



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 08:48 PM UTC

PDB ID : 6UC2 / pdb_00006uc2
EMDB ID : EMD-20725
Title : Human IMPDH2 treated with ATP and 2 mM GTP. Free canonical octamer reconstruction.
Authors : Johnson, M.C.; Kollman, J.M.
Deposited on : 2019-09-13
Resolution : 4.48 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

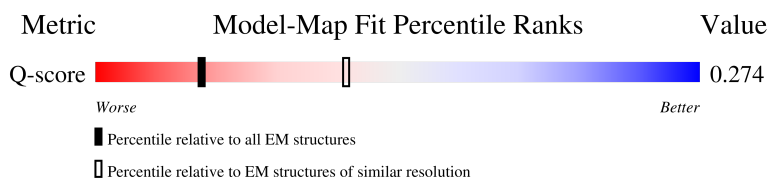
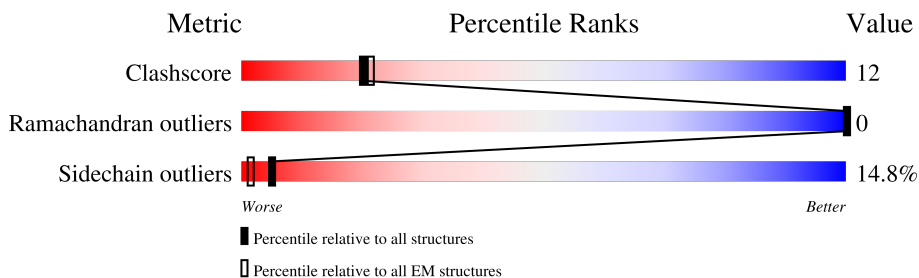
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.48 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2912 (3.99 - 4.98)

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

Mol	Chain	Length	Quality of chain
1	A	519	
1	B	519	
1	C	519	
1	D	519	

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Mol	Chain	Length	Quality of chain
1	E	519	 54% 28% 5% • 13%
1	F	519	 55% 27% 5% • 13%
1	G	519	 54% 28% 5% • 13%
1	H	519	 55% 27% 5% • 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 28408 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 Inosine-5'-monophosphate dehydrogenase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	B	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	C	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	D	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	E	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	F	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	G	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		
1	H	453	Total	C	N	O	S	0	0
			3456	2181	595	662	18		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	SER	-	expression tag	UNP P12268
A	-3	GLU	-	expression tag	UNP P12268
A	-2	PHE	-	expression tag	UNP P12268
A	-1	GLU	-	expression tag	UNP P12268
A	0	LEU	-	expression tag	UNP P12268
B	-4	SER	-	expression tag	UNP P12268
B	-3	GLU	-	expression tag	UNP P12268
B	-2	PHE	-	expression tag	UNP P12268
B	-1	GLU	-	expression tag	UNP P12268
B	0	LEU	-	expression tag	UNP P12268
C	-4	SER	-	expression tag	UNP P12268
C	-3	GLU	-	expression tag	UNP P12268
C	-2	PHE	-	expression tag	UNP P12268
C	-1	GLU	-	expression tag	UNP P12268

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	LEU	-	expression tag	UNP P12268
D	-4	SER	-	expression tag	UNP P12268
D	-3	GLU	-	expression tag	UNP P12268
D	-2	PHE	-	expression tag	UNP P12268
D	-1	GLU	-	expression tag	UNP P12268
D	0	LEU	-	expression tag	UNP P12268
E	-4	SER	-	expression tag	UNP P12268
E	-3	GLU	-	expression tag	UNP P12268
E	-2	PHE	-	expression tag	UNP P12268
E	-1	GLU	-	expression tag	UNP P12268
E	0	LEU	-	expression tag	UNP P12268
F	-4	SER	-	expression tag	UNP P12268
F	-3	GLU	-	expression tag	UNP P12268
F	-2	PHE	-	expression tag	UNP P12268
F	-1	GLU	-	expression tag	UNP P12268
F	0	LEU	-	expression tag	UNP P12268
G	-4	SER	-	expression tag	UNP P12268
G	-3	GLU	-	expression tag	UNP P12268
G	-2	PHE	-	expression tag	UNP P12268
G	-1	GLU	-	expression tag	UNP P12268
G	0	LEU	-	expression tag	UNP P12268
H	-4	SER	-	expression tag	UNP P12268
H	-3	GLU	-	expression tag	UNP P12268
H	-2	PHE	-	expression tag	UNP P12268
H	-1	GLU	-	expression tag	UNP P12268
H	0	LEU	-	expression tag	UNP P12268

- Molecule 2 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



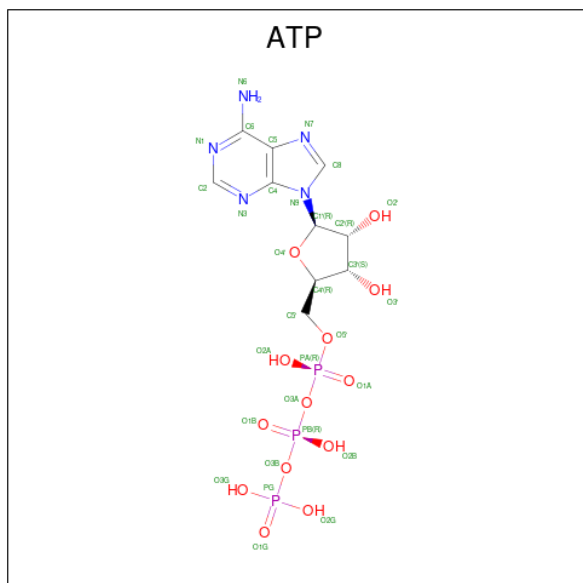
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	B	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	B	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	C	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	C	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	D	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	D	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	E	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	E	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	F	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	F	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	G	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	G	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
2	H	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	H	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

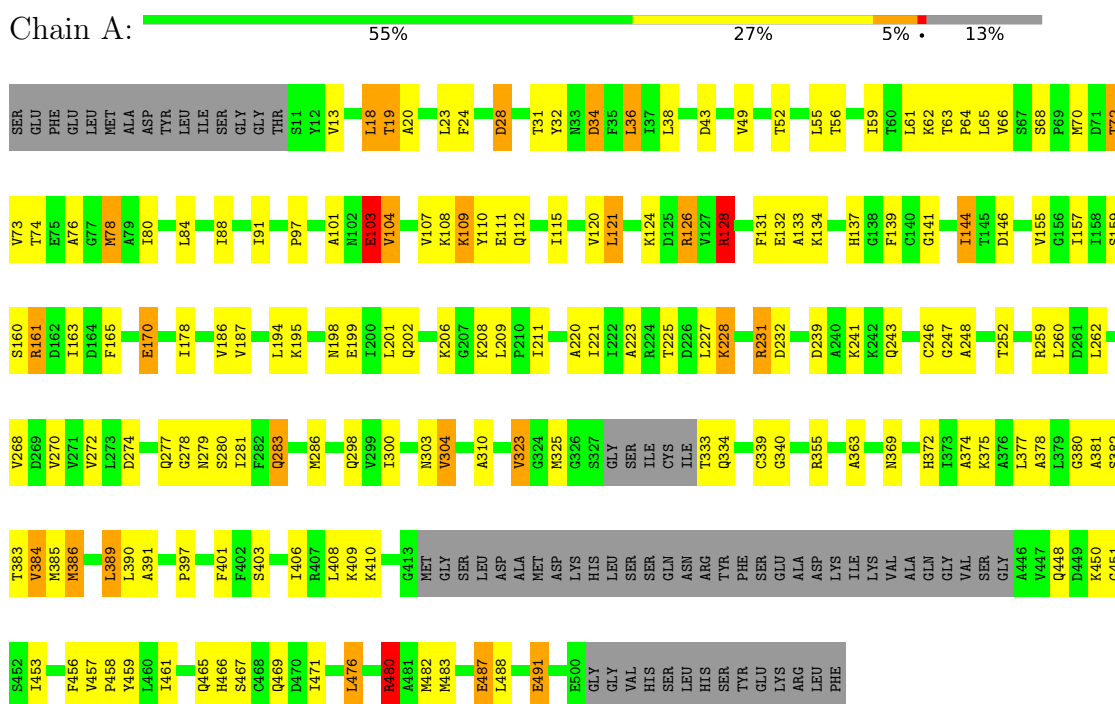


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	F	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	G	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	H	1	Total	C	N	O	P	0
			31	10	5	13	3	

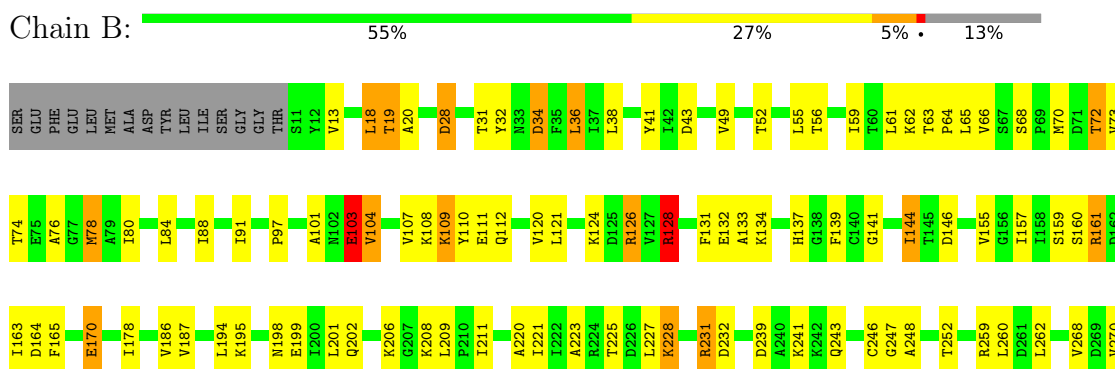
3 Residue-property plots

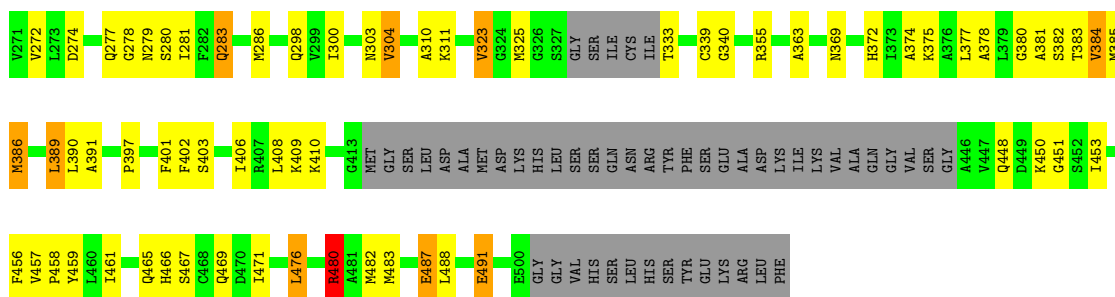
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Inosine-5'-monophosphate dehydrogenase 2



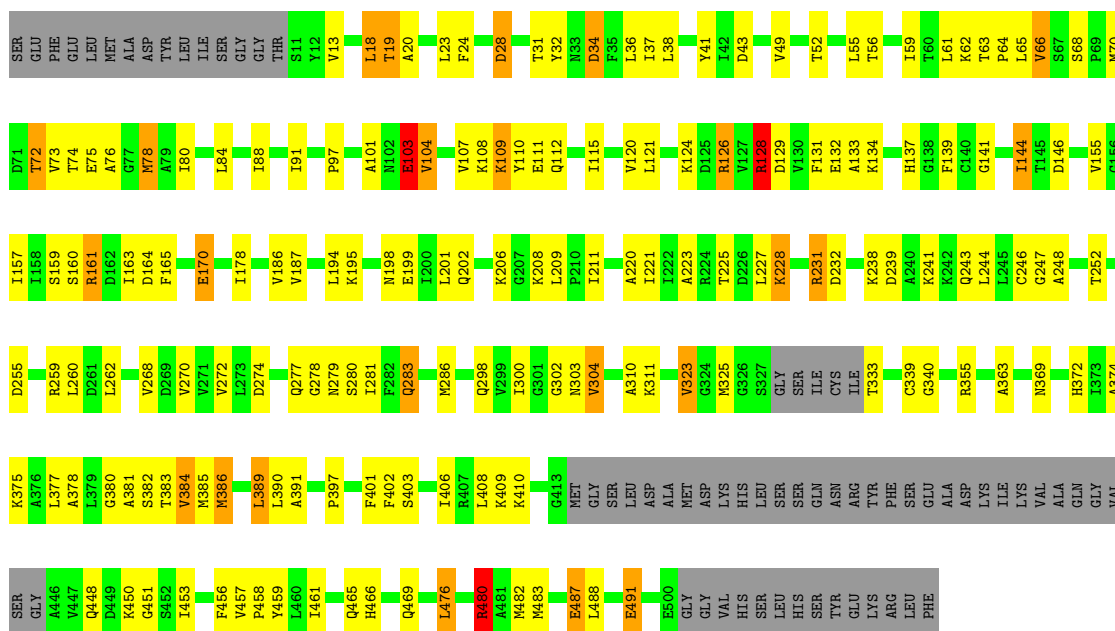
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2





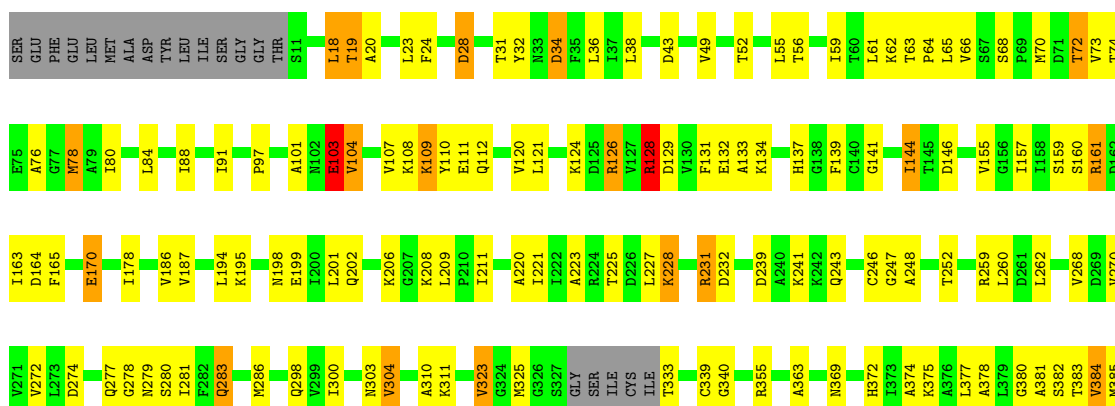
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

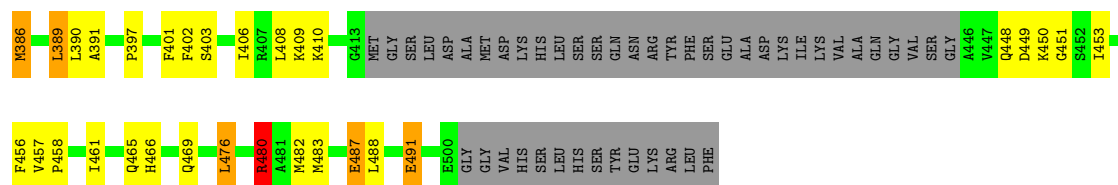
Chain C: 54% 29% 5% 13%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

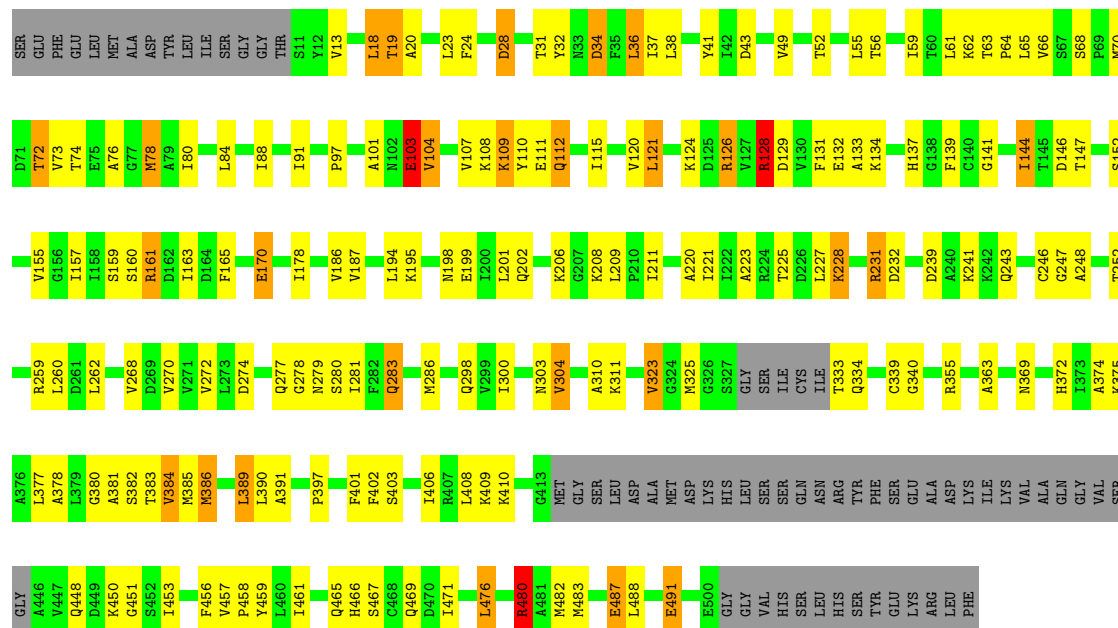
Chain D: 55% 27% 13%





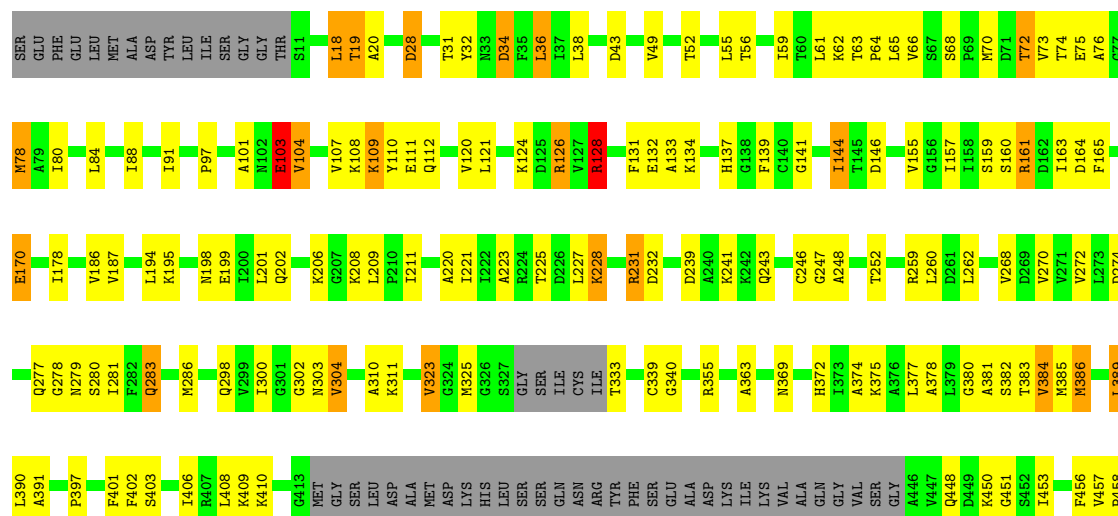
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

