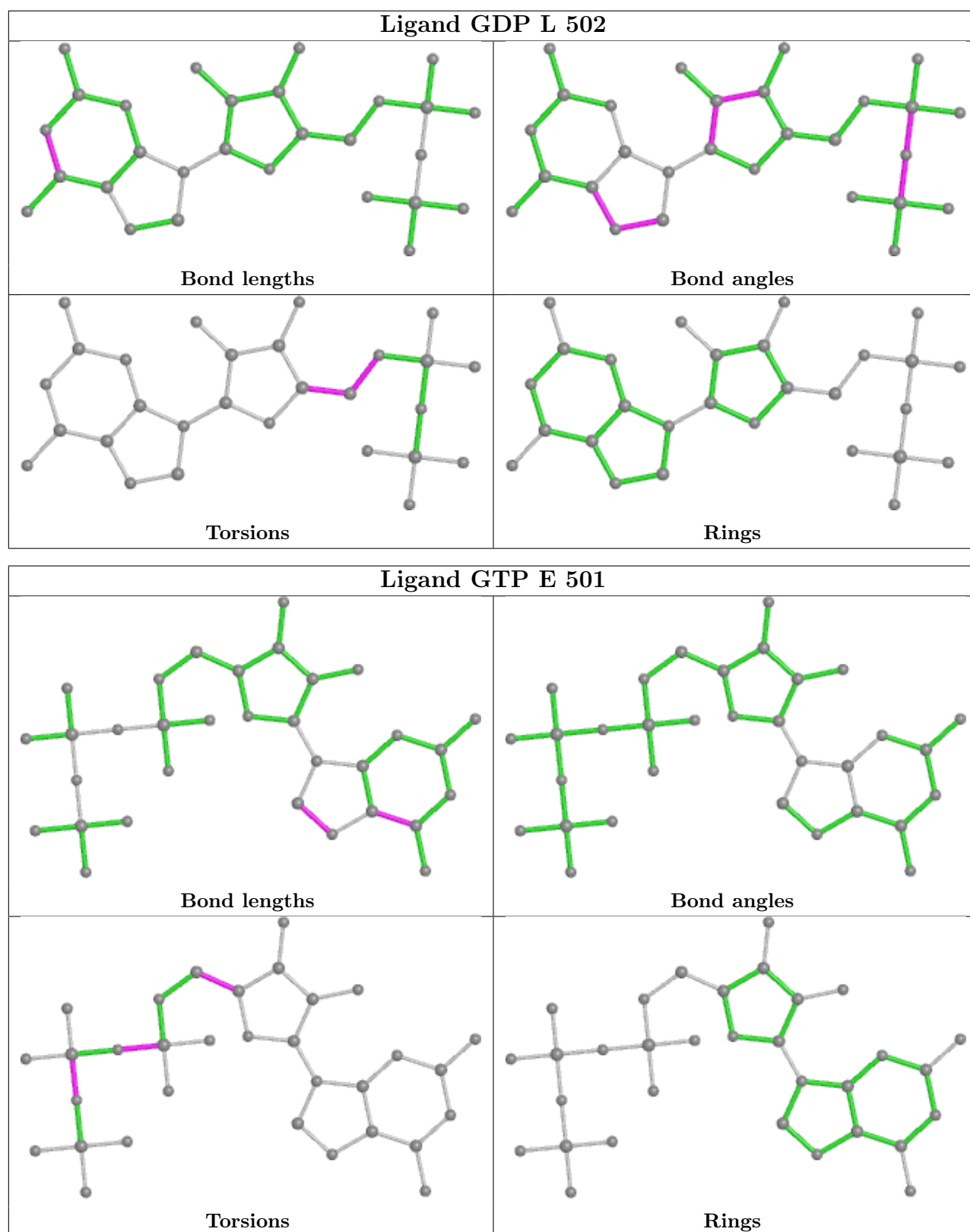


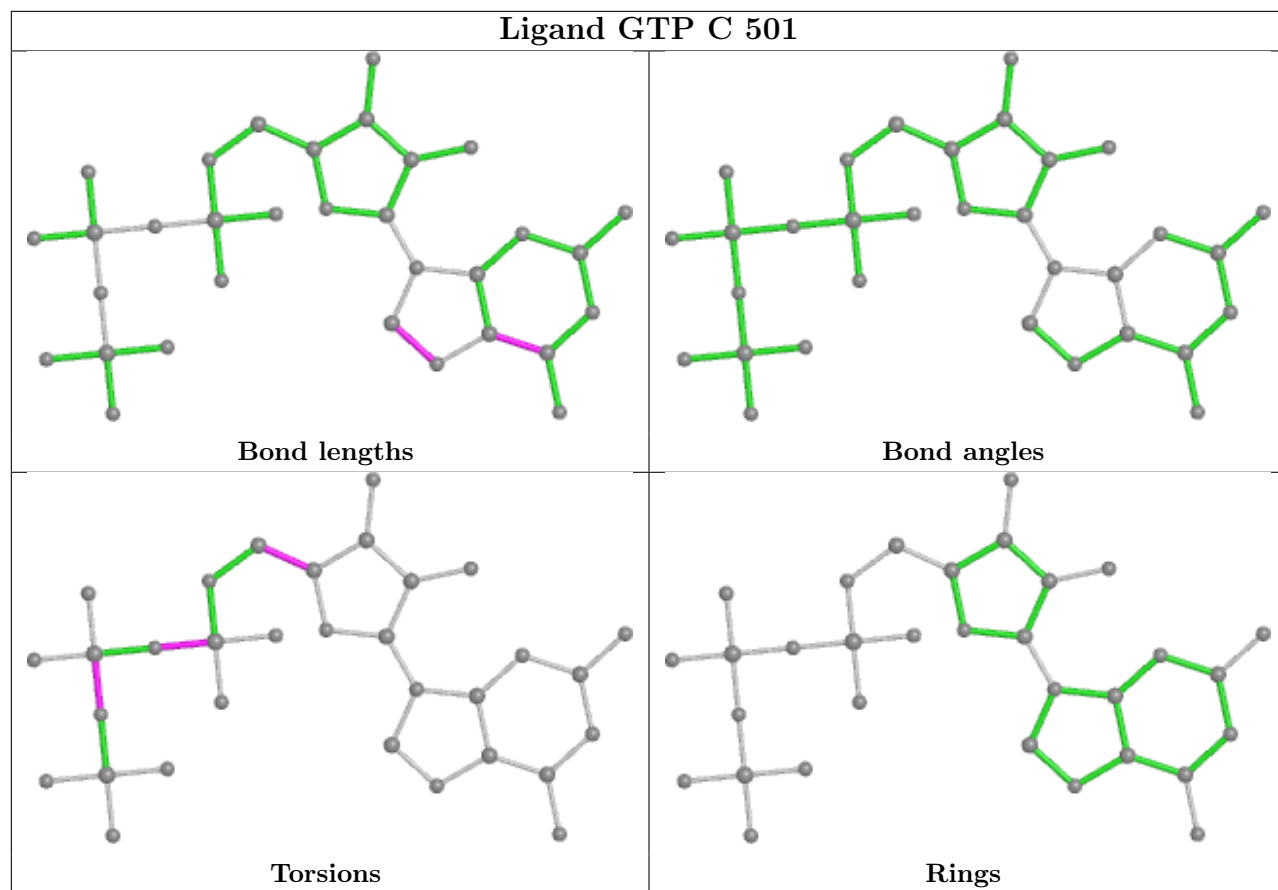