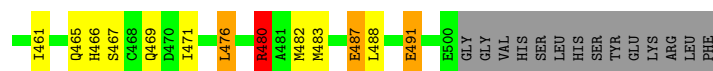
Chain E: 54% 28% 5% 13%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

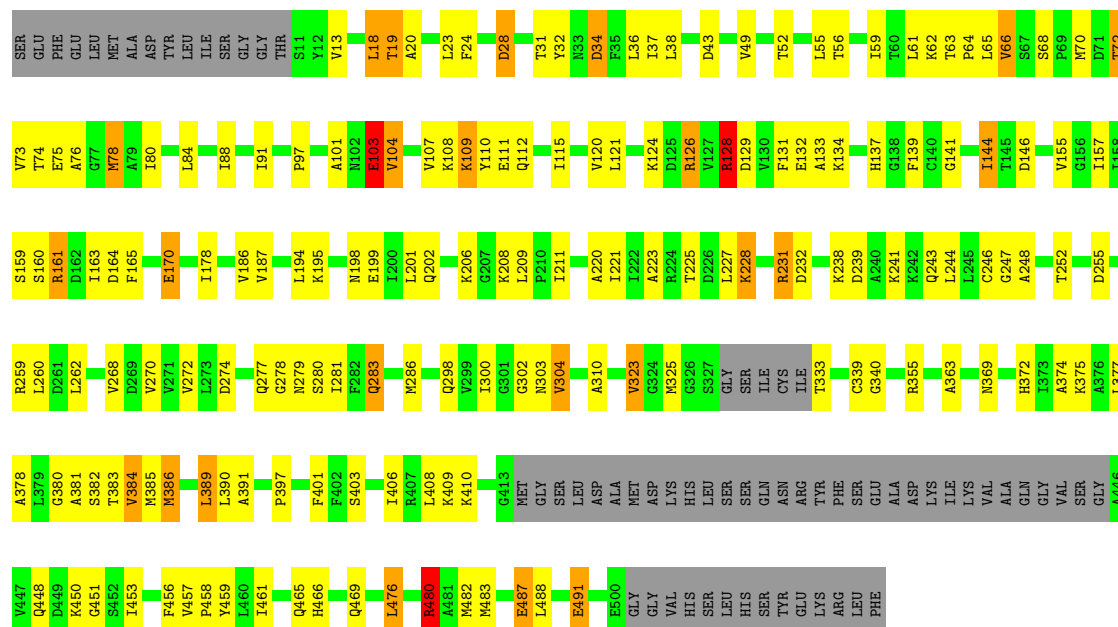
Chain F: 55% 27% 5% 13%





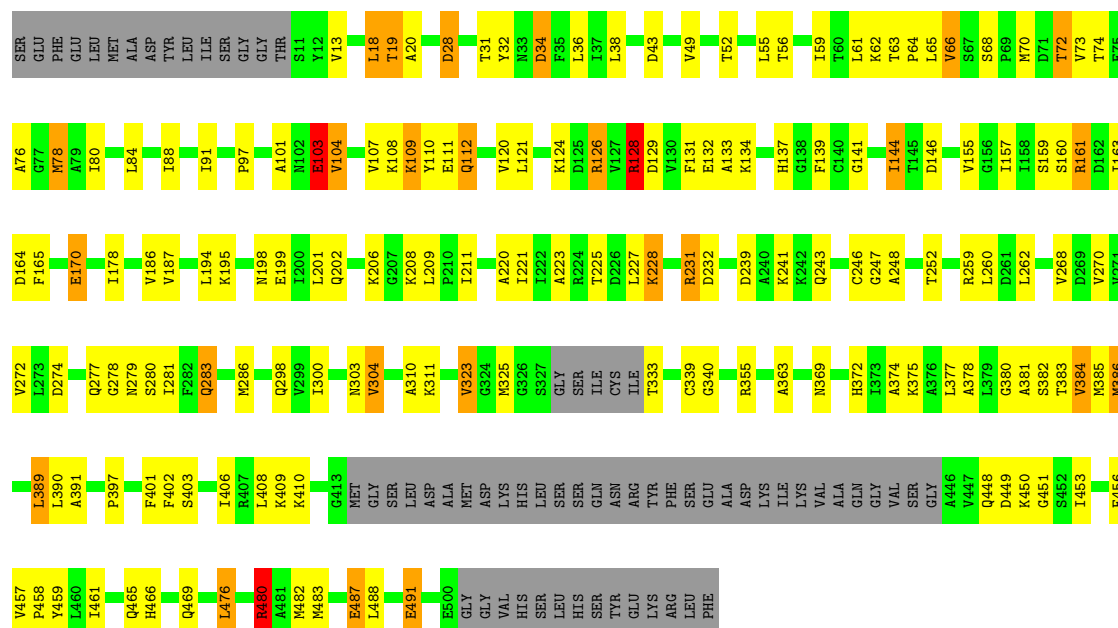
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain G: 54% 28% 5% 13%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain H: 55% 27% 5% 13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D4	Depositor
Number of particles used	26847	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 ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	96.768	Depositor
Minimum map value	-64.525	Depositor
Average map value	0.148	Depositor
Map value standard deviation	3.127	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	268.8, 268.8, 268.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/3507	0.96	12/4732 (0.3%)
1	B	0.40	0/3507	0.96	12/4732 (0.3%)
1	C	0.40	0/3507	0.96	12/4732 (0.3%)
1	D	0.40	0/3507	0.96	12/4732 (0.3%)
1	E	0.40	0/3507	0.96	12/4732 (0.3%)
1	F	0.40	0/3507	0.96	12/4732 (0.3%)
1	G	0.40	0/3507	0.96	12/4732 (0.3%)
1	H	0.40	0/3507	0.96	12/4732 (0.3%)
All	All	0.40	0/28056	0.96	96/37856 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
1	C	0	4
1	D	0	4
1	E	0	4
1	F	0	4
1	G	0	4
1	H	0	4
All	All	0	32

There are no bond length outliers.

All (96) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	480	ARG	CB-CG-CD	7.42	128.37	111.30
1	B	480	ARG	CB-CG-CD	7.42	128.35	111.30
1	C	480	ARG	CB-CG-CD	7.41	128.35	111.30
1	E	480	ARG	CB-CG-CD	7.41	128.34	111.30
1	A	480	ARG	CB-CG-CD	7.41	128.34	111.30
1	G	480	ARG	CB-CG-CD	7.40	128.32	111.30
1	F	480	ARG	CB-CG-CD	7.39	128.29	111.30
1	D	480	ARG	CB-CG-CD	7.38	128.28	111.30
1	C	385	MET	CB-CG-SD	-7.10	91.41	112.70
1	H	385	MET	CB-CG-SD	-7.10	91.41	112.70
1	G	385	MET	CB-CG-SD	-7.09	91.43	112.70
1	D	385	MET	CB-CG-SD	-7.09	91.43	112.70
1	E	385	MET	CB-CG-SD	-7.09	91.43	112.70
1	B	385	MET	CB-CG-SD	-7.08	91.45	112.70
1	A	385	MET	CB-CG-SD	-7.08	91.45	112.70
1	F	385	MET	CB-CG-SD	-7.08	91.45	112.70
1	F	18	LEU	CA-CB-CG	7.05	140.99	116.30
1	C	18	LEU	CA-CB-CG	7.04	140.95	116.30
1	H	18	LEU	CA-CB-CG	7.04	140.94	116.30
1	B	18	LEU	CA-CB-CG	7.04	140.94	116.30
1	A	18	LEU	CA-CB-CG	7.04	140.93	116.30
1	G	18	LEU	CA-CB-CG	7.04	140.92	116.30
1	E	18	LEU	CA-CB-CG	7.03	140.92	116.30
1	D	18	LEU	CA-CB-CG	7.03	140.90	116.30
1	G	451	GLY	N-CA-C	6.30	118.88	111.63
1	B	451	GLY	N-CA-C	6.30	118.87	111.63
1	D	451	GLY	N-CA-C	6.28	118.85	111.63
1	F	451	GLY	N-CA-C	6.28	118.85	111.63
1	E	451	GLY	N-CA-C	6.28	118.85	111.63
1	H	451	GLY	N-CA-C	6.28	118.85	111.63
1	C	451	GLY	N-CA-C	6.26	118.83	111.63
1	A	451	GLY	N-CA-C	6.25	118.82	111.63
1	F	491	GLU	CB-CG-CD	6.12	123.01	112.60
1	E	491	GLU	CB-CG-CD	6.12	123.00	112.60
1	C	491	GLU	CB-CG-CD	6.11	122.99	112.60
1	D	491	GLU	CB-CG-CD	6.11	122.99	112.60
1	B	491	GLU	CB-CG-CD	6.11	122.99	112.60
1	H	491	GLU	CB-CG-CD	6.11	122.99	112.60
1	A	491	GLU	CB-CG-CD	6.10	122.97	112.60
1	G	491	GLU	CB-CG-CD	6.09	122.95	112.60
1	F	72	THR	CA-CB-CG2	5.90	120.53	110.50
1	C	72	THR	CA-CB-CG2	5.90	120.52	110.50
1	A	72	THR	CA-CB-CG2	5.88	120.50	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	72	THR	CA-CB-CG2	5.88	120.50	110.50
1	H	72	THR	CA-CB-CG2	5.87	120.48	110.50
1	G	72	THR	CA-CB-CG2	5.87	120.48	110.50
1	B	72	THR	CA-CB-CG2	5.87	120.47	110.50
1	D	72	THR	CA-CB-CG2	5.85	120.45	110.50
1	E	389	LEU	CA-CB-CG	5.76	136.47	116.30
1	H	389	LEU	CA-CB-CG	5.76	136.47	116.30
1	A	389	LEU	CA-CB-CG	5.75	136.43	116.30
1	B	389	LEU	CA-CB-CG	5.75	136.43	116.30
1	G	389	LEU	CA-CB-CG	5.75	136.43	116.30
1	D	389	LEU	CA-CB-CG	5.75	136.42	116.30
1	C	389	LEU	CA-CB-CG	5.75	136.42	116.30
1	F	389	LEU	CA-CB-CG	5.74	136.40	116.30
1	F	103	GLU	CB-CG-CD	5.67	122.23	112.60
1	G	103	GLU	CB-CG-CD	5.65	122.21	112.60
1	D	103	GLU	CB-CG-CD	5.65	122.20	112.60
1	B	103	GLU	CB-CG-CD	5.64	122.19	112.60
1	H	103	GLU	CB-CG-CD	5.64	122.19	112.60
1	A	103	GLU	CB-CG-CD	5.64	122.18	112.60
1	E	103	GLU	CB-CG-CD	5.63	122.17	112.60
1	C	103	GLU	CB-CG-CD	5.63	122.17	112.60
1	G	491	GLU	CA-CB-CG	5.32	124.73	114.10
1	A	491	GLU	CA-CB-CG	5.31	124.72	114.10
1	D	491	GLU	CA-CB-CG	5.31	124.72	114.10
1	E	491	GLU	CA-CB-CG	5.30	124.71	114.10
1	C	491	GLU	CA-CB-CG	5.30	124.70	114.10
1	H	491	GLU	CA-CB-CG	5.30	124.69	114.10
1	B	491	GLU	CA-CB-CG	5.29	124.68	114.10
1	F	491	GLU	CA-CB-CG	5.29	124.68	114.10
1	G	28	ASP	CA-CB-CG	5.14	117.74	112.60
1	B	28	ASP	CA-CB-CG	5.12	117.72	112.60
1	E	28	ASP	CA-CB-CG	5.12	117.72	112.60
1	C	28	ASP	CA-CB-CG	5.12	117.72	112.60
1	F	28	ASP	CA-CB-CG	5.10	117.70	112.60
1	H	28	ASP	CA-CB-CG	5.09	117.69	112.60
1	E	34	ASP	N-CA-C	-5.09	106.48	113.30
1	A	28	ASP	CA-CB-CG	5.09	117.69	112.60
1	H	34	ASP	N-CA-C	-5.08	106.49	113.30
1	D	34	ASP	N-CA-C	-5.08	106.49	113.30
1	A	34	ASP	N-CA-C	-5.07	106.51	113.30
1	C	34	ASP	N-CA-C	-5.07	106.51	113.30
1	D	28	ASP	CA-CB-CG	5.07	117.67	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	128	ARG	CB-CG-CD	5.07	122.95	111.30
1	F	128	ARG	CB-CG-CD	5.07	122.95	111.30
1	B	128	ARG	CB-CG-CD	5.06	122.94	111.30
1	F	34	ASP	N-CA-C	-5.05	106.53	113.30
1	C	128	ARG	CB-CG-CD	5.05	122.92	111.30
1	G	34	ASP	N-CA-C	-5.05	106.53	113.30
1	G	128	ARG	CB-CG-CD	5.05	122.91	111.30
1	D	128	ARG	CB-CG-CD	5.05	122.91	111.30
1	A	128	ARG	CB-CG-CD	5.04	122.89	111.30
1	H	128	ARG	CB-CG-CD	5.04	122.89	111.30
1	B	34	ASP	N-CA-C	-5.03	106.56	113.30

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	111	GLU	Peptide
1	A	126	ARG	Peptide
1	A	165	PHE	Peptide
1	A	178	ILE	Peptide
1	B	111	GLU	Peptide
1	B	126	ARG	Peptide
1	B	165	PHE	Peptide
1	B	178	ILE	Peptide
1	C	111	GLU	Peptide
1	C	126	ARG	Peptide
1	C	165	PHE	Peptide
1	C	178	ILE	Peptide
1	D	111	GLU	Peptide
1	D	126	ARG	Peptide
1	D	165	PHE	Peptide
1	D	178	ILE	Peptide
1	E	111	GLU	Peptide
1	E	126	ARG	Peptide
1	E	165	PHE	Peptide
1	E	178	ILE	Peptide
1	F	111	GLU	Peptide
1	F	126	ARG	Peptide
1	F	165	PHE	Peptide
1	F	178	ILE	Peptide
1	G	111	GLU	Peptide
1	G	126	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	G	165	PHE	Peptide
1	G	178	ILE	Peptide
1	H	111	GLU	Peptide
1	H	126	ARG	Peptide
1	H	165	PHE	Peptide
1	H	178	ILE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3456	0	3506	92	0
1	B	3456	0	3506	88	0
1	C	3456	0	3506	97	0
1	D	3456	0	3506	87	0
1	E	3456	0	3506	97	0
1	F	3456	0	3506	90	0
1	G	3456	0	3506	92	0
1	H	3456	0	3506	90	0
2	A	64	0	22	2	0
2	B	64	0	22	2	0
2	C	64	0	22	2	0
2	D	64	0	22	2	0
2	E	64	0	22	2	0
2	F	64	0	22	2	0
2	G	64	0	22	2	0
2	H	64	0	22	2	0
3	A	31	0	12	3	0
3	B	31	0	12	2	0
3	C	31	0	12	2	0
3	D	31	0	12	2	0
3	E	31	0	12	2	0
3	F	31	0	12	2	0
3	G	31	0	12	2	0
3	H	31	0	12	2	0
All	All	28408	0	28320	695	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 12.

All (695) 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:F:109:LYS:HD3	1:F:110:TYR:H	1.52	0.75
1:B:109:LYS:HD3	1:B:110:TYR:H	1.52	0.75
1:D:109:LYS:HD3	1:D:110:TYR:H	1.52	0.75
1:C:109:LYS:HD3	1:C:110:TYR:H	1.52	0.75
1:H:109:LYS:HD3	1:H:110:TYR:H	1.52	0.75
1:G:109:LYS:HD3	1:G:110:TYR:H	1.52	0.74
1:E:109:LYS:HD3	1:E:110:TYR:H	1.52	0.74
1:A:109:LYS:HD3	1:A:110:TYR:H	1.52	0.73
1:D:206:LYS:HZ3	1:D:208:LYS:HB2	1.57	0.70
1:H:206:LYS:HZ3	1:H:208:LYS:HB2	1.57	0.70
1:B:206:LYS:HZ3	1:B:208:LYS:HB2	1.57	0.69
1:F:206:LYS:HZ3	1:F:208:LYS:HB2	1.57	0.69
1:D:448:GLN:O	1:G:448:GLN:NE2	2.24	0.69
1:D:128:ARG:O	1:D:132:GLU:HB2	1.93	0.68
1:H:128:ARG:O	1:H:132:GLU:HB2	1.93	0.68
1:G:206:LYS:HZ3	1:G:208:LYS:HB2	1.58	0.67
1:C:128:ARG:O	1:C:132:GLU:HB2	1.93	0.67
1:G:128:ARG:O	1:G:132:GLU:HB2	1.93	0.67
1:C:206:LYS:HZ3	1:C:208:LYS:HB2	1.58	0.67
1:E:128:ARG:O	1:E:132:GLU:HB2	1.93	0.67
1:C:61:LEU:HD21	1:C:88:ILE:HG13	1.76	0.67
1:F:128:ARG:O	1:F:132:GLU:HB2	1.93	0.67
1:G:61:LEU:HD21	1:G:88:ILE:HG13	1.76	0.67
1:H:61:LEU:HD21	1:H:88:ILE:HG13	1.76	0.67
1:A:128:ARG:O	1:A:132:GLU:HB2	1.93	0.67
1:B:128:ARG:O	1:B:132:GLU:HB2	1.93	0.67
1:D:61:LEU:HD21	1:D:88:ILE:HG13	1.76	0.67
1:D:78:MET:SD	1:D:78:MET:N	2.68	0.67
1:H:78:MET:SD	1:H:78:MET:N	2.68	0.67
1:B:61:LEU:HD21	1:B:88:ILE:HG13	1.76	0.66
1:F:61:LEU:HD21	1:F:88:ILE:HG13	1.76	0.66
1:D:448:GLN:NE2	1:G:448:GLN:O	2.29	0.66
1:E:78:MET:SD	1:E:78:MET:N	2.68	0.66
1:B:78:MET:SD	1:B:78:MET:N	2.68	0.66
1:F:78:MET:SD	1:F:78:MET:N	2.68	0.66
1:E:91:ILE:H	1:E:248:ALA:HA	1.61	0.66
1:A:61:LEU:HD21	1:A:88:ILE:HG13	1.76	0.66
1:A:78:MET:SD	1:A:78:MET:N	2.68	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:GLN:NE2	1:F:448:GLN:O	2.28	0.66
1:C:78:MET:SD	1:C:78:MET:N	2.68	0.66
1:G:78:MET:SD	1:G:78:MET:N	2.68	0.66
1:A:91:ILE:H	1:A:248:ALA:HA	1.61	0.66
1:C:448:GLN:NE2	1:H:448:GLN:O	2.29	0.66
1:D:91:ILE:H	1:D:248:ALA:HA	1.61	0.66
1:E:61:LEU:HD21	1:E:88:ILE:HG13	1.76	0.66
1:H:91:ILE:H	1:H:248:ALA:HA	1.61	0.66
1:B:91:ILE:H	1:B:248:ALA:HA	1.61	0.65
1:F:91:ILE:H	1:F:248:ALA:HA	1.61	0.65
1:G:91:ILE:H	1:G:248:ALA:HA	1.61	0.65
1:C:91:ILE:H	1:C:248:ALA:HA	1.61	0.65
1:A:141:GLY:O	2:A:601:GTP:N2	2.30	0.65
1:D:141:GLY:O	2:D:601:GTP:N2	2.30	0.65
1:F:141:GLY:O	2:F:601:GTP:N2	2.30	0.65
1:B:141:GLY:O	2:B:601:GTP:N2	2.30	0.65
1:E:141:GLY:O	2:E:601:GTP:N2	2.30	0.65
1:H:141:GLY:O	2:H:601:GTP:N2	2.30	0.65
1:C:141:GLY:O	2:C:601:GTP:N2	2.30	0.64
1:G:141:GLY:O	2:G:601:GTP:N2	2.30	0.64
1:A:206:LYS:HZ3	1:A:208:LYS:HB2	1.64	0.63
1:B:68:SER:HB3	1:B:73:VAL:HG21	1.81	0.63
1:F:68:SER:HB3	1:F:73:VAL:HG21	1.81	0.63
1:E:206:LYS:HZ3	1:E:208:LYS:HB2	1.64	0.62
1:H:68:SER:HB3	1:H:73:VAL:HG21	1.81	0.62
1:A:448:GLN:O	1:F:448:GLN:NE2	2.29	0.62
1:D:68:SER:HB3	1:D:73:VAL:HG21	1.81	0.62
1:E:68:SER:HB3	1:E:73:VAL:HG21	1.81	0.62
1:F:397:PRO:O	1:F:409:LYS:NZ	2.33	0.62
1:G:397:PRO:O	1:G:409:LYS:NZ	2.33	0.62
1:C:397:PRO:O	1:C:409:LYS:NZ	2.33	0.62
1:A:68:SER:HB3	1:A:73:VAL:HG21	1.81	0.61
1:A:397:PRO:O	1:A:409:LYS:NZ	2.33	0.61
1:B:391:ALA:O	1:B:450:LYS:NZ	2.33	0.61
1:C:68:SER:HB3	1:C:73:VAL:HG21	1.81	0.61
1:F:391:ALA:O	1:F:450:LYS:NZ	2.33	0.61
1:D:391:ALA:O	1:D:450:LYS:NZ	2.33	0.61
1:E:397:PRO:O	1:E:409:LYS:NZ	2.33	0.61
1:G:68:SER:HB3	1:G:73:VAL:HG21	1.81	0.61
1:H:391:ALA:O	1:H:450:LYS:NZ	2.33	0.61
1:D:186:VAL:HB	3:D:603:ATP:HN62	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:186:VAL:HB	3:H:603:ATP:HN62	1.66	0.61
1:C:391:ALA:O	1:C:450:LYS:NZ	2.33	0.61
1:G:391:ALA:O	1:G:450:LYS:NZ	2.33	0.61
1:E:56:THR:HG1	1:E:59:ILE:H	1.49	0.60
1:D:377:LEU:HD13	1:D:476:LEU:HD21	1.83	0.60
1:A:56:THR:HG1	1:A:59:ILE:H	1.49	0.60
1:G:186:VAL:HB	3:G:603:ATP:HN62	1.66	0.60
1:H:377:LEU:HD13	1:H:476:LEU:HD21	1.83	0.60
1:A:186:VAL:HB	3:A:603:ATP:HN62	1.66	0.60
1:A:391:ALA:O	1:A:450:LYS:NZ	2.33	0.60
1:E:186:VAL:HB	3:E:603:ATP:HN62	1.66	0.60
1:E:377:LEU:HD13	1:E:476:LEU:HD21	1.83	0.60
1:E:391:ALA:O	1:E:450:LYS:NZ	2.33	0.60
1:C:186:VAL:HB	3:C:603:ATP:HN62	1.66	0.60
1:F:377:LEU:HD13	1:F:476:LEU:HD21	1.83	0.60
1:A:377:LEU:HD13	1:A:476:LEU:HD21	1.83	0.59
1:C:377:LEU:HD13	1:C:476:LEU:HD21	1.83	0.59
1:B:186:VAL:HB	3:B:603:ATP:HN62	1.66	0.59
1:B:377:LEU:HD13	1:B:476:LEU:HD21	1.83	0.59
1:F:186:VAL:HB	3:F:603:ATP:HN62	1.66	0.59
1:A:74:THR:HA	1:A:78:MET:HG2	1.85	0.59
1:G:377:LEU:HD13	1:G:476:LEU:HD21	1.83	0.59
1:H:397:PRO:O	1:H:409:LYS:NZ	2.33	0.59
1:C:74:THR:HA	1:C:78:MET:HG2	1.85	0.59
1:C:448:GLN:O	1:H:448:GLN:NE2	2.36	0.59
1:D:397:PRO:O	1:D:409:LYS:NZ	2.33	0.59
1:E:74:THR:HA	1:E:78:MET:HG2	1.85	0.59
1:D:74:THR:HA	1:D:78:MET:HG2	1.85	0.59
1:C:56:THR:HG1	1:C:59:ILE:H	1.49	0.59
1:F:56:THR:HG1	1:F:59:ILE:H	1.49	0.59
1:G:74:THR:HA	1:G:78:MET:HG2	1.85	0.59
1:H:74:THR:HA	1:H:78:MET:HG2	1.85	0.59
1:C:19:THR:OG1	1:C:20:ALA:N	2.36	0.58
1:G:19:THR:OG1	1:G:20:ALA:N	2.36	0.58
1:G:246:CYS:SG	1:G:247:GLY:N	2.76	0.58
1:B:74:THR:HA	1:B:78:MET:HG2	1.85	0.58
1:C:246:CYS:SG	1:C:247:GLY:N	2.76	0.58
1:F:62:LYS:HG3	1:F:63:THR:HG23	1.85	0.58
1:F:74:THR:HA	1:F:78:MET:HG2	1.85	0.58
1:G:62:LYS:HG3	1:G:63:THR:HG23	1.85	0.58
1:B:43:ASP:HA	1:C:281:ILE:HG12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:LYS:HG3	1:B:63:THR:HG23	1.85	0.58
1:H:56:THR:HG1	1:H:59:ILE:H	1.49	0.58
1:B:56:THR:HG1	1:B:59:ILE:H	1.49	0.58
1:B:246:CYS:SG	1:B:247:GLY:N	2.76	0.58
1:C:62:LYS:HG3	1:C:63:THR:HG23	1.85	0.58
1:C:64:PRO:O	1:C:383:THR:OG1	2.21	0.58
1:D:56:THR:HG1	1:D:59:ILE:H	1.49	0.58
1:E:19:THR:OG1	1:E:20:ALA:N	2.36	0.58
1:G:56:THR:HG1	1:G:59:ILE:H	1.49	0.58
1:G:64:PRO:O	1:G:383:THR:OG1	2.21	0.58
1:F:246:CYS:SG	1:F:247:GLY:N	2.76	0.58
1:D:409:LYS:NZ	1:D:410:LYS:O	2.37	0.58
1:E:409:LYS:NZ	1:E:410:LYS:O	2.37	0.58
1:A:246:CYS:SG	1:A:247:GLY:N	2.76	0.58
1:A:409:LYS:NZ	1:A:410:LYS:O	2.37	0.58
1:B:409:LYS:NZ	1:B:410:LYS:O	2.37	0.58
1:F:409:LYS:NZ	1:F:410:LYS:O	2.37	0.58
1:B:397:PRO:O	1:B:409:LYS:NZ	2.33	0.58
1:E:246:CYS:SG	1:E:247:GLY:N	2.76	0.58
1:H:246:CYS:SG	1:H:247:GLY:N	2.76	0.58
1:H:409:LYS:NZ	1:H:410:LYS:O	2.37	0.58
1:G:409:LYS:NZ	1:G:410:LYS:O	2.37	0.57
1:C:409:LYS:NZ	1:C:410:LYS:O	2.37	0.57
1:D:246:CYS:SG	1:D:247:GLY:N	2.76	0.57
1:B:80:ILE:O	1:B:84:LEU:HB2	2.05	0.57
1:F:80:ILE:O	1:F:84:LEU:HB2	2.05	0.57
1:B:19:THR:OG1	1:B:20:ALA:N	2.36	0.57
1:E:62:LYS:HG3	1:E:63:THR:HG23	1.85	0.57
1:F:19:THR:OG1	1:F:20:ALA:N	2.36	0.57
1:A:62:LYS:HG3	1:A:63:THR:HG23	1.85	0.57
1:D:19:THR:OG1	1:D:20:ALA:N	2.36	0.57
1:H:64:PRO:O	1:H:383:THR:OG1	2.21	0.57
1:H:19:THR:OG1	1:H:20:ALA:N	2.36	0.57
1:D:62:LYS:HG3	1:D:63:THR:HG23	1.85	0.57
1:D:64:PRO:O	1:D:383:THR:OG1	2.21	0.57
1:H:62:LYS:HG3	1:H:63:THR:HG23	1.85	0.57
1:D:198:ASN:O	1:D:202:GLN:NE2	2.38	0.56
1:E:80:ILE:O	1:E:84:LEU:HB2	2.05	0.56
1:H:198:ASN:O	1:H:202:GLN:NE2	2.38	0.56
1:B:198:ASN:O	1:B:202:GLN:NE2	2.38	0.56
1:C:198:ASN:O	1:C:202:GLN:NE2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:198:ASN:O	1:F:202:GLN:NE2	2.39	0.56
1:G:198:ASN:O	1:G:202:GLN:NE2	2.38	0.56
1:G:280:SER:OG	1:G:283:GLN:NE2	2.29	0.56
1:A:80:ILE:O	1:A:84:LEU:HB2	2.05	0.56
1:C:80:ILE:O	1:C:84:LEU:HB2	2.05	0.56
1:D:278:GLY:N	1:D:303:ASN:O	2.37	0.56
1:H:278:GLY:N	1:H:303:ASN:O	2.37	0.56
1:G:80:ILE:O	1:G:84:LEU:HB2	2.05	0.56
1:A:19:THR:OG1	1:A:20:ALA:N	2.36	0.56
1:C:280:SER:OG	1:C:283:GLN:NE2	2.29	0.56
1:D:80:ILE:O	1:D:84:LEU:HB2	2.05	0.56
1:A:64:PRO:O	1:A:383:THR:OG1	2.21	0.56
1:G:278:GLY:N	1:G:303:ASN:O	2.37	0.56
1:H:80:ILE:O	1:H:84:LEU:HB2	2.05	0.56
1:B:64:PRO:O	1:B:383:THR:OG1	2.21	0.55
1:C:278:GLY:N	1:C:303:ASN:O	2.37	0.55
1:E:198:ASN:O	1:E:202:GLN:NE2	2.38	0.55
1:F:278:GLY:N	1:F:303:ASN:O	2.37	0.55
1:E:64:PRO:O	1:E:383:THR:OG1	2.21	0.55
1:F:64:PRO:O	1:F:383:THR:OG1	2.21	0.55
1:A:198:ASN:O	1:A:202:GLN:NE2	2.38	0.55
1:B:278:GLY:N	1:B:303:ASN:O	2.37	0.55
1:D:133:ALA:O	1:D:137:HIS:N	2.39	0.55
1:H:133:ALA:O	1:H:137:HIS:N	2.39	0.55
1:E:133:ALA:O	1:E:137:HIS:N	2.39	0.55
1:A:133:ALA:O	1:A:137:HIS:N	2.39	0.55
1:A:97:PRO:HG3	1:A:259:ARG:HG2	1.89	0.55
1:G:133:ALA:O	1:G:137:HIS:N	2.39	0.55
1:C:133:ALA:O	1:C:137:HIS:N	2.39	0.55
1:E:97:PRO:HG3	1:E:259:ARG:HG2	1.89	0.55
1:D:97:PRO:HG3	1:D:259:ARG:HG2	1.89	0.54
1:H:97:PRO:HG3	1:H:259:ARG:HG2	1.89	0.54
1:B:133:ALA:O	1:B:137:HIS:N	2.39	0.54
1:F:133:ALA:O	1:F:137:HIS:N	2.39	0.54
1:F:43:ASP:HA	1:G:281:ILE:HG12	1.88	0.54
1:A:281:ILE:HG12	1:D:43:ASP:HA	1.90	0.54
1:B:97:PRO:HG3	1:B:259:ARG:HG2	1.89	0.54
1:C:97:PRO:HG3	1:C:259:ARG:HG2	1.89	0.54
1:G:97:PRO:HG3	1:G:259:ARG:HG2	1.89	0.54
1:F:97:PRO:HG3	1:F:259:ARG:HG2	1.89	0.54
1:E:270:VAL:HG12	1:E:298:GLN:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:VAL:HG12	1:A:298:GLN:HB2	1.91	0.53
1:A:278:GLY:N	1:A:303:ASN:O	2.37	0.53
1:B:65:LEU:HD11	1:B:457:VAL:HG23	1.91	0.53
1:E:278:GLY:N	1:E:303:ASN:O	2.37	0.53
1:F:65:LEU:HD11	1:F:457:VAL:HG23	1.91	0.53
1:B:131:PHE:HA	1:B:134:LYS:HB3	1.91	0.53
1:F:131:PHE:HA	1:F:134:LYS:HB3	1.91	0.53
1:C:31:THR:N	1:C:34:ASP:OD2	2.36	0.52
1:H:131:PHE:HA	1:H:134:LYS:HB3	1.91	0.52
1:H:144:ILE:HG22	1:H:155:VAL:HB	1.91	0.52
1:D:144:ILE:HG22	1:D:155:VAL:HB	1.92	0.52
1:E:144:ILE:HG22	1:E:155:VAL:HB	1.92	0.52
1:C:131:PHE:HA	1:C:134:LYS:HB3	1.91	0.52
1:D:131:PHE:HA	1:D:134:LYS:HB3	1.92	0.52
1:F:270:VAL:HG12	1:F:298:GLN:HB2	1.91	0.52
1:A:144:ILE:HG22	1:A:155:VAL:HB	1.92	0.52
1:C:13:VAL:HA	1:D:311:LYS:HE2	1.90	0.52
1:E:131:PHE:HA	1:E:134:LYS:HB3	1.91	0.52
1:G:131:PHE:HA	1:G:134:LYS:HB3	1.91	0.52
1:B:270:VAL:HG12	1:B:298:GLN:HB2	1.91	0.52
1:G:31:THR:N	1:G:34:ASP:OD2	2.36	0.52
1:A:131:PHE:HA	1:A:134:LYS:HB3	1.91	0.52
1:B:458:PRO:HA	1:B:461:ILE:HG12	1.92	0.52
1:D:31:THR:N	1:D:34:ASP:OD2	2.36	0.52
1:F:458:PRO:HA	1:F:461:ILE:HG12	1.92	0.52
1:G:65:LEU:HD11	1:G:457:VAL:HG23	1.91	0.52
1:C:270:VAL:HG12	1:C:298:GLN:HB2	1.91	0.52
1:G:270:VAL:HG12	1:G:298:GLN:HB2	1.91	0.52
1:B:159:SER:OG	1:B:160:SER:N	2.43	0.52
1:D:65:LEU:HD11	1:D:457:VAL:HG23	1.91	0.52
1:F:159:SER:OG	1:F:160:SER:N	2.43	0.52
1:B:144:ILE:HG22	1:B:155:VAL:HB	1.92	0.52
1:C:65:LEU:HD11	1:C:457:VAL:HG23	1.91	0.52
1:F:144:ILE:HG22	1:F:155:VAL:HB	1.92	0.52
1:G:458:PRO:HA	1:G:461:ILE:HG12	1.92	0.52
1:H:65:LEU:HD11	1:H:457:VAL:HG23	1.91	0.52
1:H:31:THR:N	1:H:34:ASP:OD2	2.37	0.52
1:H:126:ARG:HE	1:H:128:ARG:HH12	1.57	0.52
1:A:65:LEU:HD11	1:A:457:VAL:HG23	1.91	0.51
1:C:37:ILE:O	1:D:340:GLY:N	2.41	0.51
1:C:458:PRO:HA	1:C:461:ILE:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:65:LEU:HD11	1:E:457:VAL:HG23	1.91	0.51
1:B:448:GLN:NE2	1:E:448:GLN:O	2.41	0.51
1:D:126:ARG:HE	1:D:128:ARG:HH12	1.58	0.51
1:E:52:THR:HA	1:E:62:LYS:HA	1.93	0.51
1:A:52:THR:HA	1:A:62:LYS:HA	1.93	0.51
1:B:52:THR:HA	1:B:62:LYS:HA	1.93	0.51
1:C:144:ILE:HG22	1:C:155:VAL:HB	1.92	0.51
1:D:270:VAL:HG12	1:D:298:GLN:HB2	1.91	0.51
1:F:52:THR:HA	1:F:62:LYS:HA	1.93	0.51
1:H:52:THR:HA	1:H:62:LYS:HA	1.93	0.51
1:H:270:VAL:HG12	1:H:298:GLN:HB2	1.91	0.51
1:D:52:THR:HA	1:D:62:LYS:HA	1.93	0.51
1:B:448:GLN:O	1:E:448:GLN:NE2	2.43	0.51
1:G:144:ILE:HG22	1:G:155:VAL:HB	1.92	0.51
1:C:238:LYS:HZ2	1:C:244:LEU:HG	1.74	0.51
1:E:126:ARG:HE	1:E:128:ARG:HH12	1.57	0.51
1:E:304:VAL:HG21	1:E:310:ALA:HB2	1.93	0.51
1:G:238:LYS:HZ2	1:G:244:LEU:HG	1.74	0.51
1:A:304:VAL:HG21	1:A:310:ALA:HB2	1.93	0.51
1:B:126:ARG:HE	1:B:128:ARG:HH12	1.57	0.51
1:C:52:THR:HA	1:C:62:LYS:HA	1.93	0.51
1:G:52:THR:HA	1:G:62:LYS:HA	1.93	0.51
1:G:126:ARG:HE	1:G:128:ARG:HH12	1.57	0.51
1:A:126:ARG:HE	1:A:128:ARG:HH12	1.57	0.50
1:F:126:ARG:HE	1:F:128:ARG:HH12	1.58	0.50
1:D:458:PRO:HA	1:D:461:ILE:HG12	1.92	0.50
1:F:304:VAL:HG21	1:F:310:ALA:HB2	1.93	0.50
1:F:377:LEU:HA	1:F:381:ALA:HB3	1.92	0.50
1:A:225:THR:HB	1:A:228:LYS:HE3	1.93	0.50
1:B:377:LEU:HA	1:B:381:ALA:HB3	1.92	0.50
1:C:126:ARG:HE	1:C:128:ARG:HH12	1.58	0.50
1:E:104:VAL:HA	1:E:107:VAL:HG12	1.94	0.50
1:H:458:PRO:HA	1:H:461:ILE:HG12	1.92	0.50
1:A:159:SER:OG	1:A:160:SER:N	2.43	0.50
1:B:304:VAL:HG21	1:B:310:ALA:HB2	1.94	0.50
1:A:104:VAL:HA	1:A:107:VAL:HG12	1.94	0.50
1:A:377:LEU:HA	1:A:381:ALA:HB3	1.92	0.50
1:D:211:ILE:HD11	1:D:220:ALA:HB3	1.93	0.50
1:F:104:VAL:HA	1:F:107:VAL:HG12	1.94	0.50
1:H:377:LEU:HA	1:H:381:ALA:HB3	1.92	0.50
1:A:31:THR:N	1:A:34:ASP:OD2	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:377:LEU:HA	1:D:381:ALA:HB3	1.92	0.50
1:E:159:SER:OG	1:E:160:SER:N	2.43	0.50
1:E:225:THR:HB	1:E:228:LYS:HE3	1.93	0.50
1:G:225:THR:HB	1:G:228:LYS:HE3	1.93	0.50
1:H:280:SER:OG	1:H:283:GLN:NE2	2.29	0.50
1:B:104:VAL:HA	1:B:107:VAL:HG12	1.94	0.50
1:C:225:THR:HB	1:C:228:LYS:HE3	1.93	0.50
1:D:304:VAL:HG21	1:D:310:ALA:HB2	1.93	0.50
1:E:377:LEU:HA	1:E:381:ALA:HB3	1.92	0.50
1:G:104:VAL:HA	1:G:107:VAL:HG12	1.94	0.50
1:H:211:ILE:HD11	1:H:220:ALA:HB3	1.93	0.50
1:B:374:ALA:O	1:B:378:ALA:HB2	2.12	0.49
1:C:104:VAL:HA	1:C:107:VAL:HG12	1.94	0.49
1:E:280:SER:OG	1:E:283:GLN:NE2	2.29	0.49
1:F:374:ALA:O	1:F:378:ALA:HB2	2.12	0.49
1:G:377:LEU:HA	1:G:381:ALA:HB3	1.92	0.49
1:H:304:VAL:HG21	1:H:310:ALA:HB2	1.93	0.49
1:A:211:ILE:HD11	1:A:220:ALA:HB3	1.93	0.49
1:A:228:LYS:HA	1:A:231:ARG:HG3	1.94	0.49
1:C:377:LEU:HA	1:C:381:ALA:HB3	1.92	0.49
1:C:304:VAL:HG21	1:C:310:ALA:HB2	1.93	0.49
1:C:459:TYR:CZ	1:H:402:PHE:HB3	2.47	0.49
1:E:228:LYS:HA	1:E:231:ARG:HG3	1.94	0.49
1:G:304:VAL:HG21	1:G:310:ALA:HB2	1.93	0.49
1:G:380:GLY:HA3	1:G:483:MET:HE2	1.94	0.49
1:B:228:LYS:HA	1:B:231:ARG:HG3	1.94	0.49
1:D:225:THR:HB	1:D:228:LYS:HE3	1.93	0.49
1:E:458:PRO:HA	1:E:461:ILE:HG12	1.92	0.49
1:C:380:GLY:HA3	1:C:483:MET:HE2	1.94	0.49
1:D:280:SER:OG	1:D:283:GLN:NE2	2.29	0.49
1:E:31:THR:N	1:E:34:ASP:OD2	2.36	0.49
1:E:211:ILE:HD11	1:E:220:ALA:HB3	1.93	0.49
1:F:228:LYS:HA	1:F:231:ARG:HG3	1.94	0.49
1:H:225:THR:HB	1:H:228:LYS:HE3	1.93	0.49
1:A:458:PRO:HA	1:A:461:ILE:HG12	1.92	0.49
1:B:225:THR:HB	1:B:228:LYS:HE3	1.93	0.49
1:E:374:ALA:O	1:E:378:ALA:HB2	2.12	0.49
1:H:104:VAL:HA	1:H:107:VAL:HG12	1.94	0.49
1:A:228:LYS:O	1:A:232:ASP:HB2	2.13	0.49
1:A:280:SER:OG	1:A:283:GLN:NE2	2.29	0.49
1:C:211:ILE:HD11	1:C:220:ALA:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:104:VAL:HA	1:D:107:VAL:HG12	1.94	0.49
1:D:374:ALA:O	1:D:378:ALA:HB2	2.12	0.49
1:F:225:THR:HB	1:F:228:LYS:HE3	1.93	0.49
1:A:374:ALA:O	1:A:378:ALA:HB2	2.12	0.49
1:F:211:ILE:HD11	1:F:220:ALA:HB3	1.93	0.49
1:F:380:GLY:HA2	1:F:480:ARG:HG3	1.95	0.49
1:H:228:LYS:O	1:H:232:ASP:HB2	2.13	0.49
1:H:374:ALA:O	1:H:378:ALA:HB2	2.12	0.49
1:B:211:ILE:HD11	1:B:220:ALA:HB3	1.93	0.49
1:D:228:LYS:O	1:D:232:ASP:HB2	2.13	0.49
1:E:195:LYS:HE3	2:E:602:GTP:H4'	1.95	0.49
1:E:228:LYS:O	1:E:232:ASP:HB2	2.13	0.49
1:F:380:GLY:HA3	1:F:483:MET:HE2	1.94	0.49
1:G:211:ILE:HD11	1:G:220:ALA:HB3	1.93	0.49
1:G:374:ALA:O	1:G:378:ALA:HB2	2.12	0.49
1:G:380:GLY:HA2	1:G:480:ARG:HG3	1.95	0.49
1:B:195:LYS:HE3	2:B:602:GTP:H4'	1.95	0.49
1:B:380:GLY:HA2	1:B:480:ARG:HG3	1.95	0.49
1:B:380:GLY:HA3	1:B:483:MET:HE2	1.94	0.49
1:C:374:ALA:O	1:C:378:ALA:HB2	2.12	0.49
1:C:380:GLY:HA2	1:C:480:ARG:HG3	1.95	0.49
1:G:195:LYS:HE3	2:G:602:GTP:H4'	1.95	0.49
1:A:195:LYS:HE3	2:A:602:GTP:H4'	1.95	0.48
1:C:159:SER:OG	1:C:160:SER:N	2.43	0.48
1:C:195:LYS:HE3	2:C:602:GTP:H4'	1.95	0.48
1:D:159:SER:OG	1:D:160:SER:N	2.43	0.48
1:D:228:LYS:HA	1:D:231:ARG:HG3	1.94	0.48
1:F:195:LYS:HE3	2:F:602:GTP:H4'	1.95	0.48
1:G:228:LYS:HA	1:G:231:ARG:HG3	1.94	0.48
1:A:363:ALA:HB3	1:A:384:VAL:HB	1.95	0.48
1:C:363:ALA:HB3	1:C:384:VAL:HB	1.95	0.48
1:H:195:LYS:HE3	2:H:602:GTP:H4'	1.95	0.48
1:H:228:LYS:HA	1:H:231:ARG:HG3	1.94	0.48
1:A:380:GLY:HA3	1:A:483:MET:HE2	1.94	0.48
1:B:228:LYS:O	1:B:232:ASP:HB2	2.13	0.48
1:C:228:LYS:HA	1:C:231:ARG:HG3	1.94	0.48
1:D:195:LYS:HE3	2:D:602:GTP:H4'	1.95	0.48