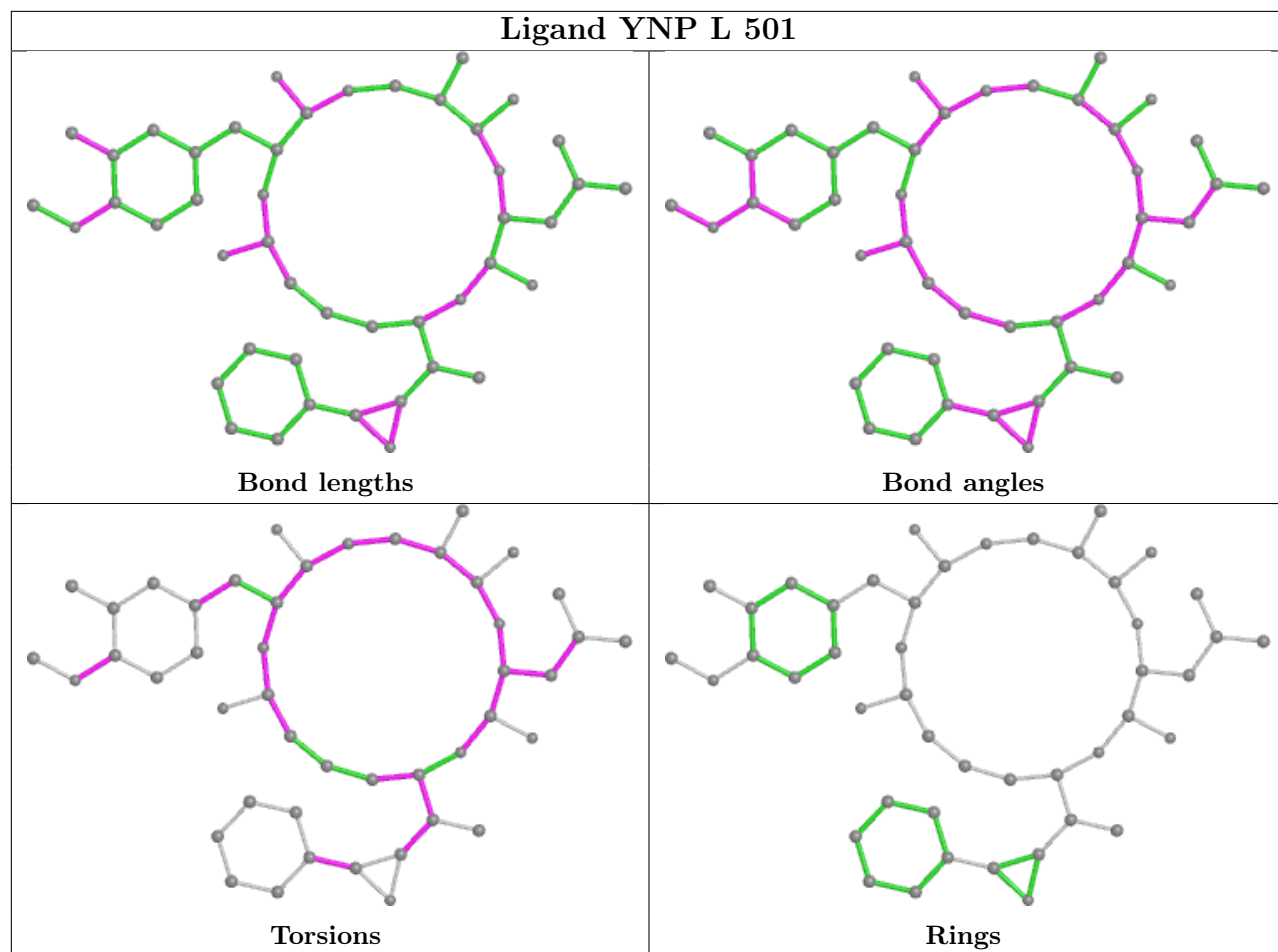


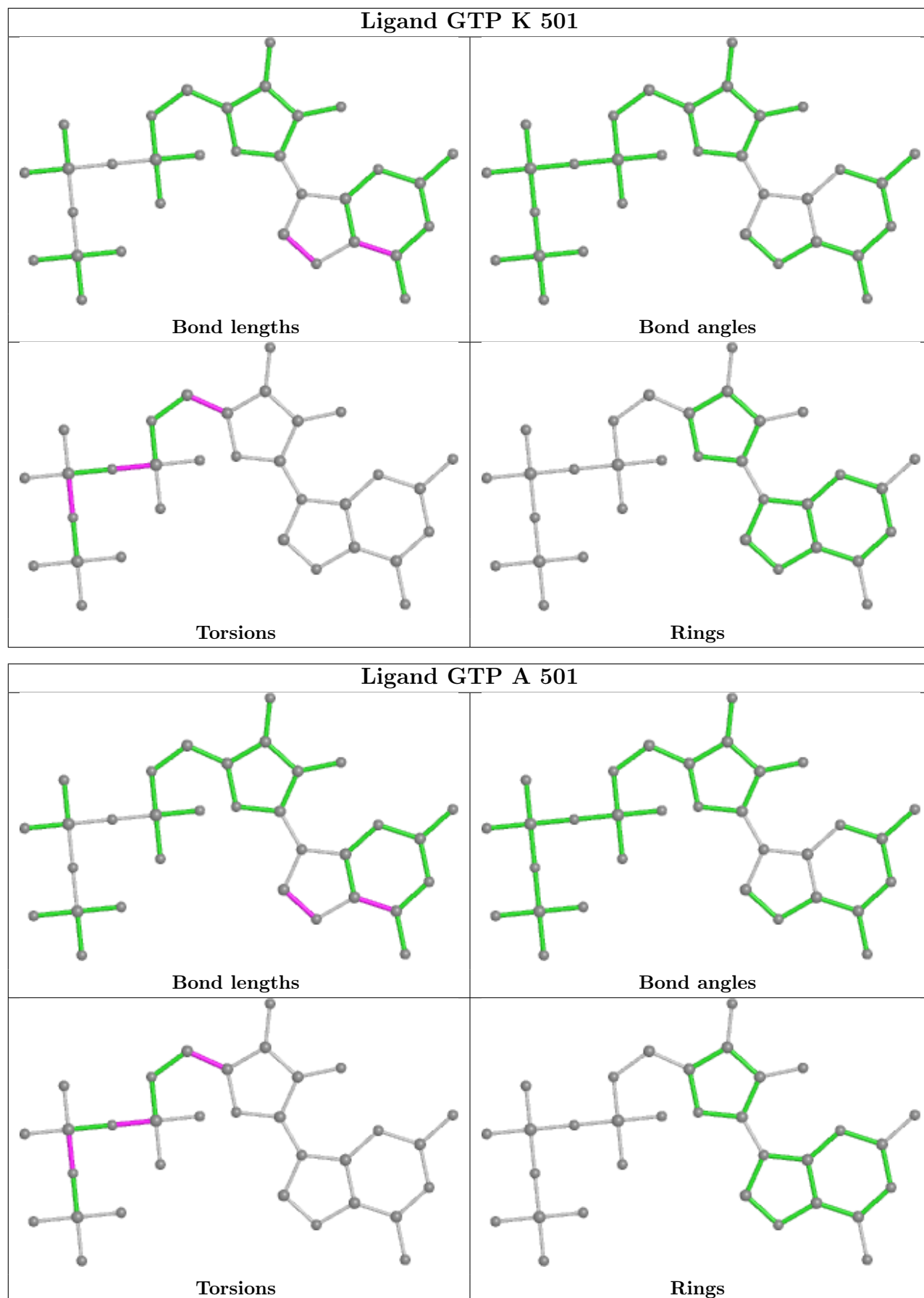


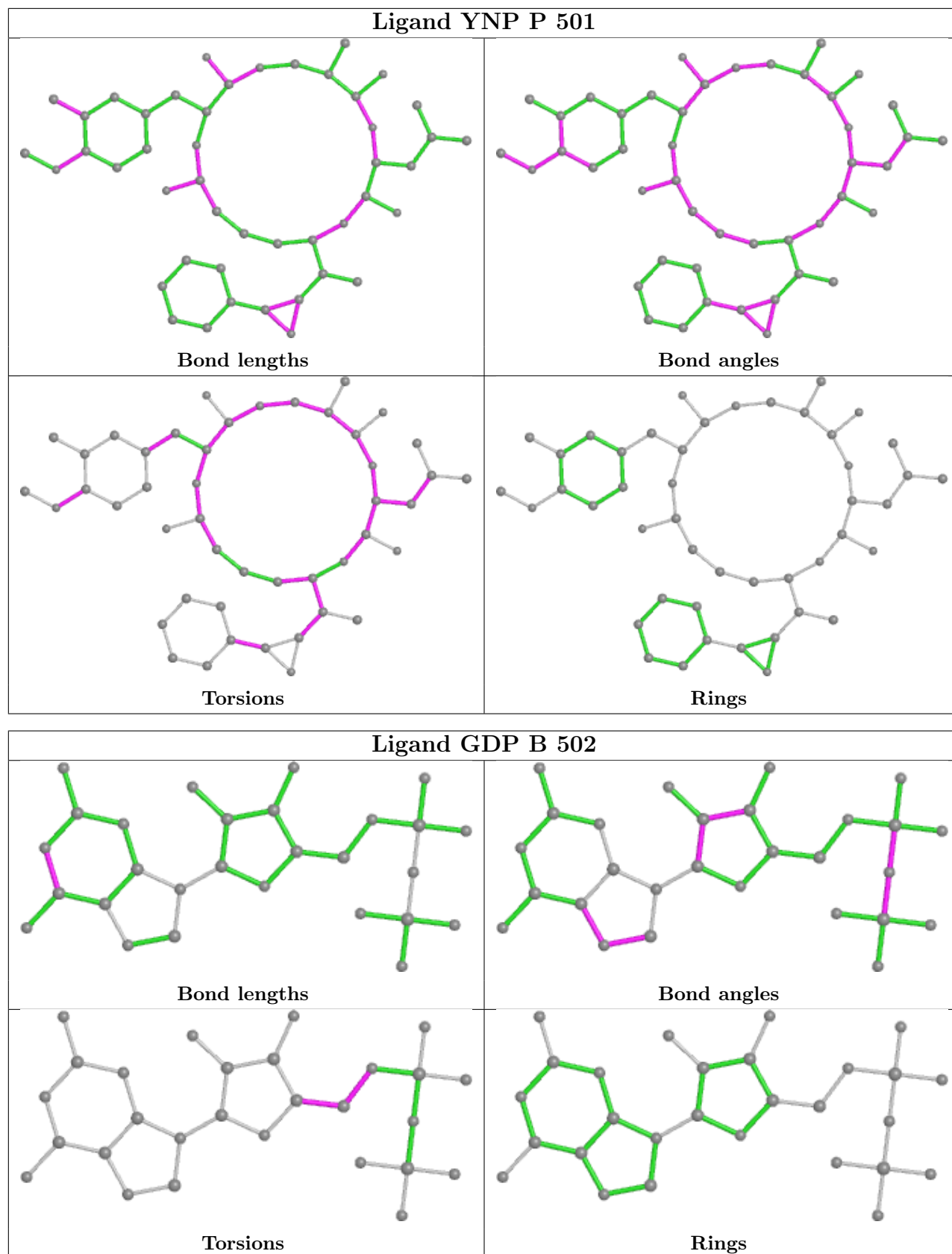