1:E:206:LYS:HZ3	1:E:208:LYS:HE2	1.78	0.48
1:G:159:SER:OG	1:G:160:SER:N	2.43	0.48
1:H:159:SER:OG	1:H:160:SER:N	2.43	0.48
1:H:380:GLY:HA3	1:H:483:MET:HE2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:380:GLY:HA3	1:D:483:MET:HE2	1.94	0.48
1:E:363:ALA:HB3	1:E:384:VAL:HB	1.95	0.48
1:E:380:GLY:HA3	1:E:483:MET:HE2	1.94	0.48
1:F:228:LYS:O	1:F:232:ASP:HB2	2.13	0.48
1:C:43:ASP:HA	1:D:281:ILE:HG12	1.96	0.48
1:C:228:LYS:O	1:C:232:ASP:HB2	2.13	0.48
1:G:363:ALA:HB3	1:G:384:VAL:HB	1.95	0.48
1:G:228:LYS:O	1:G:232:ASP:HB2	2.13	0.48
1:A:380:GLY:HA2	1:A:480:ARG:HG3	1.95	0.48
1:B:76:ALA:HB2	1:B:103:GLU:HG3	1.96	0.48
1:F:76:ALA:HB2	1:F:103:GLU:HG3	1.96	0.48
1:G:13:VAL:HA	1:H:311:LYS:HE2	1.96	0.48
1:A:206:LYS:HZ3	1:A:208:LYS:HE2	1.79	0.48
1:E:13:VAL:HA	1:F:311:LYS:HE2	1.96	0.48
1:E:76:ALA:HB2	1:E:103:GLU:HG3	1.96	0.48
1:H:363:ALA:HB3	1:H:384:VAL:HB	1.95	0.48
1:E:380:GLY:HA2	1:E:480:ARG:HG3	1.95	0.48
1:D:363:ALA:HB3	1:D:384:VAL:HB	1.95	0.48
1:G:76:ALA:HB2	1:G:103:GLU:HG3	1.96	0.48
1:A:76:ALA:HB2	1:A:103:GLU:HG3	1.96	0.47
1:C:76:ALA:HB2	1:C:103:GLU:HG3	1.96	0.47
1:D:128:ARG:O	1:D:132:GLU:CB	2.62	0.47
1:E:43:ASP:HA	1:F:281:ILE:HG12	1.96	0.47
1:D:76:ALA:HB2	1:D:103:GLU:HG3	1.96	0.47
1:F:363:ALA:HB3	1:F:384:VAL:HB	1.95	0.47
1:G:43:ASP:HA	1:H:281:ILE:HG12	1.97	0.47
1:H:76:ALA:HB2	1:H:103:GLU:HG3	1.96	0.47
1:H:128:ARG:O	1:H:132:GLU:CB	2.62	0.47
1:A:43:ASP:HA	1:B:281:ILE:HG12	1.96	0.47
1:B:363:ALA:HB3	1:B:384:VAL:HB	1.95	0.47
1:G:161:ARG:H	1:G:161:ARG:HG2	1.41	0.47
1:D:104:VAL:HG22	1:D:268:VAL:HG21	1.96	0.47
1:D:380:GLY:HA2	1:D:480:ARG:HG3	1.95	0.47
1:H:380:GLY:HA2	1:H:480:ARG:HG3	1.95	0.47
1:A:280:SER:HG	1:A:283:GLN:HE21	1.59	0.47
1:C:161:ARG:H	1:C:161:ARG:HG2	1.41	0.47
1:H:104:VAL:HG22	1:H:268:VAL:HG21	1.96	0.47
1:F:280:SER:OG	1:F:283:GLN:NE2	2.29	0.47
1:D:277:GLN:HE22	1:D:279:ASN:HB2	1.80	0.47
1:E:104:VAL:HG22	1:E:268:VAL:HG21	1.96	0.47
1:H:277:GLN:HE22	1:H:279:ASN:HB2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:453:ILE:HA	1:E:456:PHE:HB3	1.97	0.46
1:A:453:ILE:HA	1:A:456:PHE:HB3	1.98	0.46
1:D:32:TYR:HB2	1:D:375:LYS:HE3	1.98	0.46
1:D:402:PHE:HB3	1:G:459:TYR:CZ	2.50	0.46
1:E:161:ARG:H	1:E:161:ARG:HG2	1.41	0.46
1:A:104:VAL:HG22	1:A:268:VAL:HG21	1.96	0.46
1:C:32:TYR:HB2	1:C:375:LYS:HE3	1.98	0.46
1:B:280:SER:OG	1:B:283:GLN:NE2	2.29	0.46
1:C:66:VAL:O	1:C:386:MET:N	2.36	0.46
1:E:277:GLN:HE22	1:E:279:ASN:HB2	1.80	0.46
1:F:302:GLY:HA2	1:F:303:ASN:HA	1.79	0.46
1:G:32:TYR:HB2	1:G:375:LYS:HE3	1.98	0.46
1:H:32:TYR:HB2	1:H:375:LYS:HE3	1.98	0.46
1:A:277:GLN:HE22	1:A:279:ASN:HB2	1.80	0.46
1:G:37:ILE:O	1:H:340:GLY:N	2.47	0.46
1:G:66:VAL:O	1:G:386:MET:N	2.36	0.46
1:A:161:ARG:H	1:A:161:ARG:HG2	1.41	0.46
1:E:161:ARG:NH2	3:E:603:ATP:O5'	2.44	0.46
1:G:277:GLN:HE22	1:G:279:ASN:HB2	1.80	0.46
1:B:104:VAL:HG22	1:B:268:VAL:HG21	1.96	0.46
1:G:104:VAL:HG22	1:G:268:VAL:HG21	1.96	0.46
1:C:104:VAL:HG22	1:C:268:VAL:HG21	1.96	0.46
1:C:277:GLN:HE22	1:C:279:ASN:HB2	1.80	0.46
1:C:339:CYS:SG	1:C:340:GLY:N	2.89	0.46
1:D:65:LEU:HD12	1:D:386:MET:HG2	1.98	0.46
1:F:104:VAL:HG22	1:F:268:VAL:HG21	1.96	0.46
1:H:65:LEU:HD12	1:H:386:MET:HG2	1.98	0.46
1:F:453:ILE:HA	1:F:456:PHE:HB3	1.98	0.46
1:G:339:CYS:SG	1:G:340:GLY:N	2.89	0.46
1:A:32:TYR:HB2	1:A:375:LYS:HE3	1.98	0.45
1:A:161:ARG:NH2	3:A:603:ATP:O5'	2.44	0.45
1:B:31:THR:N	1:B:34:ASP:OD2	2.36	0.45
1:B:401:PHE:HD1	1:B:410:LYS:HB2	1.81	0.45
1:B:453:ILE:HA	1:B:456:PHE:HB3	1.98	0.45
1:B:277:GLN:HE22	1:B:279:ASN:HB2	1.80	0.45
1:E:32:TYR:HB2	1:E:375:LYS:HE3	1.98	0.45
1:F:31:THR:N	1:F:34:ASP:OD2	2.37	0.45
1:F:401:PHE:HD1	1:F:410:LYS:HB2	1.82	0.45
1:C:448:GLN:HG3	1:H:449:ASP:O	2.17	0.45
1:D:453:ILE:HA	1:D:456:PHE:HB3	1.98	0.45
1:H:66:VAL:O	1:H:386:MET:N	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:453:ILE:HA	1:H:456:PHE:HB3	1.98	0.45
1:A:13:VAL:HA	1:B:311:LYS:HE2	1.98	0.45
1:A:128:ARG:O	1:A:132:GLU:CB	2.62	0.45
1:B:339:CYS:SG	1:B:340:GLY:N	2.89	0.45
1:D:339:CYS:SG	1:D:340:GLY:N	2.89	0.45
1:F:277:GLN:HE22	1:F:279:ASN:HB2	1.80	0.45
1:F:339:CYS:SG	1:F:340:GLY:N	2.89	0.45
1:G:453:ILE:HA	1:G:456:PHE:HB3	1.97	0.45
1:B:32:TYR:HB2	1:B:375:LYS:HE3	1.98	0.45
1:F:128:ARG:O	1:F:132:GLU:CB	2.62	0.45
1:H:339:CYS:SG	1:H:340:GLY:N	2.89	0.45
1:B:128:ARG:O	1:B:132:GLU:CB	2.62	0.45
1:C:453:ILE:HA	1:C:456:PHE:HB3	1.98	0.45
1:E:128:ARG:O	1:E:132:GLU:CB	2.62	0.45
1:F:32:TYR:HB2	1:F:375:LYS:HE3	1.98	0.45
1:F:161:ARG:NH2	3:F:603:ATP:O5'	2.44	0.45
1:A:55:LEU:HD13	1:A:88:ILE:HD12	1.99	0.45
1:C:65:LEU:HD12	1:C:386:MET:HG2	1.98	0.45
1:C:459:TYR:CE1	1:H:402:PHE:HB3	2.51	0.45
1:E:55:LEU:HD13	1:E:88:ILE:HD12	1.99	0.45
1:G:65:LEU:HD12	1:G:386:MET:HG2	1.98	0.45
1:B:161:ARG:NH2	3:B:603:ATP:O5'	2.44	0.44
1:C:401:PHE:HD1	1:C:410:LYS:HB2	1.81	0.44
1:B:208:LYS:HG3	1:B:223:ALA:HA	1.99	0.44
1:D:401:PHE:HD1	1:D:410:LYS:HB2	1.82	0.44
1:E:65:LEU:HD12	1:E:386:MET:HG2	1.98	0.44
1:E:112:GLN:H	1:E:112:GLN:HG2	1.62	0.44
1:E:339:CYS:SG	1:E:340:GLY:N	2.89	0.44
1:H:401:PHE:HD1	1:H:410:LYS:HB2	1.81	0.44
1:A:65:LEU:HD12	1:A:386:MET:HG2	1.98	0.44
1:A:252:THR:HA	1:A:286:MET:HE1	1.99	0.44
1:A:339:CYS:SG	1:A:340:GLY:N	2.89	0.44
1:B:323:VAL:HG12	1:B:363:ALA:HA	1.99	0.44
1:F:208:LYS:HG3	1:F:223:ALA:HA	1.99	0.44
1:G:401:PHE:HD1	1:G:410:LYS:HB2	1.82	0.44
1:A:401:PHE:HD1	1:A:410:LYS:HB2	1.81	0.44
1:E:401:PHE:HD1	1:E:410:LYS:HB2	1.81	0.44
1:B:65:LEU:HD12	1:B:386:MET:HG2	1.98	0.44
1:F:65:LEU:HD12	1:F:386:MET:HG2	1.98	0.44
1:F:323:VAL:HG12	1:F:363:ALA:HA	1.99	0.44
1:A:459:TYR:CZ	1:F:402:PHE:HB3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:LEU:HD13	1:C:88:ILE:HD12	1.99	0.44
1:E:252:THR:HA	1:E:286:MET:HE1	1.99	0.44
1:G:55:LEU:HD13	1:G:88:ILE:HD12	1.99	0.44
1:H:161:ARG:NH2	3:H:603:ATP:O5'	2.44	0.44
1:B:402:PHE:HB3	1:E:459:TYR:CE1	2.53	0.44
1:G:208:LYS:HG3	1:G:223:ALA:HA	1.99	0.44
1:G:252:THR:HA	1:G:286:MET:HE1	1.99	0.44
1:H:112:GLN:H	1:H:112:GLN:HG2	1.62	0.44
1:B:41:TYR:HA	1:C:279:ASN:ND2	2.32	0.44
1:B:161:ARG:H	1:B:161:ARG:HG2	1.41	0.44
1:C:252:THR:HA	1:C:286:MET:HE1	1.99	0.44
1:D:487:GLU:OE1	1:D:488:LEU:N	2.51	0.44
1:E:323:VAL:HG12	1:E:363:ALA:HA	1.99	0.44
1:G:128:ARG:O	1:G:132:GLU:CB	2.62	0.44
1:A:323:VAL:HG12	1:A:363:ALA:HA	1.99	0.43
1:B:386:MET:HB3	1:B:390:LEU:HD22	2.00	0.43
1:D:161:ARG:NH2	3:D:603:ATP:O5'	2.44	0.43
1:D:323:VAL:HG12	1:D:363:ALA:HA	1.99	0.43
1:F:386:MET:HB3	1:F:390:LEU:HD22	2.00	0.43
1:H:487:GLU:OE1	1:H:488:LEU:N	2.51	0.43
1:A:208:LYS:HG3	1:A:223:ALA:HA	1.99	0.43
1:C:128:ARG:O	1:C:132:GLU:CB	2.62	0.43
1:C:208:LYS:HG3	1:C:223:ALA:HA	1.99	0.43
1:D:206:LYS:HZ3	1:D:208:LYS:HE2	1.83	0.43
1:E:208:LYS:HG3	1:E:223:ALA:HA	1.99	0.43
1:E:325:MET:O	1:E:334:GLN:NE2	2.48	0.43
1:G:206:LYS:HZ3	1:G:208:LYS:HE2	1.82	0.43
1:H:55:LEU:HD13	1:H:88:ILE:HD12	1.99	0.43
1:H:206:LYS:HZ3	1:H:208:LYS:HE2	1.83	0.43
1:H:323:VAL:HG12	1:H:363:ALA:HA	1.99	0.43
1:A:325:MET:O	1:A:334:GLN:NE2	2.48	0.43
1:B:252:THR:HA	1:B:286:MET:HE1	1.99	0.43
1:D:55:LEU:HD13	1:D:88:ILE:HD12	1.99	0.43
1:F:161:ARG:H	1:F:161:ARG:HG2	1.41	0.43
1:F:252:THR:HA	1:F:286:MET:HE1	1.99	0.43
1:B:487:GLU:OE1	1:B:488:LEU:N	2.51	0.43
1:C:115:ILE:H	1:C:115:ILE:HG13	1.71	0.43
1:C:206:LYS:HZ3	1:C:208:LYS:HE2	1.82	0.43
1:C:402:PHE:HB3	1:H:459:TYR:CE1	2.53	0.43
1:D:208:LYS:HG3	1:D:223:ALA:HA	1.99	0.43
1:E:487:GLU:OE1	1:E:488:LEU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:LEU:HD13	1:B:88:ILE:HD12	1.99	0.43
1:B:206:LYS:HZ3	1:B:208:LYS:HE2	1.83	0.43
1:C:487:GLU:OE1	1:C:488:LEU:N	2.51	0.43
1:D:252:THR:HA	1:D:286:MET:HE1	1.99	0.43
1:F:487:GLU:OE1	1:F:488:LEU:N	2.51	0.43
1:G:487:GLU:OE1	1:G:488:LEU:N	2.51	0.43
1:H:208:LYS:HG3	1:H:223:ALA:HA	1.99	0.43
1:H:252:THR:HA	1:H:286:MET:HE1	1.99	0.43
1:H:466:HIS:HD2	1:H:469:GLN:HE21	1.67	0.43
1:A:487:GLU:OE1	1:A:488:LEU:N	2.51	0.43
1:C:466:HIS:HD2	1:C:469:GLN:HE21	1.67	0.43
1:D:466:HIS:HD2	1:D:469:GLN:HE21	1.67	0.43
1:E:281:ILE:HG12	1:H:43:ASP:HA	2.01	0.43
1:B:410:LYS:HE2	1:B:410:LYS:HB3	1.87	0.43
1:F:55:LEU:HD13	1:F:88:ILE:HD12	1.99	0.43
1:F:206:LYS:HZ3	1:F:208:LYS:HE2	1.83	0.43
1:G:466:HIS:HD2	1:G:469:GLN:HE21	1.67	0.43
1:B:198:ASN:HA	1:B:201:LEU:HD12	2.01	0.43
1:C:386:MET:HB3	1:C:390:LEU:HD22	2.00	0.43
1:D:372:HIS:HA	1:D:375:LYS:HE2	2.01	0.43
1:F:198:ASN:HA	1:F:201:LEU:HD12	2.01	0.43
1:G:386:MET:HB3	1:G:390:LEU:HD22	2.00	0.43
1:H:372:HIS:HA	1:H:375:LYS:HE2	2.01	0.43
1:A:466:HIS:HD2	1:A:469:GLN:HE21	1.67	0.43
1:C:323:VAL:HG12	1:C:363:ALA:HA	1.99	0.43
1:E:372:HIS:HA	1:E:375:LYS:HE2	2.01	0.43
1:E:466:HIS:HD2	1:E:469:GLN:HE21	1.67	0.43
1:A:372:HIS:HA	1:A:375:LYS:HE2	2.01	0.42
1:B:325:MET:HE2	1:B:340:GLY:HA3	2.01	0.42
1:E:147:THR:OG1	1:E:152:SER:OG	2.37	0.42
1:F:372:HIS:HA	1:F:375:LYS:HE2	2.01	0.42
1:G:115:ILE:H	1:G:115:ILE:HG13	1.71	0.42
1:C:372:HIS:HA	1:C:375:LYS:HE2	2.01	0.42
1:E:37:ILE:O	1:F:340:GLY:N	2.48	0.42
1:F:164:ASP:OD1	1:F:164:ASP:N	2.52	0.42
1:F:325:MET:HE2	1:F:340:GLY:HA3	2.01	0.42
1:F:410:LYS:HE2	1:F:410:LYS:HB3	1.87	0.42
1:G:323:VAL:HG12	1:G:363:ALA:HA	2.00	0.42
1:H:325:MET:HE2	1:H:340:GLY:HA3	2.01	0.42
1:A:115:ILE:H	1:A:115:ILE:HG13	1.71	0.42
1:A:386:MET:HB3	1:A:390:LEU:HD22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:ASP:OD1	1:B:164:ASP:N	2.52	0.42
1:B:372:HIS:HA	1:B:375:LYS:HE2	2.01	0.42
1:E:386:MET:HB3	1:E:390:LEU:HD22	2.00	0.42
1:G:372:HIS:HA	1:G:375:LYS:HE2	2.01	0.42
1:C:302:GLY:HA2	1:C:303:ASN:HA	1.79	0.42
1:D:101:ALA:HA	1:D:104:VAL:HG12	2.01	0.42
1:D:325:MET:HE2	1:D:340:GLY:HA3	2.01	0.42
1:G:164:ASP:N	1:G:164:ASP:OD1	2.52	0.42
1:H:101:ALA:HA	1:H:104:VAL:HG12	2.01	0.42
1:C:164:ASP:OD1	1:C:164:ASP:N	2.52	0.42
1:D:403:SER:OG	1:D:406:ILE:O	2.37	0.42
1:D:449:ASP:O	1:G:448:GLN:HG3	2.19	0.42
1:E:311:LYS:HE2	1:H:13:VAL:HA	2.00	0.42
1:F:466:HIS:HD2	1:F:469:GLN:HE21	1.67	0.42
1:G:161:ARG:NH2	3:G:603:ATP:O5'	2.44	0.42
1:H:403:SER:OG	1:H:406:ILE:O	2.38	0.42
1:A:206:LYS:NZ	1:A:208:LYS:HB2	2.33	0.42
1:B:466:HIS:HD2	1:B:469:GLN:HE21	1.67	0.42
1:C:198:ASN:HA	1:C:201:LEU:HD12	2.01	0.42
1:D:128:ARG:HH11	1:D:170:GLU:HB2	1.85	0.42
1:E:41:TYR:HA	1:F:279:ASN:ND2	2.34	0.42
1:G:198:ASN:HA	1:G:201:LEU:HD12	2.01	0.42
1:D:386:MET:HB3	1:D:390:LEU:HD22	2.00	0.42
1:E:115:ILE:H	1:E:115:ILE:HG13	1.71	0.42
1:E:239:ASP:OD1	1:E:243:GLN:N	2.53	0.42
1:F:36:LEU:HD12	1:F:36:LEU:HA	1.98	0.42
1:G:239:ASP:OD1	1:G:243:GLN:N	2.53	0.42
1:G:302:GLY:HA2	1:G:303:ASN:HA	1.80	0.42
1:H:128:ARG:HH11	1:H:170:GLU:HB2	1.84	0.42
1:H:386:MET:HB3	1:H:390:LEU:HD22	2.00	0.42
1:A:239:ASP:OD1	1:A:243:GLN:N	2.53	0.42
1:C:101:ALA:HA	1:C:104:VAL:HG12	2.01	0.42
1:C:161:ARG:NH2	3:C:603:ATP:O5'	2.44	0.42
1:C:239:ASP:OD1	1:C:243:GLN:N	2.53	0.42
1:E:206:LYS:NZ	1:E:208:LYS:HB2	2.33	0.42
1:H:239:ASP:OD1	1:H:243:GLN:N	2.53	0.42
1:B:36:LEU:HD12	1:B:36:LEU:HA	1.98	0.41
1:B:101:ALA:HA	1:B:104:VAL:HG12	2.01	0.41
1:D:239:ASP:OD1	1:D:243:GLN:N	2.53	0.41
1:F:101:ALA:HA	1:F:104:VAL:HG12	2.01	0.41
1:A:128:ARG:HH11	1:A:170:GLU:HB2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:ARG:HH11	1:C:170:GLU:HB2	1.84	0.41
1:E:128:ARG:HH11	1:E:170:GLU:HB2	1.85	0.41
1:E:325:MET:HE2	1:E:340:GLY:HA3	2.01	0.41
1:G:101:ALA:HA	1:G:104:VAL:HG12	2.01	0.41
1:A:325:MET:HE2	1:A:340:GLY:HA3	2.01	0.41
1:B:128:ARG:HH11	1:B:170:GLU:HB2	1.84	0.41
1:D:198:ASN:HA	1:D:201:LEU:HD12	2.01	0.41
1:E:303:ASN:HD22	1:E:304:VAL:H	1.68	0.41
1:H:198:ASN:HA	1:H:201:LEU:HD12	2.01	0.41
1:A:303:ASN:HD22	1:A:304:VAL:H	1.68	0.41
1:B:459:TYR:CE1	1:E:402:PHE:HB3	2.56	0.41
1:G:128:ARG:HH11	1:G:170:GLU:HB2	1.84	0.41
1:H:164:ASP:OD1	1:H:164:ASP:N	2.52	0.41
1:C:41:TYR:HA	1:D:279:ASN:ND2	2.36	0.41
1:E:410:LYS:HB3	1:E:410:LYS:HE2	1.87	0.41
1:G:325:MET:HE2	1:G:340:GLY:HA3	2.01	0.41
1:A:198:ASN:HA	1:A:201:LEU:HD12	2.01	0.41
1:A:403:SER:OG	1:A:406:ILE:O	2.37	0.41
1:B:403:SER:O	1:B:406:ILE:N	2.54	0.41
1:C:255:ASP:OD1	1:C:255:ASP:N	2.54	0.41
1:D:146:ASP:OD1	1:D:146:ASP:N	2.54	0.41
1:D:164:ASP:OD1	1:D:164:ASP:N	2.52	0.41
1:E:198:ASN:HA	1:E:201:LEU:HD12	2.01	0.41
1:F:128:ARG:HH11	1:F:170:GLU:HB2	1.84	0.41
1:F:239:ASP:OD1	1:F:243:GLN:N	2.53	0.41
1:H:146:ASP:OD1	1:H:146:ASP:N	2.54	0.41
1:A:121:LEU:HD13	1:A:121:LEU:HA	1.94	0.41
1:B:239:ASP:OD1	1:B:243:GLN:N	2.53	0.41
1:C:325:MET:HE2	1:C:340:GLY:HA3	2.01	0.41
1:E:137:HIS:HB3	1:E:139:PHE:CE1	2.56	0.41
1:F:403:SER:O	1:F:406:ILE:N	2.54	0.41
1:G:255:ASP:OD1	1:G:255:ASP:N	2.54	0.41
1:H:137:HIS:HB3	1:H:139:PHE:CE1	2.56	0.41
1:A:137:HIS:HB3	1:A:139:PHE:CE1	2.56	0.41
1:D:137:HIS:HB3	1:D:139:PHE:CE1	2.56	0.41
1:H:129:ASP:OD1	1:H:129:ASP:N	2.54	0.41
1:A:101:ALA:HA	1:A:104:VAL:HG12	2.01	0.41
1:B:13:VAL:HA	1:C:311:LYS:HE2	2.02	0.41
1:B:280:SER:HG	1:B:283:GLN:HE21	1.62	0.41
1:C:137:HIS:HB3	1:C:139:PHE:CE1	2.56	0.41
1:C:403:SER:O	1:C:406:ILE:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:129:ASP:OD1	1:D:129:ASP:N	2.54	0.41
1:D:410:LYS:HE2	1:D:410:LYS:HB3	1.87	0.41
1:E:403:SER:OG	1:E:406:ILE:O	2.38	0.41
1:G:137:HIS:HB3	1:G:139:PHE:CE1	2.56	0.41
1:E:36:LEU:HD12	1:E:36:LEU:HA	1.98	0.41
1:E:101:ALA:HA	1:E:104:VAL:HG12	2.01	0.41
1:G:403:SER:O	1:G:406:ILE:N	2.54	0.41
1:A:146:ASP:N	1:A:146:ASP:OD1	2.54	0.40
1:C:23:LEU:HD22	1:C:24:PHE:CZ	2.57	0.40
1:F:146:ASP:N	1:F:146:ASP:OD1	2.54	0.40
1:G:146:ASP:OD1	1:G:146:ASP:N	2.54	0.40
1:A:36:LEU:HD12	1:A:36:LEU:HA	1.98	0.40
1:A:160:SER:OG	3:A:603:ATP:O2B	2.34	0.40
1:B:467:SER:O	1:B:471:ILE:HD12	2.21	0.40
1:C:303:ASN:HD22	1:C:304:VAL:H	1.68	0.40
1:E:121:LEU:HD13	1:E:121:LEU:HA	1.94	0.40
1:F:280:SER:HG	1:F:283:GLN:HE21	1.62	0.40
1:F:467:SER:O	1:F:471:ILE:HD12	2.21	0.40
1:A:410:LYS:HB3	1:A:410:LYS:HE2	1.88	0.40
1:B:146:ASP:OD1	1:B:146:ASP:N	2.54	0.40
1:C:146:ASP:OD1	1:C:146:ASP:N	2.54	0.40
1:E:467:SER:O	1:E:471:ILE:HD12	2.21	0.40
1:G:23:LEU:HD22	1:G:24:PHE:CZ	2.57	0.40
1:G:75:GLU:HG2	1:G:397:PRO:HA	2.04	0.40
1:H:410:LYS:HE2	1:H:410:LYS:HB3	1.87	0.40
1:C:75:GLU:HG2	1:C:397:PRO:HA	2.04	0.40
1:E:129:ASP:OD1	1:E:129:ASP:N	2.54	0.40
1:E:146:ASP:N	1:E:146:ASP:OD1	2.54	0.40
1:F:137:HIS:HB3	1:F:139:PHE:CE1	2.56	0.40
1:G:303:ASN:HD22	1:G:304:VAL:H	1.69	0.40
1:H:126:ARG:NE	1:H:128:ARG:HH12	2.18	0.40
1:A:23:LEU:HD22	1:A:24:PHE:CZ	2.57	0.40
1:A:459:TYR:CE1	1:F:402:PHE:HB3	2.56	0.40
1:A:467:SER:O	1:A:471:ILE:HD12	2.21	0.40
1:B:137:HIS:HB3	1:B:139:PHE:CE1	2.56	0.40
1:C:129:ASP:OD1	1:C:129:ASP:N	2.54	0.40
1:D:23:LEU:HD22	1:D:24:PHE:CZ	2.56	0.40
1:D:126:ARG:NE	1:D:128:ARG:HH12	2.18	0.40
1:E:23:LEU:HD22	1:E:24:PHE:CZ	2.57	0.40
1:E:126:ARG:NE	1:E:128:ARG:HH12	2.18	0.40
1:F:75:GLU:HG2	1:F:397:PRO:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:129:ASP:OD1	1:G:129:ASP:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	B	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	C	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	D	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	E	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	F	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	G	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
1	H	447/519 (86%)	413 (92%)	34 (8%)	0	100	100
All	All	3576/4152 (86%)	3304 (92%)	272 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	A	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	B	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	C	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	D	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	E	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	F	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	G	371/425 (87%)	316 (85%)	55 (15%)	3	14
1	H	371/425 (87%)	316 (85%)	55 (15%)	3	14
All	All	2968/3400 (87%)	2528 (85%)	440 (15%)	5	14

All (440) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LEU
1	A	19	THR
1	A	28	ASP
1	A	36	LEU
1	A	38	LEU
1	A	49	VAL
1	A	66	VAL
1	A	70	MET
1	A	72	THR
1	A	78	MET
1	A	103	GLU
1	A	104	VAL
1	A	108	LYS
1	A	109	LYS
1	A	112	GLN
1	A	120	VAL
1	A	121	LEU
1	A	124	LYS
1	A	128	ARG
1	A	144	ILE
1	A	157	ILE
1	A	161	ARG
1	A	163	ILE
1	A	170	GLU
1	A	187	VAL
1	A	194	LEU
1	A	199	GLU

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Mol	Chain	Res	Type
1	A	209	LEU
1	A	221	ILE
1	A	227	LEU
1	A	228	LYS
1	A	231	ARG
1	A	241	LYS
1	A	260	LEU
1	A	262	LEU
1	A	272	VAL
1	A	274	ASP
1	A	283	GLN
1	A	300	ILE
1	A	304	VAL
1	A	323	VAL
1	A	333	THR
1	A	355	ARG
1	A	369	ASN
1	A	382	SER
1	A	384	VAL
1	A	386	MET
1	A	389	LEU
1	A	408	LEU
1	A	465	GLN
1	A	476	LEU
1	A	480	ARG
1	A	482	MET
1	A	487	GLU
1	A	491	GLU
1	B	18	LEU
1	B	19	THR
1	B	28	ASP
1	B	36	LEU
1	B	38	LEU
1	B	49	VAL
1	B	66	VAL
1	B	70	MET
1	B	72	THR
1	B	78	MET
1	B	103	GLU
1	B	104	VAL
1	B	108	LYS
1	B	109	LYS