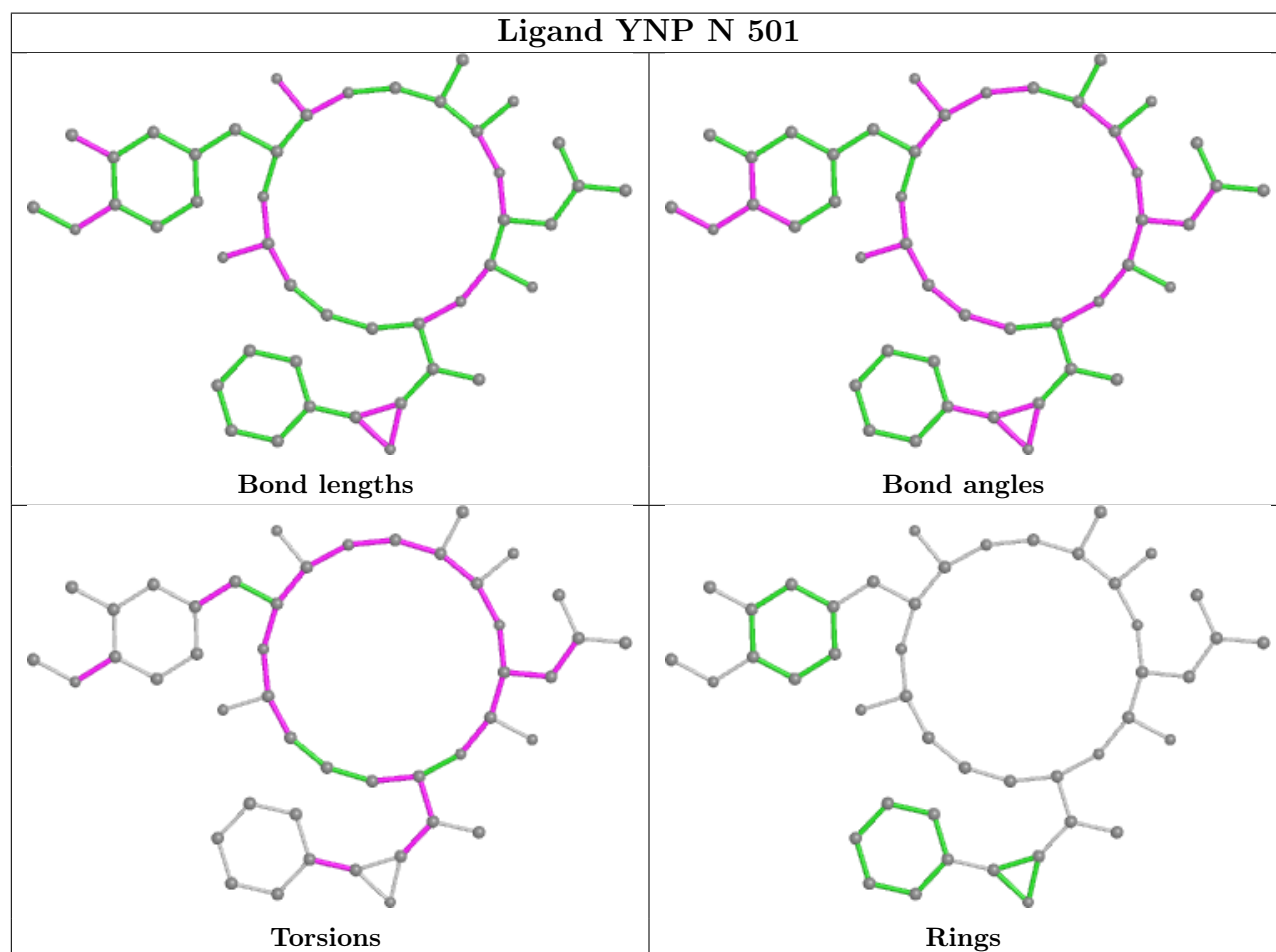
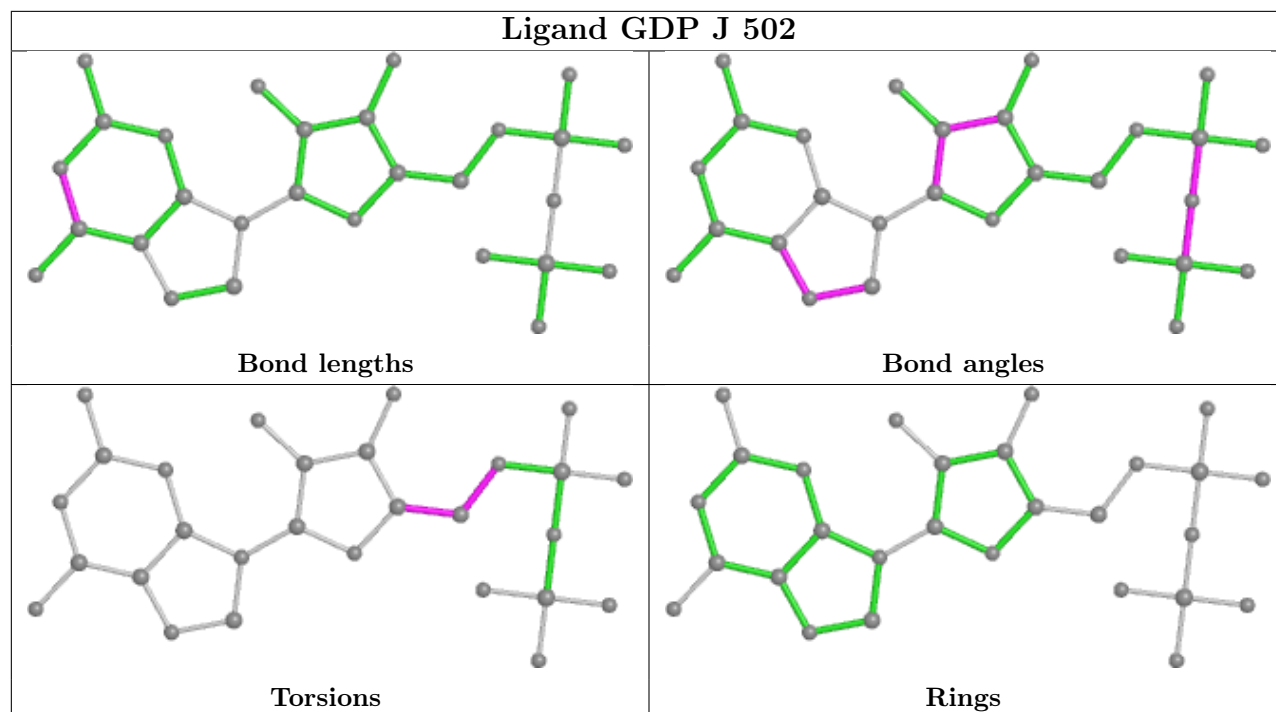