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Mol	Chain	Res	Type
1	B	112	GLN
1	B	120	VAL
1	B	121	LEU
1	B	124	LYS
1	B	128	ARG
1	B	144	ILE
1	B	157	ILE
1	B	161	ARG
1	B	163	ILE
1	B	170	GLU
1	B	187	VAL
1	B	194	LEU
1	B	199	GLU
1	B	209	LEU
1	B	221	ILE
1	B	227	LEU
1	B	228	LYS
1	B	231	ARG
1	B	241	LYS
1	B	260	LEU
1	B	262	LEU
1	B	272	VAL
1	B	274	ASP
1	B	283	GLN
1	B	300	ILE
1	B	304	VAL
1	B	323	VAL
1	B	333	THR
1	B	355	ARG
1	B	369	ASN
1	B	382	SER
1	B	384	VAL
1	B	386	MET
1	B	389	LEU
1	B	408	LEU
1	B	465	GLN
1	B	476	LEU
1	B	480	ARG
1	B	482	MET
1	B	487	GLU
1	B	491	GLU
1	C	18	LEU

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Mol	Chain	Res	Type
1	C	19	THR
1	C	28	ASP
1	C	36	LEU
1	C	38	LEU
1	C	49	VAL
1	C	66	VAL
1	C	70	MET
1	C	72	THR
1	C	78	MET
1	C	103	GLU
1	C	104	VAL
1	C	108	LYS
1	C	109	LYS
1	C	112	GLN
1	C	120	VAL
1	C	121	LEU
1	C	124	LYS
1	C	128	ARG
1	C	144	ILE
1	C	157	ILE
1	C	161	ARG
1	C	163	ILE
1	C	170	GLU
1	C	187	VAL
1	C	194	LEU
1	C	199	GLU
1	C	209	LEU
1	C	221	ILE
1	C	227	LEU
1	C	228	LYS
1	C	231	ARG
1	C	241	LYS
1	C	260	LEU
1	C	262	LEU
1	C	272	VAL
1	C	274	ASP
1	C	283	GLN
1	C	300	ILE
1	C	304	VAL
1	C	323	VAL
1	C	333	THR
1	C	355	ARG

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Mol	Chain	Res	Type
1	C	369	ASN
1	C	382	SER
1	C	384	VAL
1	C	386	MET
1	C	389	LEU
1	C	408	LEU
1	C	465	GLN
1	C	476	LEU
1	C	480	ARG
1	C	482	MET
1	C	487	GLU
1	C	491	GLU
1	D	18	LEU
1	D	19	THR
1	D	28	ASP
1	D	36	LEU
1	D	38	LEU
1	D	49	VAL
1	D	66	VAL
1	D	70	MET
1	D	72	THR
1	D	78	MET
1	D	103	GLU
1	D	104	VAL
1	D	108	LYS
1	D	109	LYS
1	D	112	GLN
1	D	120	VAL
1	D	121	LEU
1	D	124	LYS
1	D	128	ARG
1	D	144	ILE
1	D	157	ILE
1	D	161	ARG
1	D	163	ILE
1	D	170	GLU
1	D	187	VAL
1	D	194	LEU
1	D	199	GLU
1	D	209	LEU
1	D	221	ILE
1	D	227	LEU

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Mol	Chain	Res	Type
1	D	228	LYS
1	D	231	ARG
1	D	241	LYS
1	D	260	LEU
1	D	262	LEU
1	D	272	VAL
1	D	274	ASP
1	D	283	GLN
1	D	300	ILE
1	D	304	VAL
1	D	323	VAL
1	D	333	THR
1	D	355	ARG
1	D	369	ASN
1	D	382	SER
1	D	384	VAL
1	D	386	MET
1	D	389	LEU
1	D	408	LEU
1	D	465	GLN
1	D	476	LEU
1	D	480	ARG
1	D	482	MET
1	D	487	GLU
1	D	491	GLU
1	E	18	LEU
1	E	19	THR
1	E	28	ASP
1	E	36	LEU
1	E	38	LEU
1	E	49	VAL
1	E	66	VAL
1	E	70	MET
1	E	72	THR
1	E	78	MET
1	E	103	GLU
1	E	104	VAL
1	E	108	LYS
1	E	109	LYS
1	E	112	GLN
1	E	120	VAL
1	E	121	LEU

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Mol	Chain	Res	Type
1	E	124	LYS
1	E	128	ARG
1	E	144	ILE
1	E	157	ILE
1	E	161	ARG
1	E	163	ILE
1	E	170	GLU
1	E	187	VAL
1	E	194	LEU
1	E	199	GLU
1	E	209	LEU
1	E	221	ILE
1	E	227	LEU
1	E	228	LYS
1	E	231	ARG
1	E	241	LYS
1	E	260	LEU
1	E	262	LEU
1	E	272	VAL
1	E	274	ASP
1	E	283	GLN
1	E	300	ILE
1	E	304	VAL
1	E	323	VAL
1	E	333	THR
1	E	355	ARG
1	E	369	ASN
1	E	382	SER
1	E	384	VAL
1	E	386	MET
1	E	389	LEU
1	E	408	LEU
1	E	465	GLN
1	E	476	LEU
1	E	480	ARG
1	E	482	MET
1	E	487	GLU
1	E	491	GLU
1	F	18	LEU
1	F	19	THR
1	F	28	ASP
1	F	36	LEU

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Mol	Chain	Res	Type
1	F	38	LEU
1	F	49	VAL
1	F	66	VAL
1	F	70	MET
1	F	72	THR
1	F	78	MET
1	F	103	GLU
1	F	104	VAL
1	F	108	LYS
1	F	109	LYS
1	F	112	GLN
1	F	120	VAL
1	F	121	LEU
1	F	124	LYS
1	F	128	ARG
1	F	144	ILE
1	F	157	ILE
1	F	161	ARG
1	F	163	ILE
1	F	170	GLU
1	F	187	VAL
1	F	194	LEU
1	F	199	GLU
1	F	209	LEU
1	F	221	ILE
1	F	227	LEU
1	F	228	LYS
1	F	231	ARG
1	F	241	LYS
1	F	260	LEU
1	F	262	LEU
1	F	272	VAL
1	F	274	ASP
1	F	283	GLN
1	F	300	ILE
1	F	304	VAL
1	F	323	VAL
1	F	333	THR
1	F	355	ARG
1	F	369	ASN
1	F	382	SER
1	F	384	VAL

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Mol	Chain	Res	Type
1	F	386	MET
1	F	389	LEU
1	F	408	LEU
1	F	465	GLN
1	F	476	LEU
1	F	480	ARG
1	F	482	MET
1	F	487	GLU
1	F	491	GLU
1	G	18	LEU
1	G	19	THR
1	G	28	ASP
1	G	36	LEU
1	G	38	LEU
1	G	49	VAL
1	G	66	VAL
1	G	70	MET
1	G	72	THR
1	G	78	MET
1	G	103	GLU
1	G	104	VAL
1	G	108	LYS
1	G	109	LYS
1	G	112	GLN
1	G	120	VAL
1	G	121	LEU
1	G	124	LYS
1	G	128	ARG
1	G	144	ILE
1	G	157	ILE
1	G	161	ARG
1	G	163	ILE
1	G	170	GLU
1	G	187	VAL
1	G	194	LEU
1	G	199	GLU
1	G	209	LEU
1	G	221	ILE
1	G	227	LEU
1	G	228	LYS
1	G	231	ARG
1	G	241	LYS

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Mol	Chain	Res	Type
1	G	260	LEU
1	G	262	LEU
1	G	272	VAL
1	G	274	ASP
1	G	283	GLN
1	G	300	ILE
1	G	304	VAL
1	G	323	VAL
1	G	333	THR
1	G	355	ARG
1	G	369	ASN
1	G	382	SER
1	G	384	VAL
1	G	386	MET
1	G	389	LEU
1	G	408	LEU
1	G	465	GLN
1	G	476	LEU
1	G	480	ARG
1	G	482	MET
1	G	487	GLU
1	G	491	GLU
1	H	18	LEU
1	H	19	THR
1	H	28	ASP
1	H	36	LEU
1	H	38	LEU
1	H	49	VAL
1	H	66	VAL
1	H	70	MET
1	H	72	THR
1	H	78	MET
1	H	103	GLU
1	H	104	VAL
1	H	108	LYS
1	H	109	LYS
1	H	112	GLN
1	H	120	VAL
1	H	121	LEU
1	H	124	LYS
1	H	128	ARG
1	H	144	ILE

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Mol	Chain	Res	Type
1	H	157	ILE
1	H	161	ARG
1	H	163	ILE
1	H	170	GLU
1	H	187	VAL
1	H	194	LEU
1	H	199	GLU
1	H	209	LEU
1	H	221	ILE
1	H	227	LEU
1	H	228	LYS
1	H	231	ARG
1	H	241	LYS
1	H	260	LEU
1	H	262	LEU
1	H	272	VAL
1	H	274	ASP
1	H	283	GLN
1	H	300	ILE
1	H	304	VAL
1	H	323	VAL
1	H	333	THR
1	H	355	ARG
1	H	369	ASN
1	H	382	SER
1	H	384	VAL
1	H	386	MET
1	H	389	LEU
1	H	408	LEU
1	H	465	GLN
1	H	476	LEU
1	H	480	ARG
1	H	482	MET
1	H	487	GLU
1	H	491	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	GLN
1	A	202	GLN
1	A	283	GLN

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Mol	Chain	Res	Type
1	A	285	ASN
1	A	298	GLN
1	A	303	ASN
1	A	469	GLN
1	B	100	GLN
1	B	202	GLN
1	B	285	ASN
1	B	298	GLN
1	B	303	ASN
1	B	469	GLN
1	C	100	GLN
1	C	202	GLN
1	C	285	ASN
1	C	298	GLN
1	C	303	ASN
1	C	469	GLN
1	D	100	GLN
1	D	202	GLN
1	D	285	ASN
1	D	298	GLN
1	D	303	ASN
1	D	469	GLN
1	E	100	GLN
1	E	202	GLN
1	E	285	ASN
1	E	298	GLN
1	E	303	ASN
1	E	469	GLN
1	F	100	GLN
1	F	202	GLN
1	F	285	ASN
1	F	298	GLN
1	F	303	ASN
1	F	469	GLN
1	G	100	GLN
1	G	202	GLN
1	G	285	ASN
1	G	298	GLN
1	G	303	ASN
1	G	469	GLN
1	H	100	GLN
1	H	202	GLN

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Mol	Chain	Res	Type
1	H	285	ASN
1	H	298	GLN
1	H	303	ASN
1	H	469	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
2	GTP	G	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)
2	GTP	B	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)
2	GTP	D	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)
3	ATP	D	603	-	32,33,33	3.21	15 (46%)	48,52,52	2.84	14 (29%)
2	GTP	H	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)
3	ATP	H	603	-	32,33,33	3.21	15 (46%)	48,52,52	2.84	13 (27%)
3	ATP	C	603	-	32,33,33	3.21	15 (46%)	48,52,52	2.84	14 (29%)
2	GTP	C	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.87	16 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GTP	D	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.69	13 (26%)
2	GTP	F	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)
3	ATP	F	603	-	32,33,33	3.20	15 (46%)	48,52,52	2.84	13 (27%)
2	GTP	A	602	-	33,34,34	3.86	20 (60%)	50,54,54	1.68	13 (26%)
2	GTP	C	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.69	13 (26%)
2	GTP	E	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.68	13 (26%)
2	GTP	F	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.68	13 (26%)
3	ATP	E	603	-	32,33,33	3.20	15 (46%)	48,52,52	2.84	13 (27%)
2	GTP	A	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)
2	GTP	G	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.69	13 (26%)
3	ATP	G	603	-	32,33,33	3.21	15 (46%)	48,52,52	2.84	13 (27%)
2	GTP	H	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.68	13 (26%)
2	GTP	B	602	-	33,34,34	3.87	20 (60%)	50,54,54	1.68	13 (26%)
3	ATP	B	603	-	32,33,33	3.20	15 (46%)	48,52,52	2.84	14 (29%)
3	ATP	A	603	-	32,33,33	3.20	15 (46%)	48,52,52	2.84	13 (27%)
2	GTP	E	601	-	33,34,34	3.82	20 (60%)	50,54,54	1.88	16 (32%)

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
2	GTP	G	601	-	-	11/22/38/38	0/3/3/3
2	GTP	B	601	-	-	11/22/38/38	0/3/3/3
2	GTP	D	601	-	-	11/22/38/38	0/3/3/3
3	ATP	D	603	-	-	1/22/38/38	0/3/3/3
2	GTP	H	601	-	-	11/22/38/38	0/3/3/3
3	ATP	H	603	-	-	1/22/38/38	0/3/3/3
3	ATP	C	603	-	-	1/22/38/38	0/3/3/3
2	GTP	C	601	-	-	11/22/38/38	0/3/3/3
2	GTP	D	602	-	-	6/22/38/38	0/3/3/3
2	GTP	F	601	-	-	11/22/38/38	0/3/3/3
3	ATP	F	603	-	-	1/22/38/38	0/3/3/3
2	GTP	A	602	-	-	6/22/38/38	0/3/3/3
2	GTP	C	602	-	-	5/22/38/38	0/3/3/3
2	GTP	E	602	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GTP	F	602	-	-	6/22/38/38	0/3/3/3
3	ATP	E	603	-	-	1/22/38/38	0/3/3/3
2	GTP	A	601	-	-	11/22/38/38	0/3/3/3
2	GTP	G	602	-	-	5/22/38/38	0/3/3/3
3	ATP	G	603	-	-	1/22/38/38	0/3/3/3
2	GTP	H	602	-	-	5/22/38/38	0/3/3/3
2	GTP	B	602	-	-	5/22/38/38	0/3/3/3
3	ATP	B	603	-	-	1/22/38/38	0/3/3/3
3	ATP	A	603	-	-	1/22/38/38	0/3/3/3
2	GTP	E	601	-	-	11/22/38/38	0/3/3/3