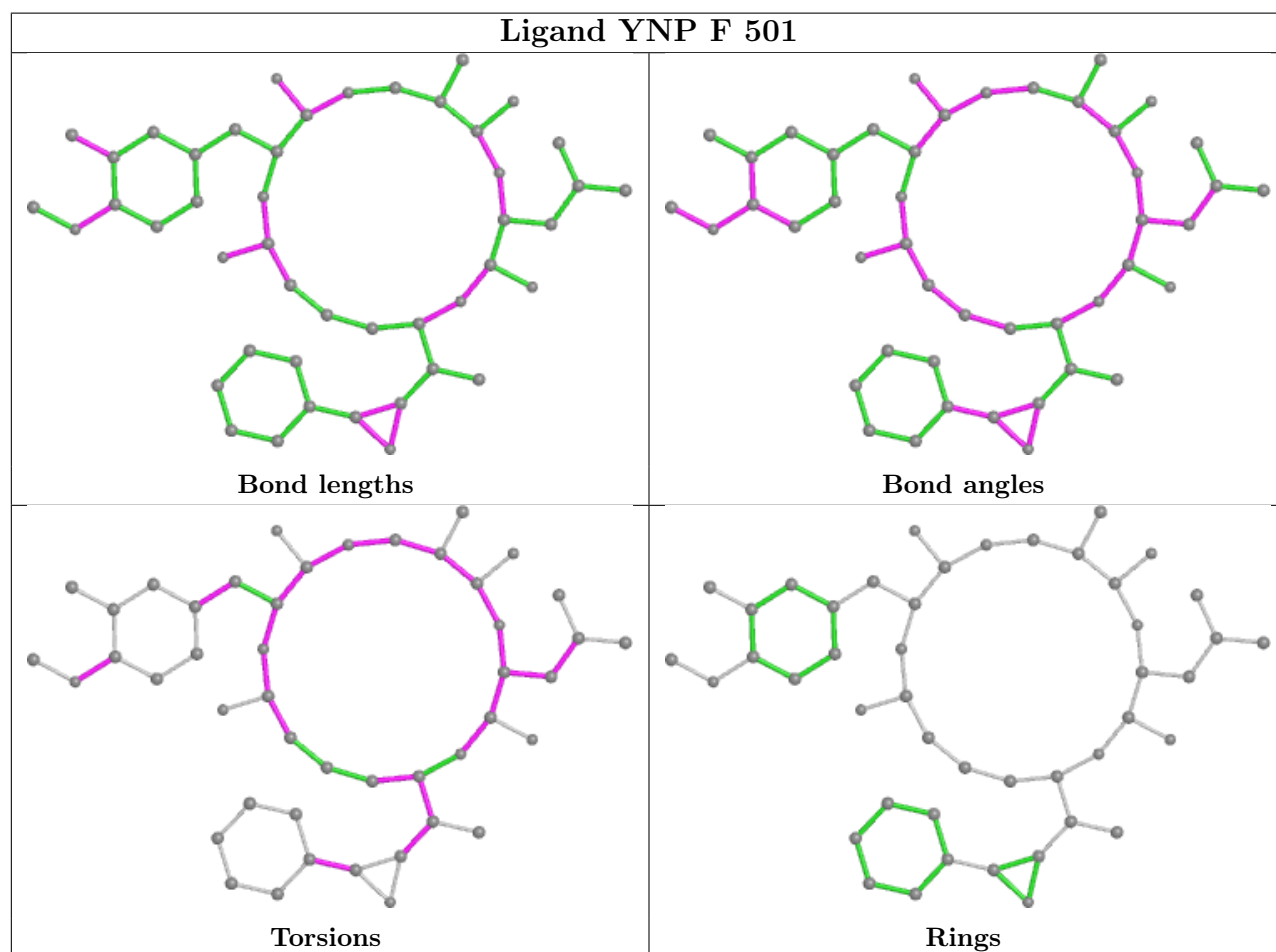
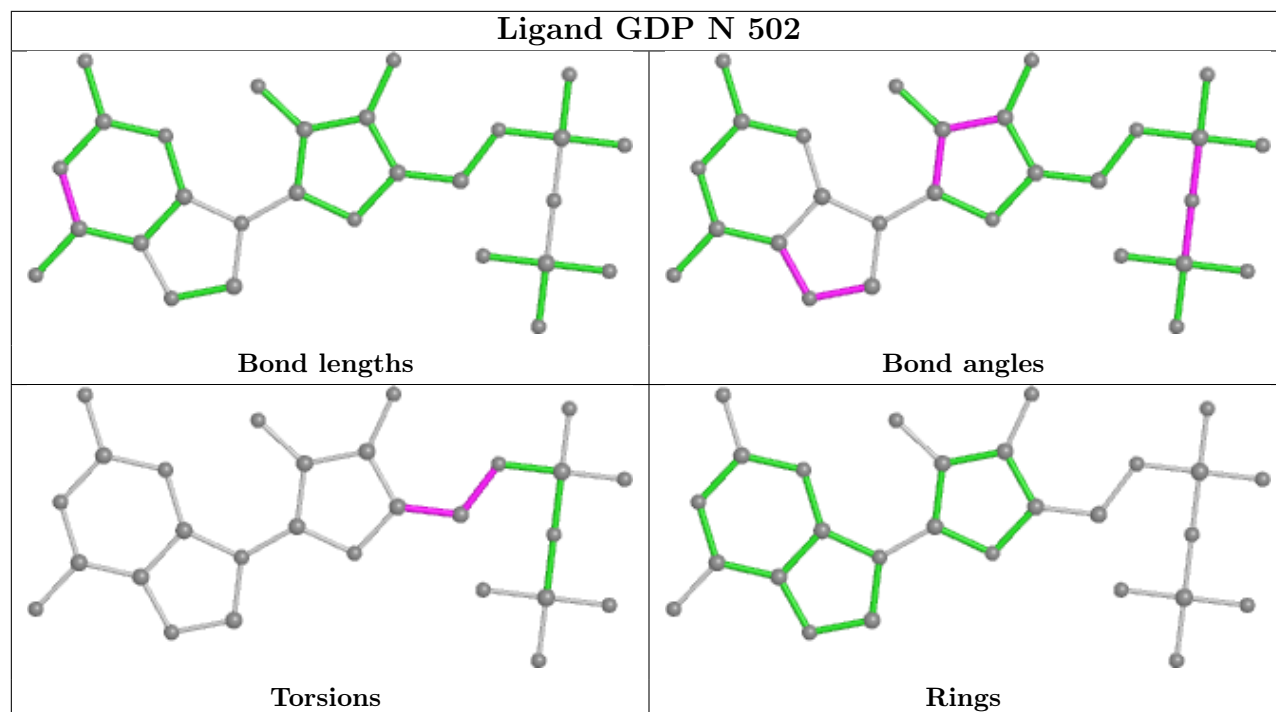


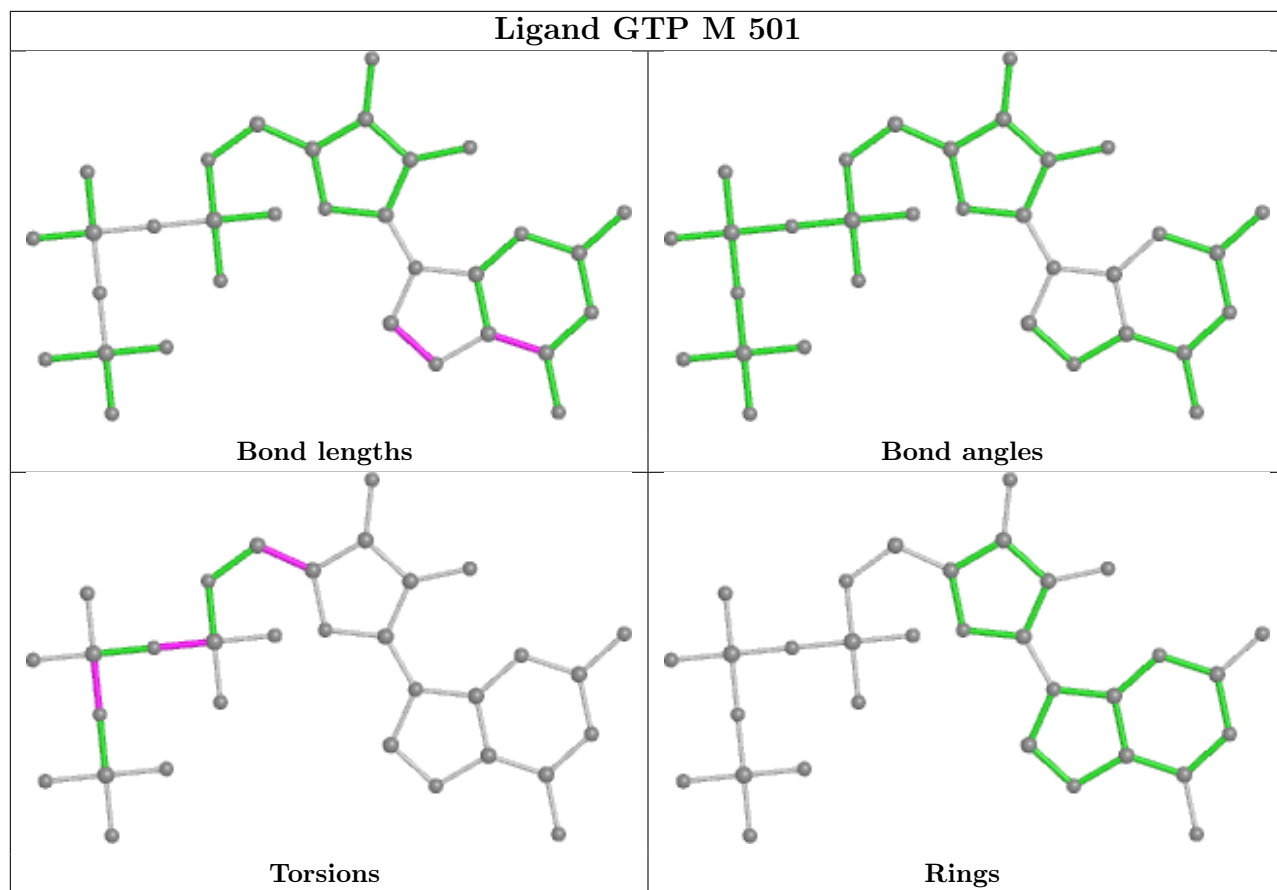


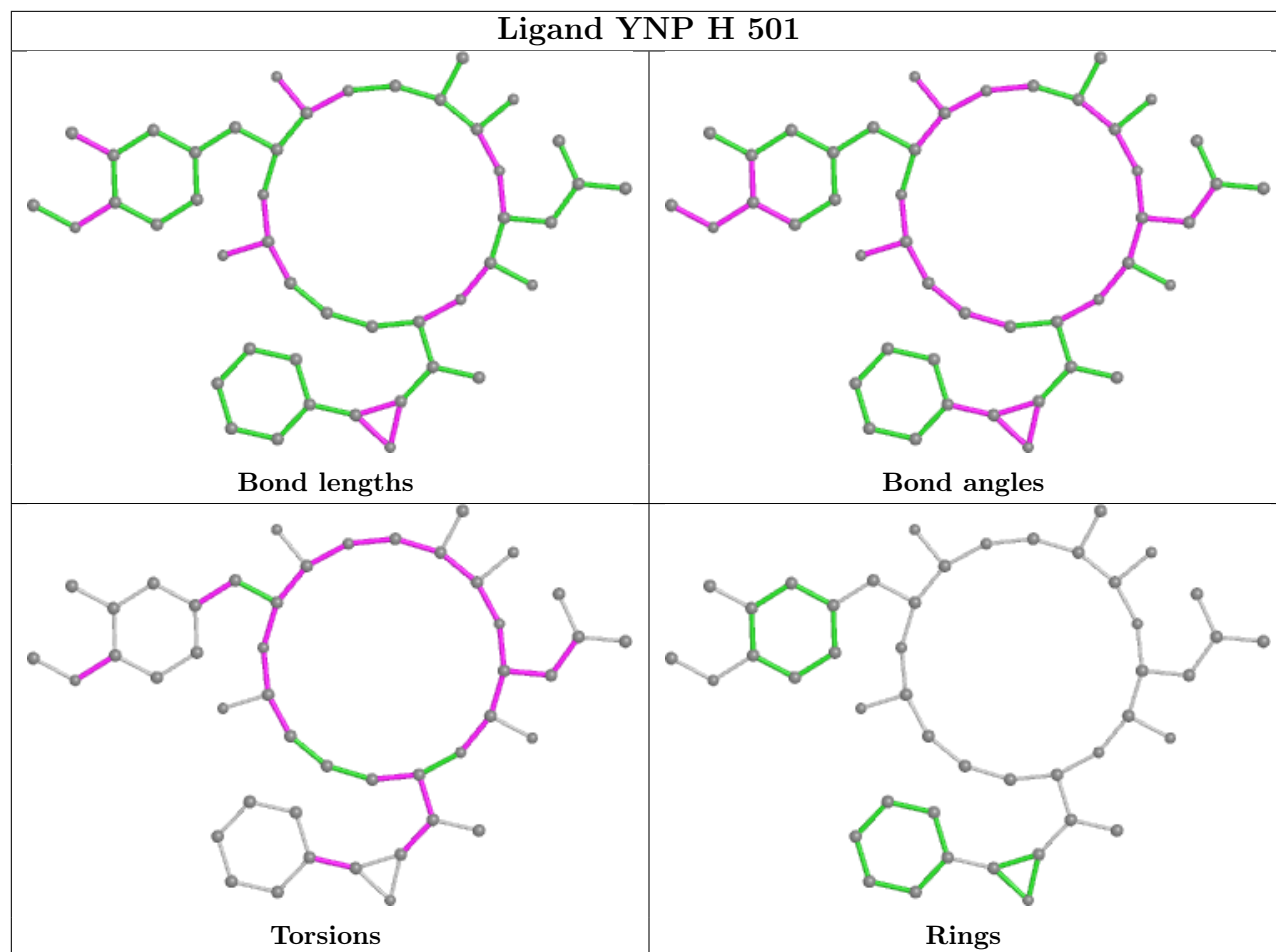












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

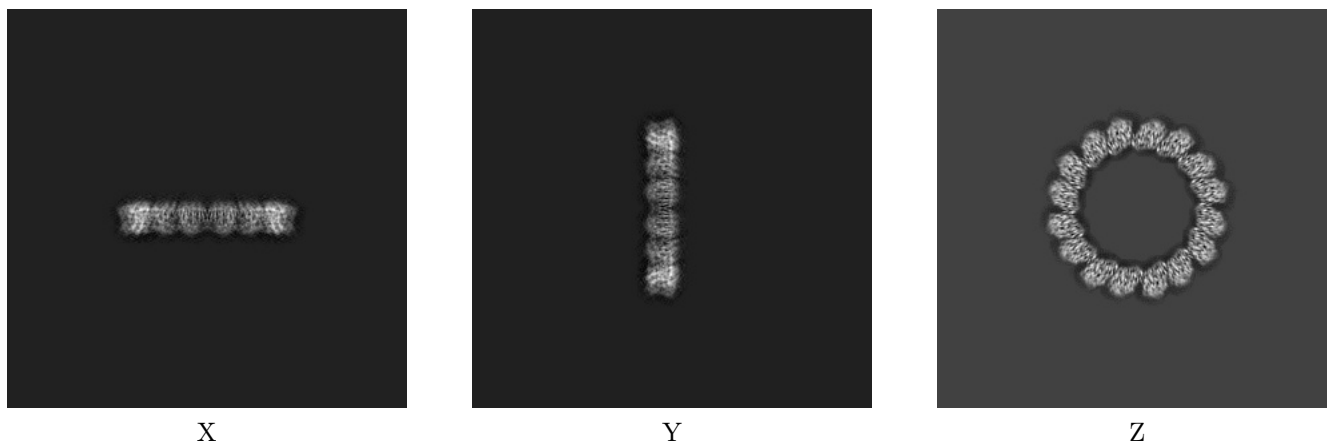
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23615. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

### 6.1 Orthogonal projections [i](#)

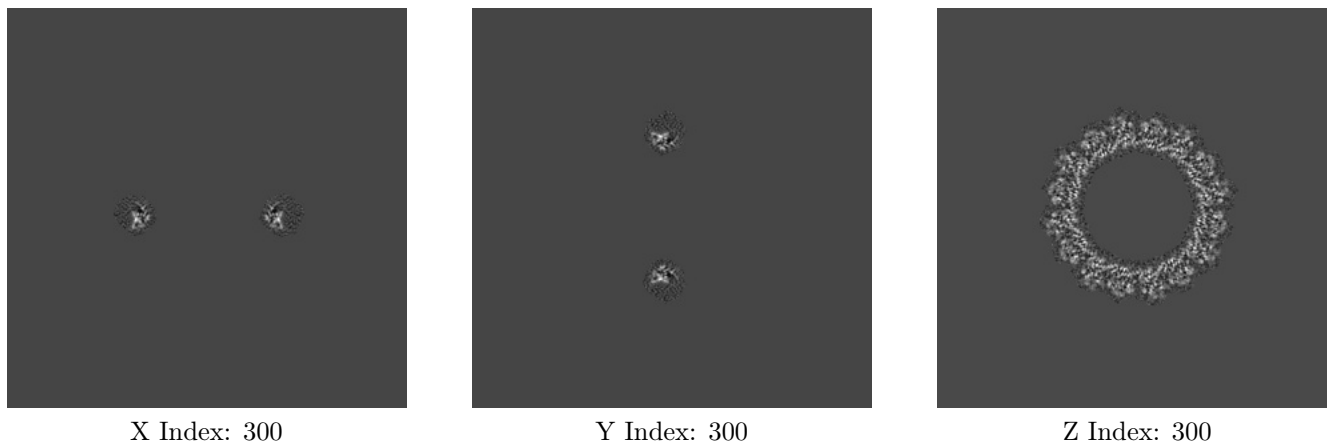
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