All (440) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	601	GTP	C2'-C3'	-10.85	1.24	1.53
2	C	601	GTP	C2'-C3'	-10.83	1.24	1.53
2	H	601	GTP	C2'-C3'	-10.82	1.24	1.53
2	A	601	GTP	C2'-C3'	-10.82	1.24	1.53
2	F	601	GTP	C2'-C3'	-10.82	1.24	1.53
2	B	601	GTP	C2'-C3'	-10.82	1.24	1.53
2	G	602	GTP	C2'-C3'	-10.80	1.24	1.53
2	D	602	GTP	C2'-C3'	-10.79	1.24	1.53
2	B	602	GTP	C2'-C3'	-10.79	1.24	1.53
2	D	601	GTP	C2'-C3'	-10.79	1.24	1.53
2	A	602	GTP	C2'-C3'	-10.79	1.24	1.53
2	C	602	GTP	C2'-C3'	-10.78	1.24	1.53
2	G	601	GTP	C2'-C3'	-10.78	1.24	1.53
2	H	602	GTP	C2'-C3'	-10.78	1.24	1.53
2	E	602	GTP	C2'-C3'	-10.77	1.24	1.53
2	F	602	GTP	C2'-C3'	-10.76	1.24	1.53
3	D	603	ATP	C2'-C3'	-10.16	1.25	1.53
3	E	603	ATP	C2'-C3'	-10.15	1.25	1.53
3	B	603	ATP	C2'-C3'	-10.14	1.25	1.53
3	A	603	ATP	C2'-C3'	-10.14	1.25	1.53
3	C	603	ATP	C2'-C3'	-10.14	1.25	1.53
3	H	603	ATP	C2'-C3'	-10.13	1.25	1.53
3	G	603	ATP	C2'-C3'	-10.11	1.26	1.53
3	F	603	ATP	C2'-C3'	-10.10	1.26	1.53
2	C	601	GTP	O4'-C4'	-6.77	1.29	1.45
2	D	601	GTP	O4'-C4'	-6.77	1.29	1.45
2	A	601	GTP	O4'-C4'	-6.75	1.30	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	602	GTP	O4'-C4'	-6.75	1.30	1.45
2	F	602	GTP	O4'-C4'	-6.75	1.30	1.45
2	F	601	GTP	O4'-C4'	-6.75	1.30	1.45
2	H	601	GTP	O4'-C4'	-6.75	1.30	1.45
2	A	602	GTP	O4'-C4'	-6.75	1.30	1.45
2	E	601	GTP	O4'-C4'	-6.75	1.30	1.45
2	B	602	GTP	O4'-C4'	-6.74	1.30	1.45
2	G	601	GTP	O4'-C4'	-6.74	1.30	1.45
2	E	602	GTP	O4'-C4'	-6.74	1.30	1.45
2	G	602	GTP	O4'-C4'	-6.73	1.30	1.45
2	B	601	GTP	O4'-C4'	-6.73	1.30	1.45
2	H	602	GTP	O4'-C4'	-6.73	1.30	1.45
2	C	602	GTP	O4'-C4'	-6.72	1.30	1.45
3	G	603	ATP	PA-O3A	6.44	1.66	1.59
2	D	602	GTP	C4-N3	6.41	1.48	1.34
3	C	603	ATP	PA-O3A	6.41	1.66	1.59
2	C	602	GTP	C4-N3	6.41	1.48	1.34
3	F	603	ATP	PA-O3A	6.40	1.66	1.59
3	H	603	ATP	PA-O3A	6.40	1.66	1.59
2	A	602	GTP	C4-N3	6.40	1.48	1.34
2	G	602	GTP	C4-N3	6.38	1.48	1.34
2	B	602	GTP	C4-N3	6.38	1.48	1.34
2	E	602	GTP	C4-N3	6.36	1.48	1.34
2	F	602	GTP	C4-N3	6.36	1.48	1.34
2	H	602	GTP	C4-N3	6.36	1.48	1.34
3	D	603	ATP	PA-O3A	6.35	1.66	1.59
3	E	603	ATP	PA-O3A	6.31	1.66	1.59
3	A	603	ATP	PA-O3A	6.28	1.66	1.59
3	B	603	ATP	PA-O3A	6.27	1.66	1.59
2	A	601	GTP	C4-N3	6.25	1.48	1.34
2	H	601	GTP	C4-N3	6.25	1.48	1.34
2	B	601	GTP	C4-N3	6.23	1.48	1.34
2	F	601	GTP	C4-N3	6.23	1.48	1.34
2	G	601	GTP	C4-N3	6.23	1.48	1.34
2	C	601	GTP	C4-N3	6.22	1.48	1.34
2	D	601	GTP	C4-N3	6.22	1.48	1.34
2	E	601	GTP	C4-N3	6.19	1.48	1.34
3	B	603	ATP	PB-O3A	6.11	1.66	1.59
3	H	603	ATP	PB-O3A	6.06	1.66	1.59
3	C	603	ATP	PB-O3A	6.06	1.66	1.59
3	E	603	ATP	PB-O3A	6.04	1.66	1.59
3	A	603	ATP	PB-O3A	6.02	1.66	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	603	ATP	PB-O3A	6.02	1.66	1.59
3	G	603	ATP	PB-O3A	6.00	1.66	1.59
3	F	603	ATP	PB-O3A	5.96	1.65	1.59
2	C	601	GTP	C1'-N9	-5.88	1.30	1.47
2	F	601	GTP	C1'-N9	-5.87	1.30	1.47
2	D	601	GTP	C1'-N9	-5.87	1.30	1.47
2	H	601	GTP	C1'-N9	-5.87	1.30	1.47
2	G	601	GTP	C1'-N9	-5.86	1.30	1.47
2	B	601	GTP	C1'-N9	-5.86	1.30	1.47
2	A	601	GTP	C1'-N9	-5.86	1.30	1.47
2	E	601	GTP	C1'-N9	-5.84	1.31	1.47
2	G	601	GTP	PB-O3B	5.76	1.65	1.59
2	A	601	GTP	PB-O3B	5.72	1.65	1.59
2	B	601	GTP	PB-O3B	5.70	1.65	1.59
2	D	601	GTP	PB-O3B	5.69	1.65	1.59
2	F	601	GTP	PB-O3B	5.69	1.65	1.59
2	C	601	GTP	PB-O3B	5.68	1.65	1.59
2	H	601	GTP	PB-O3B	5.67	1.65	1.59
2	C	602	GTP	PA-O3A	5.66	1.65	1.59
2	G	602	GTP	PB-O3B	5.65	1.65	1.59
2	E	601	GTP	PB-O3B	5.64	1.65	1.59
2	D	602	GTP	PA-O3A	5.64	1.65	1.59
2	F	602	GTP	PA-O3A	5.64	1.65	1.59
2	G	602	GTP	PA-O3A	5.63	1.65	1.59
2	E	602	GTP	PB-O3A	5.63	1.65	1.59
2	H	602	GTP	PB-O3B	5.62	1.65	1.59
2	H	602	GTP	PA-O3A	5.62	1.65	1.59
2	A	602	GTP	PA-O3A	5.61	1.65	1.59
2	B	602	GTP	PA-O3A	5.61	1.65	1.59
2	E	602	GTP	PB-O3B	5.60	1.65	1.59
2	C	602	GTP	PB-O3B	5.60	1.65	1.59
2	B	602	GTP	PB-O3B	5.59	1.65	1.59
2	H	602	GTP	PB-O3A	5.57	1.65	1.59
2	D	602	GTP	PB-O3B	5.57	1.65	1.59
2	F	602	GTP	PB-O3B	5.57	1.65	1.59
2	A	602	GTP	PB-O3B	5.56	1.65	1.59
2	E	602	GTP	PA-O3A	5.55	1.65	1.59
2	B	602	GTP	PB-O3A	5.54	1.65	1.59
2	G	602	GTP	PB-O3A	5.53	1.65	1.59
2	F	602	GTP	C1'-N9	-5.52	1.31	1.47
2	B	602	GTP	C1'-N9	-5.51	1.31	1.47
2	D	602	GTP	PB-O3A	5.51	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	602	GTP	PB-O3A	5.51	1.65	1.59
2	G	602	GTP	C1'-N9	-5.51	1.31	1.47
2	A	602	GTP	PB-O3A	5.50	1.65	1.59
2	A	602	GTP	C1'-N9	-5.49	1.32	1.47
2	D	602	GTP	C1'-N9	-5.49	1.32	1.47
2	E	602	GTP	C1'-N9	-5.49	1.32	1.47
2	H	602	GTP	C1'-N9	-5.49	1.32	1.47
2	C	602	GTP	PB-O3A	5.49	1.65	1.59
2	C	602	GTP	C1'-N9	-5.48	1.32	1.47
2	B	601	GTP	C3'-C4'	5.46	1.66	1.53
2	A	601	GTP	C3'-C4'	5.46	1.66	1.53
2	E	601	GTP	C3'-C4'	5.45	1.66	1.53
2	C	601	GTP	C3'-C4'	5.44	1.66	1.53
2	F	601	GTP	C3'-C4'	5.43	1.66	1.53
2	D	601	GTP	C3'-C4'	5.43	1.66	1.53
2	H	601	GTP	C3'-C4'	5.43	1.66	1.53
2	G	601	GTP	C3'-C4'	5.42	1.66	1.53
2	G	602	GTP	C3'-C4'	5.41	1.66	1.53
2	H	602	GTP	C3'-C4'	5.40	1.66	1.53
2	D	602	GTP	C3'-C4'	5.40	1.66	1.53
2	F	602	GTP	C3'-C4'	5.40	1.66	1.53
2	A	602	GTP	C3'-C4'	5.39	1.66	1.53
2	C	602	GTP	C3'-C4'	5.38	1.66	1.53
2	B	602	GTP	C3'-C4'	5.37	1.66	1.53
2	E	602	GTP	C3'-C4'	5.37	1.66	1.53
2	D	602	GTP	C2-N3	5.35	1.46	1.33
2	E	602	GTP	C2-N3	5.35	1.46	1.33
2	F	602	GTP	C2-N3	5.35	1.46	1.33
2	A	602	GTP	C2-N3	5.35	1.46	1.33
2	H	602	GTP	C2-N3	5.35	1.46	1.33
2	B	602	GTP	C2-N3	5.34	1.46	1.33
2	G	602	GTP	C2-N3	5.34	1.46	1.33
2	C	602	GTP	C2-N3	5.33	1.46	1.33
2	C	602	GTP	C2-N2	5.21	1.46	1.34
2	D	602	GTP	C2-N2	5.19	1.46	1.34
2	F	602	GTP	C2-N2	5.17	1.46	1.34
2	G	602	GTP	C2-N2	5.16	1.46	1.34
2	B	602	GTP	C2-N2	5.16	1.46	1.34
2	E	602	GTP	C2-N2	5.16	1.46	1.34
2	A	602	GTP	C2-N2	5.15	1.46	1.34
2	H	602	GTP	C2-N2	5.14	1.46	1.34
2	B	601	GTP	PB-O3A	5.13	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	GTP	PB-O3A	5.11	1.65	1.59
2	G	601	GTP	PB-O3A	5.09	1.65	1.59
2	A	601	GTP	PB-O3A	5.08	1.65	1.59
2	D	601	GTP	PB-O3A	5.08	1.65	1.59
2	F	601	GTP	PB-O3A	5.08	1.65	1.59
2	H	601	GTP	PB-O3A	5.08	1.65	1.59
2	E	601	GTP	PB-O3A	5.08	1.65	1.59
2	B	601	GTP	C2-N3	5.05	1.45	1.33
2	H	601	GTP	C2-N3	5.03	1.45	1.33
2	A	601	GTP	C2-N3	5.02	1.45	1.33
2	E	601	GTP	C2-N3	5.01	1.45	1.33
2	C	601	GTP	C2-N3	5.01	1.45	1.33
2	G	601	GTP	C2-N3	5.00	1.45	1.33
2	F	601	GTP	C2-N3	5.00	1.45	1.33
2	D	601	GTP	C2-N3	5.00	1.45	1.33
2	D	601	GTP	C2-N2	4.91	1.45	1.34
2	G	601	GTP	C2-N2	4.90	1.45	1.34
2	H	601	GTP	C2-N2	4.88	1.45	1.34
2	A	601	GTP	C2-N2	4.87	1.45	1.34
2	E	601	GTP	C2-N2	4.87	1.45	1.34
2	B	601	GTP	C2-N2	4.87	1.45	1.34
2	F	601	GTP	C2-N2	4.87	1.45	1.34
2	C	601	GTP	C2-N2	4.85	1.45	1.34
2	F	601	GTP	PA-O3A	4.82	1.64	1.59
2	H	601	GTP	PA-O3A	4.79	1.64	1.59
2	C	601	GTP	PA-O3A	4.77	1.64	1.59
2	G	601	GTP	PA-O3A	4.75	1.64	1.59
2	B	601	GTP	PA-O3A	4.73	1.64	1.59
2	A	601	GTP	PA-O3A	4.71	1.64	1.59
2	E	601	GTP	PA-O3A	4.71	1.64	1.59
2	D	601	GTP	PA-O3A	4.70	1.64	1.59
3	D	603	ATP	C2'-C1'	4.20	1.66	1.53
3	A	603	ATP	C2'-C1'	4.19	1.66	1.53
3	G	603	ATP	C2'-C1'	4.19	1.66	1.53
3	F	603	ATP	C2'-C1'	4.18	1.66	1.53
3	E	603	ATP	C2'-C1'	4.18	1.66	1.53
3	B	603	ATP	C2'-C1'	4.17	1.66	1.53
3	C	603	ATP	C2'-C1'	4.17	1.66	1.53
3	E	603	ATP	C5'-C4'	-4.17	1.39	1.51
3	H	603	ATP	C2'-C1'	4.17	1.66	1.53
3	A	603	ATP	C5'-C4'	-4.16	1.39	1.51
3	G	603	ATP	C5'-C4'	-4.15	1.39	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	603	ATP	C5'-C4'	-4.15	1.39	1.51
3	D	603	ATP	C5'-C4'	-4.15	1.39	1.51
3	F	603	ATP	C5'-C4'	-4.15	1.39	1.51
3	B	603	ATP	C5'-C4'	-4.14	1.39	1.51
3	C	603	ATP	C5'-C4'	-4.13	1.39	1.51
3	G	603	ATP	O4'-C1'	-4.13	1.32	1.42
3	H	603	ATP	O4'-C1'	-4.12	1.32	1.42
3	F	603	ATP	O4'-C1'	-4.11	1.32	1.42
3	D	603	ATP	O4'-C1'	-4.11	1.32	1.42
3	B	603	ATP	O4'-C1'	-4.10	1.32	1.42
3	E	603	ATP	O4'-C1'	-4.10	1.32	1.42
3	C	603	ATP	O4'-C1'	-4.08	1.32	1.42
3	A	603	ATP	O4'-C1'	-4.08	1.32	1.42
3	G	603	ATP	C6-N6	3.70	1.43	1.34
3	A	603	ATP	C6-N6	3.69	1.43	1.34
3	D	603	ATP	C6-N6	3.69	1.43	1.34
3	F	603	ATP	C6-N6	3.69	1.43	1.34
3	B	603	ATP	C6-N6	3.69	1.43	1.34
3	C	603	ATP	C6-N6	3.69	1.43	1.34
3	E	603	ATP	C6-N6	3.69	1.43	1.34
3	H	603	ATP	C6-N6	3.67	1.43	1.34
2	H	601	GTP	O4'-C1'	3.55	1.50	1.42
2	C	601	GTP	O4'-C1'	3.55	1.50	1.42
2	B	601	GTP	O4'-C1'	3.55	1.50	1.42
2	D	601	GTP	O4'-C1'	3.55	1.50	1.42
2	F	601	GTP	O4'-C1'	3.55	1.50	1.42
2	A	601	GTP	O4'-C1'	3.53	1.50	1.42
2	E	601	GTP	O4'-C1'	3.52	1.50	1.42
2	G	601	GTP	O4'-C1'	3.51	1.50	1.42
2	H	602	GTP	O4'-C1'	3.50	1.50	1.42
2	A	602	GTP	O4'-C1'	3.49	1.50	1.42
2	G	602	GTP	O4'-C1'	3.49	1.50	1.42
2	E	602	GTP	O4'-C1'	3.48	1.50	1.42
2	B	602	GTP	O4'-C1'	3.48	1.50	1.42
2	C	602	GTP	O4'-C1'	3.48	1.50	1.42
2	D	602	GTP	O4'-C1'	3.48	1.50	1.42
2	F	602	GTP	O4'-C1'	3.46	1.50	1.42
2	F	601	GTP	O2'-C2'	3.40	1.51	1.43
2	H	601	GTP	O2'-C2'	3.40	1.51	1.43
2	A	601	GTP	O2'-C2'	3.39	1.51	1.43
2	D	601	GTP	O2'-C2'	3.37	1.51	1.43
2	C	601	GTP	O2'-C2'	3.36	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	601	GTP	O2'-C2'	3.35	1.51	1.43
2	G	601	GTP	O2'-C2'	3.35	1.51	1.43
2	B	601	GTP	O2'-C2'	3.33	1.51	1.43
2	F	602	GTP	O2'-C2'	3.32	1.51	1.43
2	B	602	GTP	O2'-C2'	3.31	1.51	1.43
2	C	602	GTP	O2'-C2'	3.31	1.51	1.43
2	A	602	GTP	O2'-C2'	3.30	1.51	1.43
2	D	602	GTP	O2'-C2'	3.30	1.51	1.43
2	H	602	GTP	O2'-C2'	3.29	1.51	1.43
2	G	602	GTP	O2'-C2'	3.28	1.51	1.43
2	E	602	GTP	O2'-C2'	3.28	1.51	1.43
3	G	603	ATP	O3'-C3'	3.27	1.51	1.43
3	H	603	ATP	O3'-C3'	3.27	1.51	1.43
3	D	603	ATP	O3'-C3'	3.27	1.51	1.43
3	F	603	ATP	O3'-C3'	3.26	1.51	1.43
3	C	603	ATP	O3'-C3'	3.25	1.51	1.43
3	E	603	ATP	O3'-C3'	3.25	1.51	1.43
3	B	603	ATP	O3'-C3'	3.23	1.51	1.43
3	A	603	ATP	O3'-C3'	3.23	1.51	1.43
3	C	603	ATP	C5-C4	-3.23	1.33	1.39
3	B	603	ATP	C5-C4	-3.22	1.33	1.39
3	A	603	ATP	C5-C4	-3.22	1.33	1.39
3	F	603	ATP	C5-C4	-3.21	1.33	1.39
3	G	603	ATP	C5-C4	-3.19	1.33	1.39
3	E	603	ATP	C5-C4	-3.19	1.33	1.39
3	D	603	ATP	C5-C4	-3.19	1.33	1.39
3	H	603	ATP	C5-C4	-3.18	1.33	1.39
3	A	603	ATP	C3'-C4'	3.10	1.60	1.53
3	E	603	ATP	C3'-C4'	3.08	1.60	1.53
3	F	603	ATP	C3'-C4'	3.08	1.60	1.53
3	G	603	ATP	C3'-C4'	3.08	1.60	1.53
3	B	603	ATP	C3'-C4'	3.07	1.60	1.53
3	H	603	ATP	C3'-C4'	3.07	1.60	1.53
3	D	603	ATP	C3'-C4'	3.07	1.60	1.53
3	C	603	ATP	C3'-C4'	3.06	1.60	1.53
2	H	602	GTP	C2-N1	2.96	1.44	1.37
2	E	602	GTP	C2-N1	2.96	1.44	1.37
2	A	602	GTP	C2-N1	2.95	1.44	1.37
2	C	602	GTP	C2-N1	2.95	1.44	1.37
2	G	602	GTP	C2-N1	2.95	1.44	1.37
2	B	602	GTP	C2-N1	2.95	1.44	1.37
3	D	603	ATP	C5-N7	-2.94	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	602	GTP	C2-N1	2.94	1.44	1.37
2	F	602	GTP	C2-N1	2.94	1.44	1.37
3	G	603	ATP	C5-N7	-2.93	1.33	1.39
3	A	603	ATP	C5-N7	-2.92	1.33	1.39
3	C	603	ATP	C5-N7	-2.91	1.33	1.39
3	H	603	ATP	C5-N7	-2.90	1.33	1.39
3	F	603	ATP	C5-N7	-2.90	1.33	1.39
3	B	603	ATP	C5-N7	-2.89	1.33	1.39
3	E	603	ATP	C5-N7	-2.89	1.33	1.39
2	G	601	GTP	C5-N7	-2.85	1.33	1.39
2	B	601	GTP	C5-N7	-2.82	1.33	1.39
2	A	601	GTP	C5-N7	-2.82	1.33	1.39
2	D	601	GTP	C5-N7	-2.81	1.33	1.39
2	E	601	GTP	C5-N7	-2.81	1.33	1.39
2	F	601	GTP	C5-N7	-2.81	1.33	1.39
2	H	601	GTP	C5-N7	-2.80	1.33	1.39
2	C	601	GTP	C5-N7	-2.78	1.33	1.39
2	F	601	GTP	C2-N1	2.76	1.44	1.37
2	B	601	GTP	C2-N1	2.75	1.44	1.37
2	C	601	GTP	C2-N1	2.74	1.44	1.37
2	G	601	GTP	C2-N1	2.74	1.44	1.37
2	A	601	GTP	C2-N1	2.74	1.44	1.37
2	D	601	GTP	C2-N1	2.73	1.44	1.37
2	E	601	GTP	C2-N1	2.72	1.44	1.37
2	B	602	GTP	C5-N7	-2.72	1.33	1.39
2	H	601	GTP	C2-N1	2.70	1.44	1.37
2	E	602	GTP	C5-N7	-2.70	1.33	1.39
2	F	602	GTP	C5-N7	-2.69	1.33	1.39
2	A	602	GTP	C5-N7	-2.69	1.33	1.39
2	D	602	GTP	C5-N7	-2.67	1.33	1.39
2	H	602	GTP	C5-N7	-2.67	1.33	1.39
2	C	602	GTP	C5-N7	-2.67	1.33	1.39
3	C	603	ATP	C8-N9	-2.66	1.33	1.37
2	B	602	GTP	C5-C6	2.66	1.54	1.44
3	A	603	ATP	C8-N9	-2.66	1.33	1.37
3	B	603	ATP	C8-N9	-2.65	1.33	1.37
2	G	602	GTP	C5-N7	-2.65	1.33	1.39
3	D	603	ATP	C8-N9	-2.64	1.33	1.37
2	F	602	GTP	C5-C6	2.64	1.54	1.44
2	H	602	GTP	C5-C6	2.64	1.54	1.44
2	E	602	GTP	C5-C6	2.64	1.54	1.44
2	D	601	GTP	C6-N1	2.64	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	602	GTP	C5-C6	2.63	1.54	1.44
2	A	602	GTP	C5-C6	2.63	1.54	1.44
2	G	602	GTP	C5-C6	2.63	1.54	1.44
3	H	603	ATP	C8-N9	-2.63	1.33	1.37
3	E	603	ATP	C8-N9	-2.63	1.33	1.37
2	G	601	GTP	C6-N1	2.62	1.43	1.38
2	C	602	GTP	C5-C6	2.62	1.54	1.44
3	F	603	ATP	C8-N9	-2.61	1.33	1.37
2	E	601	GTP	C6-N1	2.61	1.43	1.38
2	H	601	GTP	C6-N1	2.61	1.43	1.38
2	A	601	GTP	C6-N1	2.60	1.43	1.38
3	G	603	ATP	C8-N9	-2.59	1.33	1.37
2	B	601	GTP	C6-N1	2.59	1.43	1.38
2	F	601	GTP	C6-N1	2.59	1.43	1.38
2	C	601	GTP	C6-N1	2.56	1.43	1.38
2	A	601	GTP	C5-C6	2.52	1.53	1.44
2	B	601	GTP	C5-C6	2.52	1.53	1.44
2	C	601	GTP	C5-C6	2.52	1.53	1.44
2	E	601	GTP	C5-C6	2.52	1.53	1.44
2	G	601	GTP	C2'-C1'	2.52	1.61	1.53
2	D	601	GTP	C5-C6	2.51	1.53	1.44
2	F	601	GTP	C5-C6	2.51	1.53	1.44
2	A	601	GTP	C2'-C1'	2.51	1.61	1.53
2	G	601	GTP	C5-C6	2.51	1.53	1.44
2	E	601	GTP	C2'-C1'	2.51	1.61	1.53
2	B	601	GTP	C2'-C1'	2.51	1.61	1.53
2	H	601	GTP	C5-C6	2.51	1.53	1.44
2	C	601	GTP	C2'-C1'	2.50	1.61	1.53
2	F	601	GTP	C2'-C1'	2.50	1.61	1.53
2	H	601	GTP	C2'-C1'	2.49	1.61	1.53
2	D	601	GTP	C2'-C1'	2.49	1.61	1.53
3	D	603	ATP	PA-O5'	2.47	1.69	1.59
3	G	603	ATP	PA-O5'	2.46	1.69	1.59
2	F	602	GTP	C6-N1	2.46	1.43	1.38
3	B	603	ATP	PA-O5'	2.46	1.69	1.59
3	F	603	ATP	PA-O5'	2.45	1.69	1.59
2	H	602	GTP	C6-N1	2.45	1.43	1.38
3	C	603	ATP	PA-O5'	2.45	1.69	1.59
3	H	603	ATP	PA-O5'	2.44	1.68	1.59
3	A	603	ATP	PA-O5'	2.44	1.68	1.59
3	E	603	ATP	PA-O5'	2.43	1.68	1.59
2	C	601	GTP	O3'-C3'	2.43	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	602	GTP	C6-N1	2.42	1.43	1.38
2	E	601	GTP	O3'-C3'	2.42	1.49	1.43
2	F	601	GTP	O3'-C3'	2.42	1.49	1.43
2	B	601	GTP	O3'-C3'	2.42	1.49	1.43
2	G	601	GTP	O3'-C3'	2.41	1.48	1.43
2	H	601	GTP	O3'-C3'	2.41	1.48	1.43
2	D	601	GTP	O3'-C3'	2.40	1.48	1.43
2	D	602	GTP	C6-N1	2.40	1.43	1.38
2	G	602	GTP	C6-N1	2.40	1.43	1.38
2	A	601	GTP	O3'-C3'	2.39	1.48	1.43
2	C	602	GTP	C6-N1	2.39	1.43	1.38
2	B	602	GTP	C6-N1	2.39	1.43	1.38
2	F	602	GTP	O6-C6	-2.38	1.19	1.23
2	H	602	GTP	O6-C6	-2.38	1.19	1.23
2	A	602	GTP	C6-N1	2.38	1.43	1.38
2	G	602	GTP	O6-C6	-2.37	1.19	1.23
2	B	602	GTP	O6-C6	-2.37	1.19	1.23
2	C	602	GTP	C4-N9	-2.36	1.32	1.38
3	E	603	ATP	O4'-C4'	2.36	1.50	1.45
3	C	603	ATP	O4'-C4'	2.36	1.50	1.45
2	E	602	GTP	O6-C6	-2.35	1.19	1.23
2	C	602	GTP	O6-C6	-2.35	1.19	1.23
3	H	603	ATP	O4'-C4'	2.34	1.50	1.45
2	D	602	GTP	C4-N9	-2.34	1.32	1.38
2	H	602	GTP	C4-N9	-2.34	1.32	1.38
2	A	602	GTP	C4-N9	-2.34	1.32	1.38
2	B	602	GTP	C4-N9	-2.34	1.32	1.38
2	G	602	GTP	C4-N9	-2.34	1.32	1.38
2	E	602	GTP	C4-N9	-2.34	1.32	1.38
2	E	601	GTP	O6-C6	-2.34	1.19	1.23
3	G	603	ATP	O4'-C4'	2.33	1.50	1.45
3	E	603	ATP	PB-O3B	2.33	1.62	1.59
2	D	601	GTP	O6-C6	-2.33	1.19	1.23
2	F	601	GTP	O6-C6	-2.33	1.19	1.23
2	A	602	GTP	O6-C6	-2.32	1.19	1.23
2	H	601	GTP	O6-C6	-2.32	1.19	1.23
3	B	603	ATP	O4'-C4'	2.32	1.50	1.45
2	B	601	GTP	O6-C6	-2.32	1.19	1.23
3	A	603	ATP	O4'-C4'	2.32	1.50	1.45
3	D	603	ATP	PB-O3B	2.32	1.62	1.59
2	A	601	GTP	O6-C6	-2.32	1.19	1.23
2	G	601	GTP	O6-C6	-2.31	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	603	ATP	O4'-C4'	2.31	1.50	1.45
3	F	603	ATP	O4'-C4'	2.31	1.50	1.45
2	D	602	GTP	O6-C6	-2.31	1.19	1.23
2	C	601	GTP	O6-C6	-2.31	1.19	1.23
2	A	601	GTP	C4-N9	-2.31	1.32	1.38
2	F	602	GTP	C4-N9	-2.30	1.32	1.38
2	B	601	GTP	C4-N9	-2.30	1.32	1.38
3	C	603	ATP	PB-O3B	2.30	1.62	1.59
3	G	603	ATP	PB-O3B	2.29	1.62	1.59
2	E	601	GTP	C4-N9	-2.29	1.32	1.38
2	H	602	GTP	C2'-C1'	2.28	1.60	1.53
3	A	603	ATP	PB-O3B	2.28	1.62	1.59
2	A	602	GTP	C2'-C1'	2.28	1.60	1.53
2	F	602	GTP	C2'-C1'	2.28	1.60	1.53
3	B	603	ATP	PB-O3B	2.28	1.62	1.59
2	H	601	GTP	C4-N9	-2.28	1.32	1.38
2	E	602	GTP	C2'-C1'	2.27	1.60	1.53
2	C	602	GTP	C2'-C1'	2.27	1.60	1.53
2	G	601	GTP	C4-N9	-2.26	1.32	1.38
2	F	601	GTP	C4-N9	-2.26	1.32	1.38
2	B	602	GTP	C2'-C1'	2.26	1.60	1.53
2	D	601	GTP	C4-N9	-2.26	1.32	1.38
2	C	601	GTP	C4-N9	-2.26	1.32	1.38
2	G	602	GTP	C2'-C1'	2.25	1.60	1.53
2	D	602	GTP	C2'-C1'	2.25	1.60	1.53
2	B	602	GTP	O3'-C3'	2.24	1.48	1.43
2	D	602	GTP	O3'-C3'	2.24	1.48	1.43
2	C	602	GTP	O3'-C3'	2.23	1.48	1.43
3	H	603	ATP	PB-O3B	2.22	1.61	1.59
2	F	602	GTP	O3'-C3'	2.22	1.48	1.43
3	F	603	ATP	PB-O3B	2.22	1.61	1.59
2	G	602	GTP	O3'-C3'	2.21	1.48	1.43
2	E	602	GTP	O3'-C3'	2.20	1.48	1.43
2	A	602	GTP	O3'-C3'	2.20	1.48	1.43
2	H	602	GTP	O3'-C3'	2.20	1.48	1.43