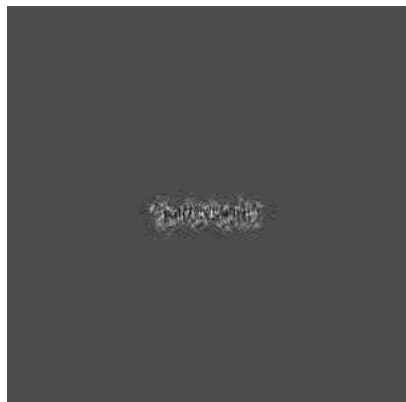
#### 6.2.1 Primary map



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: 398



Y Index: 398

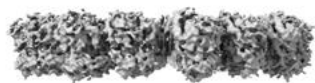


Z Index: 288

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

## 6.4 Orthogonal surface views [i](#)

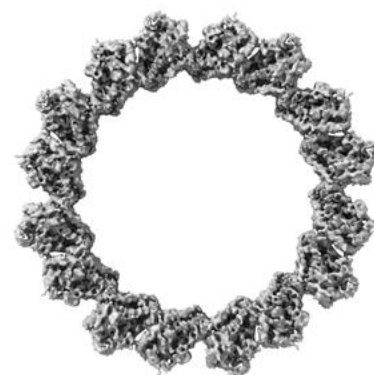
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

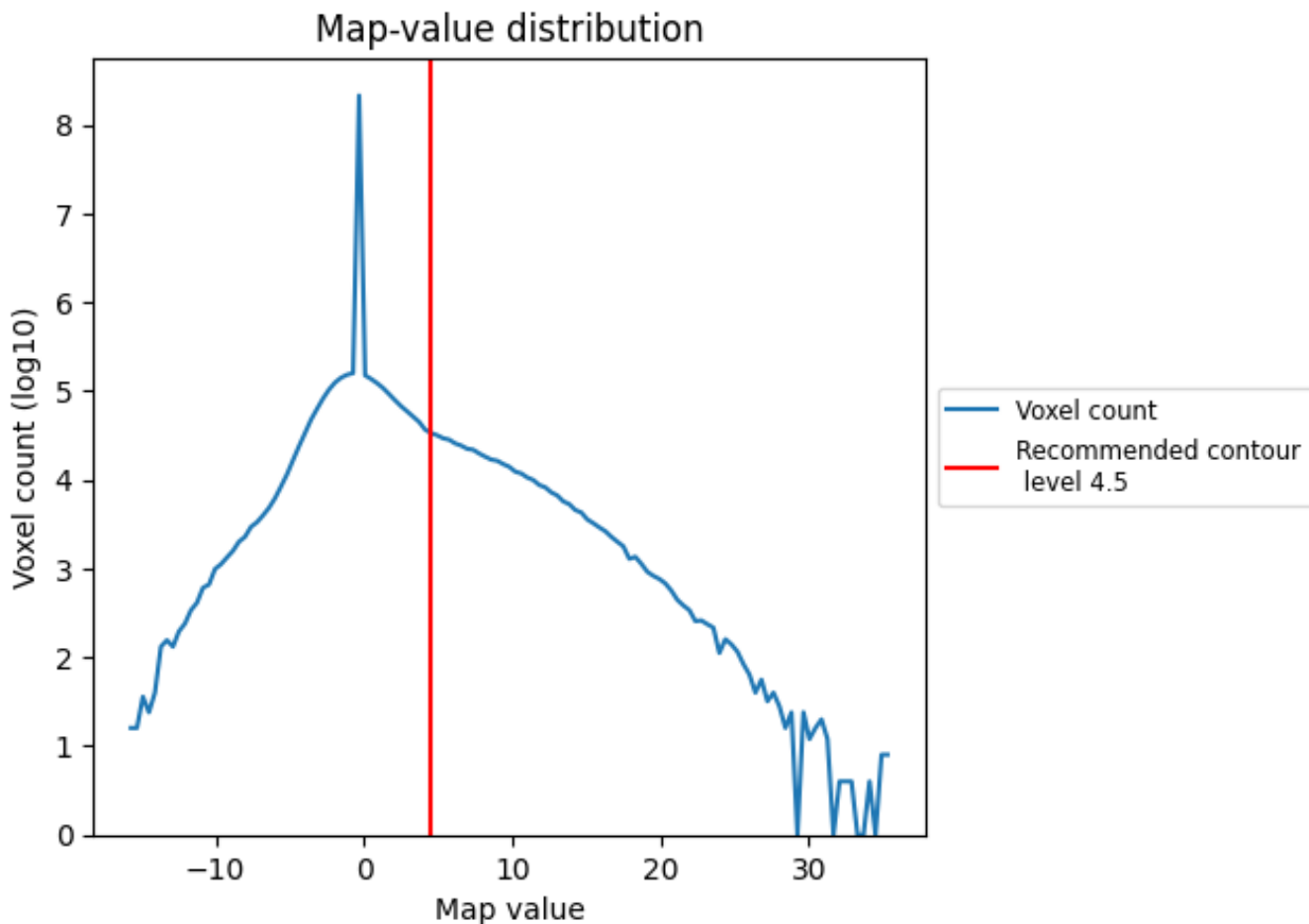
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

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

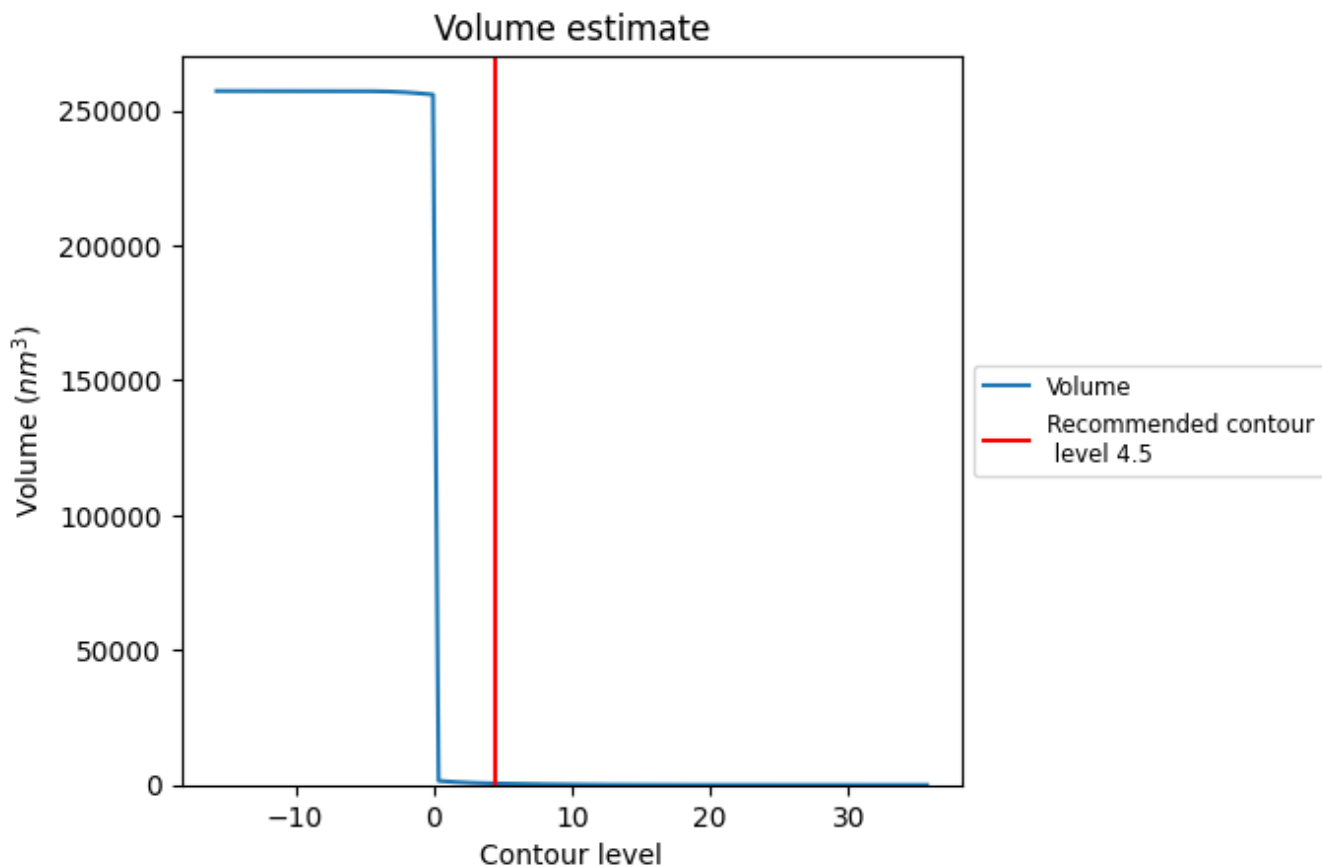
### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



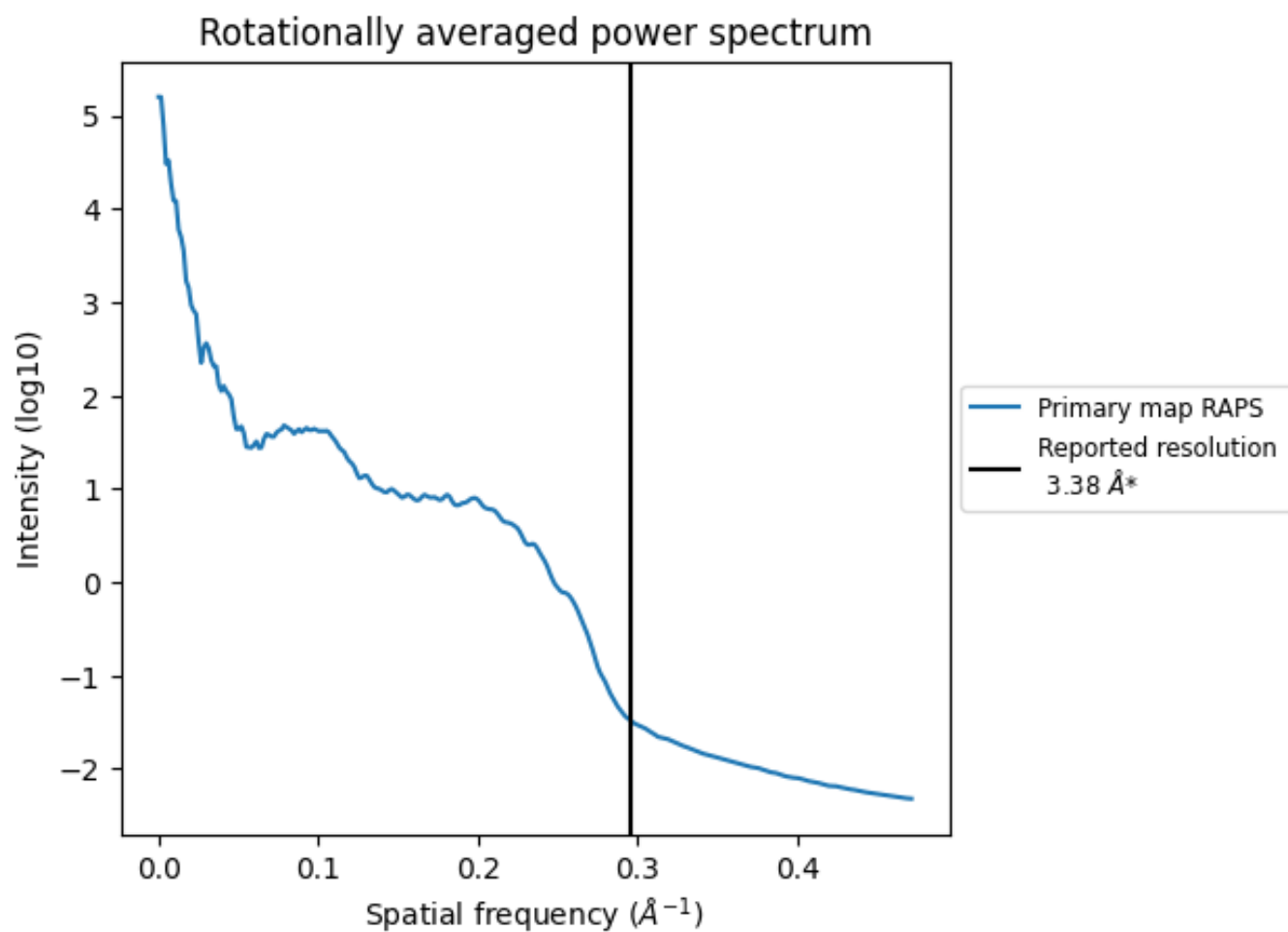
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 530  $\text{nm}^3$ ; this corresponds to an approximate mass of 479 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](#)

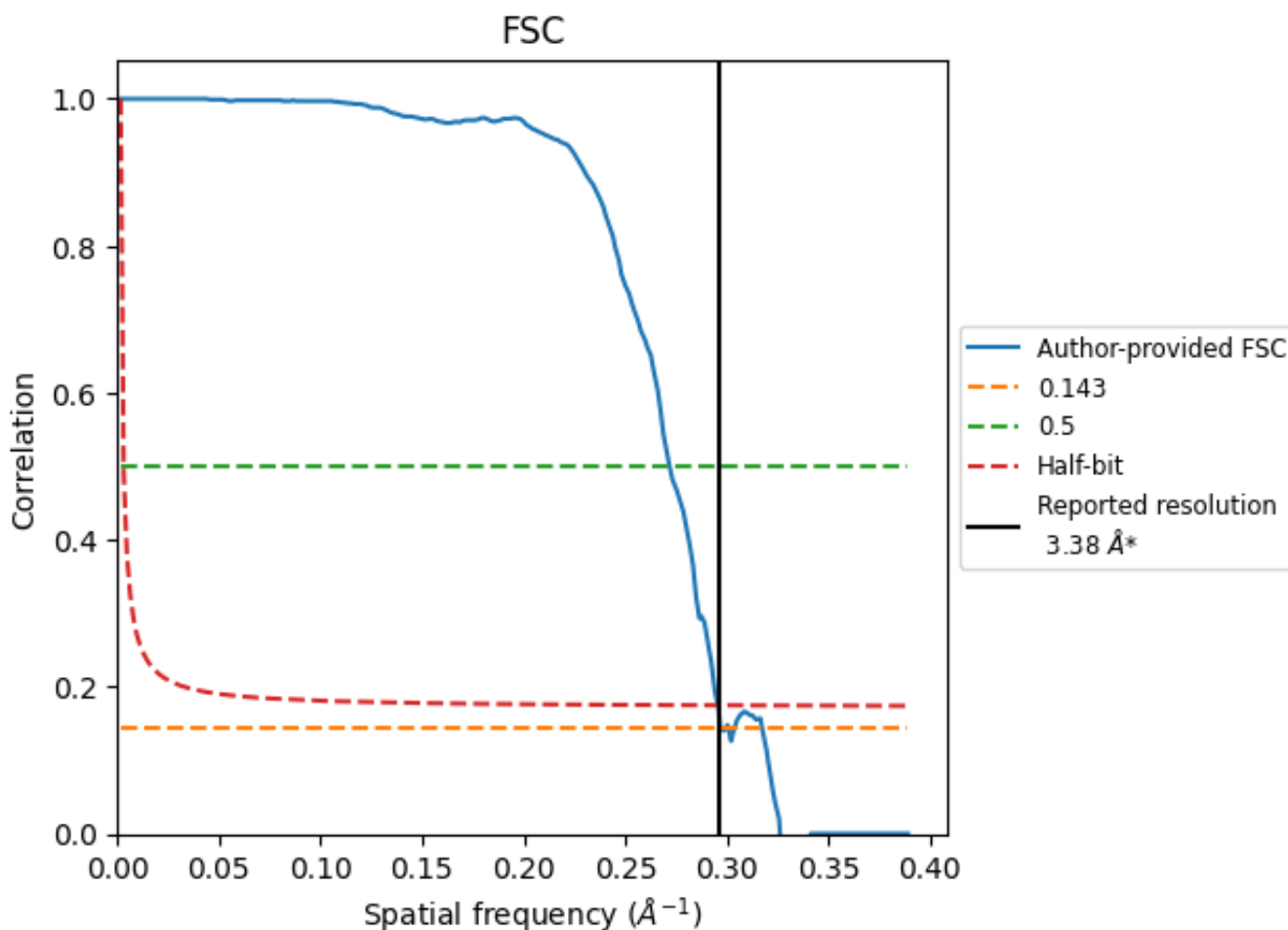


\*Reported resolution corresponds to spatial frequency of 0.296 Å<sup>-1</sup>

## 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 0.296 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

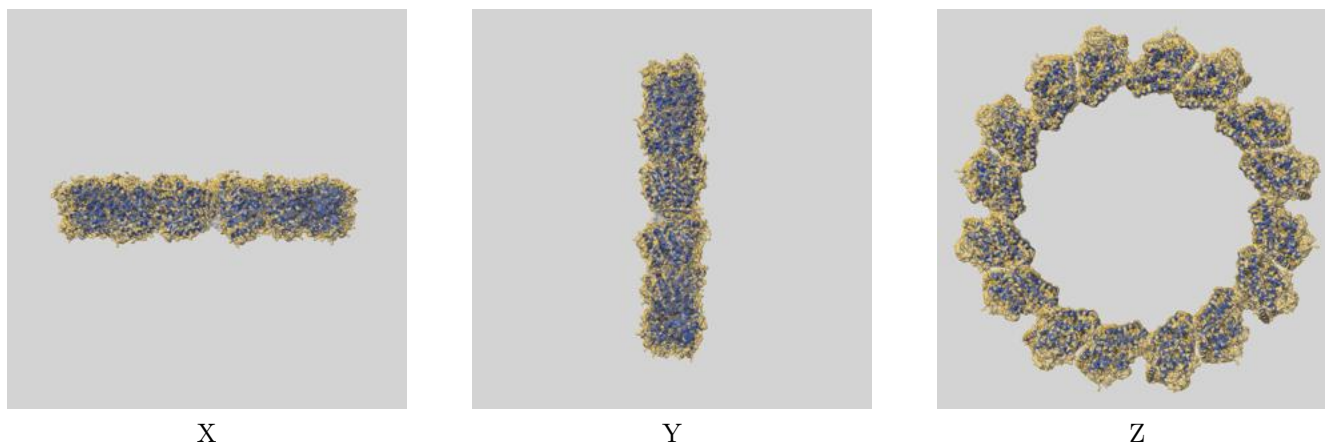
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.38	-	-
Author-provided FSC curve	3.36	3.68	3.38
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

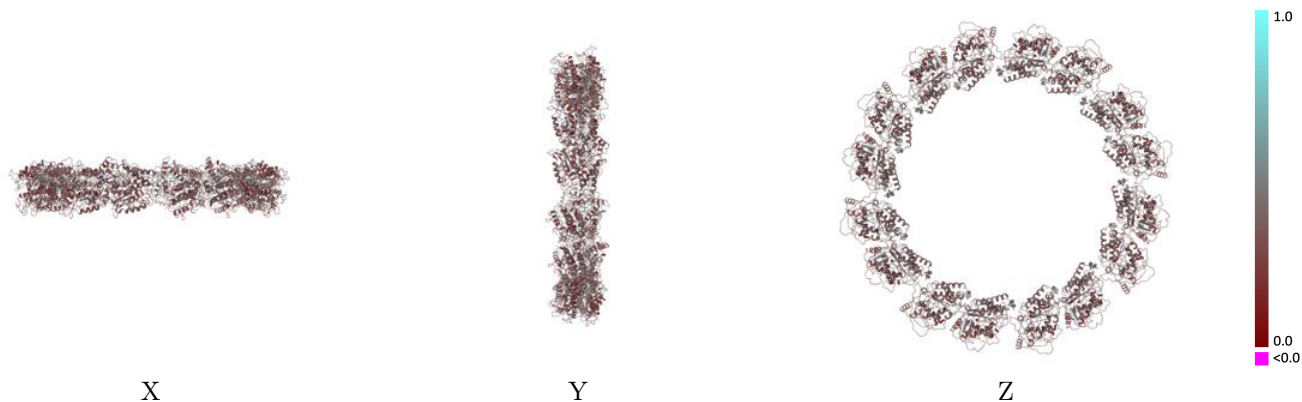
This section contains information regarding the fit between EMDB map EMD-23615 and PDB model 7M18. Per-residue inclusion information can be found in section [3](#) on page [8](#).

### 9.1 Map-model overlay [i](#)



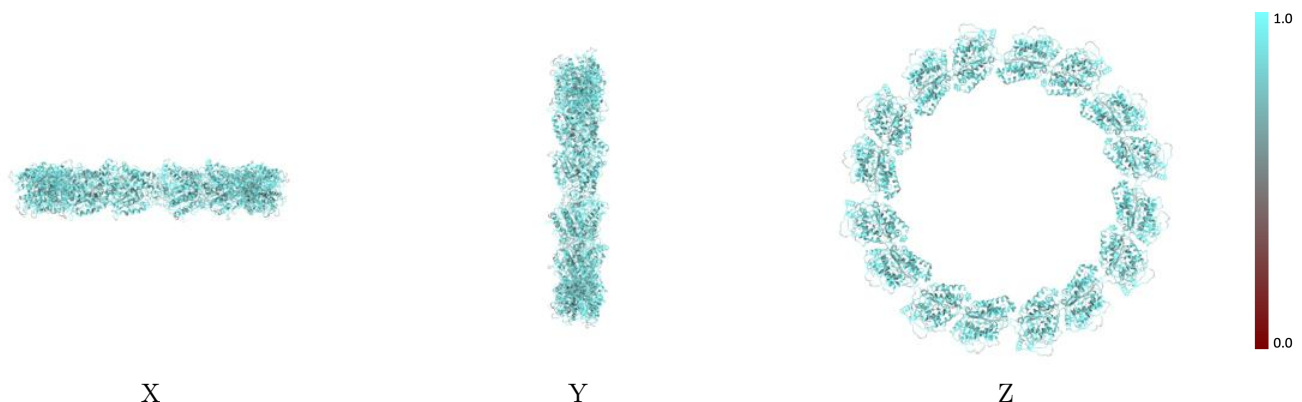
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



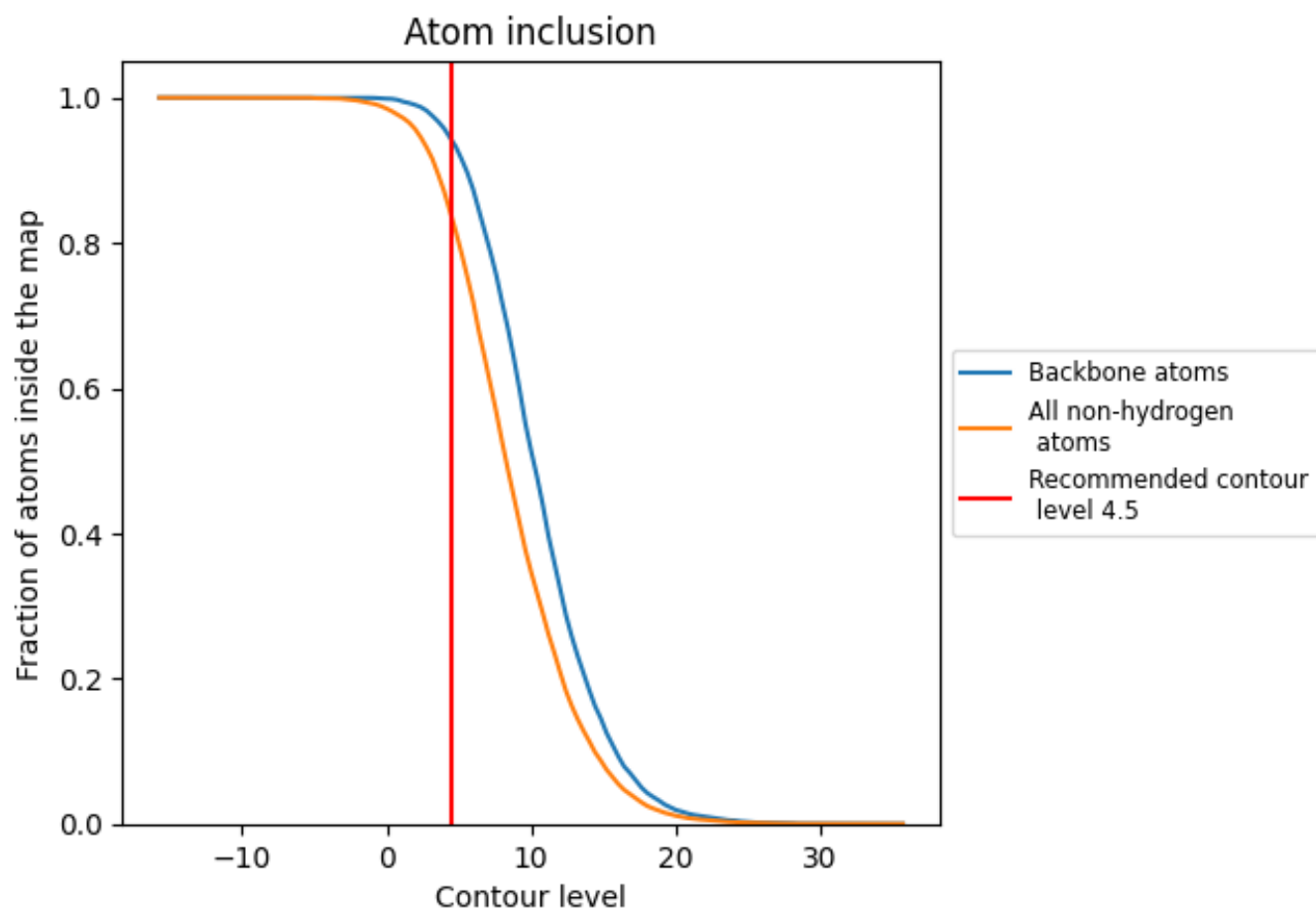
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).



































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 84% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8358	 0.3600
A	 0.8388	 0.3640
B	 0.8339	 0.3560
C	 0.8349	 0.3620
D	 0.8357	 0.3560
E	 0.8388	 0.3660
F	 0.8339	 0.3580
G	 0.8349	 0.3630
H	 0.8354	 0.3570
I	 0.8388	 0.3640
J	 0.8339	 0.3580
K	 0.8349	 0.3630
L	 0.8357	 0.3560
M	 0.8388	 0.3650
N	 0.8339	 0.3580
O	 0.8349	 0.3620
P	 0.8351	 0.3560