All (339) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	603	ATP	N6-C6-N1	-8.42	99.62	118.38
3	G	603	ATP	N6-C6-N1	-8.42	99.62	118.38
3	H	603	ATP	N6-C6-N1	-8.41	99.64	118.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	603	ATP	N6-C6-N1	-8.41	99.65	118.38
3	A	603	ATP	N6-C6-N1	-8.41	99.65	118.38
3	D	603	ATP	N6-C6-N1	-8.40	99.67	118.38
3	E	603	ATP	N6-C6-N1	-8.40	99.67	118.38
3	C	603	ATP	N6-C6-N1	-8.40	99.67	118.38
3	D	603	ATP	C4-N9-C1'	-7.30	109.56	126.63
3	C	603	ATP	C4-N9-C1'	-7.28	109.59	126.63
3	A	603	ATP	C4-N9-C1'	-7.28	109.60	126.63
3	F	603	ATP	C4-N9-C1'	-7.28	109.60	126.63
3	G	603	ATP	C4-N9-C1'	-7.28	109.60	126.63
3	H	603	ATP	C4-N9-C1'	-7.28	109.60	126.63
3	E	603	ATP	C4-N9-C1'	-7.27	109.62	126.63
3	B	603	ATP	C4-N9-C1'	-7.27	109.63	126.63
3	H	603	ATP	C5-C6-N6	6.99	140.59	123.29
3	F	603	ATP	C5-C6-N6	6.98	140.58	123.29
3	B	603	ATP	C5-C6-N6	6.98	140.57	123.29
3	A	603	ATP	C5-C6-N6	6.98	140.56	123.29
3	G	603	ATP	C5-C6-N6	6.97	140.53	123.29
3	E	603	ATP	C5-C6-N6	6.96	140.52	123.29
3	C	603	ATP	C5-C6-N6	6.96	140.51	123.29
3	D	603	ATP	C5-C6-N6	6.95	140.51	123.29
3	D	603	ATP	N9-C8-N7	-5.75	105.78	113.94
3	C	603	ATP	N9-C8-N7	-5.75	105.78	113.94
3	E	603	ATP	N9-C8-N7	-5.73	105.81	113.94
3	G	603	ATP	N9-C8-N7	-5.73	105.81	113.94
3	H	603	ATP	N9-C8-N7	-5.73	105.81	113.94
3	F	603	ATP	N9-C8-N7	-5.72	105.82	113.94
3	A	603	ATP	N9-C8-N7	-5.71	105.83	113.94
3	B	603	ATP	N9-C8-N7	-5.69	105.86	113.94
3	A	603	ATP	C1'-N9-C8	5.66	139.66	127.09
3	D	603	ATP	C1'-N9-C8	5.65	139.65	127.09
3	G	603	ATP	C1'-N9-C8	5.65	139.65	127.09
3	F	603	ATP	C1'-N9-C8	5.65	139.64	127.09
3	B	603	ATP	C1'-N9-C8	5.65	139.64	127.09
3	H	603	ATP	C1'-N9-C8	5.64	139.62	127.09
3	C	603	ATP	C1'-N9-C8	5.64	139.62	127.09
3	E	603	ATP	C1'-N9-C8	5.63	139.58	127.09
3	C	603	ATP	N3-C2-N1	-5.29	120.58	128.58
3	G	603	ATP	N3-C2-N1	-5.29	120.58	128.58
3	B	603	ATP	N3-C2-N1	-5.29	120.58	128.58
3	E	603	ATP	N3-C2-N1	-5.29	120.58	128.58
3	A	603	ATP	N3-C2-N1	-5.27	120.60	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	603	ATP	N3-C2-N1	-5.26	120.62	128.58
3	H	603	ATP	N3-C2-N1	-5.26	120.62	128.58
3	D	603	ATP	N3-C2-N1	-5.25	120.63	128.58
2	A	601	GTP	C5-C4-N3	-4.96	120.50	128.39
2	E	601	GTP	C5-C4-N3	-4.95	120.51	128.39
2	H	601	GTP	C5-C4-N3	-4.95	120.52	128.39
2	G	601	GTP	C5-C4-N3	-4.94	120.52	128.39
2	B	601	GTP	C5-C4-N3	-4.94	120.53	128.39
2	C	601	GTP	C5-C4-N3	-4.93	120.54	128.39
2	D	601	GTP	C5-C4-N3	-4.93	120.54	128.39
2	F	601	GTP	C5-C4-N3	-4.93	120.55	128.39
3	H	603	ATP	C5-C4-N3	-4.87	120.02	126.72
3	E	603	ATP	C5-C4-N3	-4.86	120.02	126.72
3	A	603	ATP	C5-C4-N3	-4.86	120.03	126.72
3	B	603	ATP	C5-C4-N3	-4.86	120.03	126.72
3	C	603	ATP	C5-C4-N3	-4.85	120.03	126.72
3	F	603	ATP	C5-C4-N3	-4.85	120.04	126.72
3	G	603	ATP	C5-C4-N3	-4.85	120.04	126.72
3	E	603	ATP	C4-N9-C8	4.82	110.80	105.74
3	D	603	ATP	C5-C4-N3	-4.81	120.09	126.72
3	C	603	ATP	C4-N9-C8	4.81	110.79	105.74
3	D	603	ATP	C4-N9-C8	4.81	110.79	105.74
3	H	603	ATP	C4-N9-C8	4.80	110.77	105.74
3	F	603	ATP	C4-N9-C8	4.77	110.75	105.74
3	G	603	ATP	C4-N9-C8	4.77	110.75	105.74
3	A	603	ATP	C4-N9-C8	4.76	110.73	105.74
3	B	603	ATP	C4-N9-C8	4.75	110.73	105.74
2	D	602	GTP	C5-C4-N3	-4.33	121.50	128.39
2	C	602	GTP	C5-C4-N3	-4.33	121.50	128.39
2	G	602	GTP	C5-C4-N3	-4.32	121.52	128.39
2	B	602	GTP	C5-C4-N3	-4.31	121.53	128.39
2	A	602	GTP	C5-C4-N3	-4.31	121.54	128.39
2	F	602	GTP	C5-C4-N3	-4.29	121.56	128.39
2	H	602	GTP	C5-C4-N3	-4.29	121.56	128.39
2	E	602	GTP	C5-C4-N3	-4.29	121.56	128.39
2	E	601	GTP	C2-N3-C4	4.22	119.56	112.30
2	G	601	GTP	C2-N3-C4	4.20	119.54	112.30
2	D	601	GTP	C2-N3-C4	4.20	119.54	112.30
2	A	601	GTP	C2-N3-C4	4.19	119.52	112.30
2	C	601	GTP	C2-N3-C4	4.19	119.51	112.30
2	F	601	GTP	C2-N3-C4	4.19	119.51	112.30
2	B	601	GTP	C2-N3-C4	4.18	119.51	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	601	GTP	C2-N3-C4	4.17	119.49	112.30
3	E	603	ATP	N3-C4-N9	4.11	134.16	127.17
3	H	603	ATP	N3-C4-N9	4.11	134.15	127.17
3	F	603	ATP	N3-C4-N9	4.10	134.14	127.17
3	G	603	ATP	N3-C4-N9	4.10	134.14	127.17
3	C	603	ATP	N3-C4-N9	4.10	134.13	127.17
3	D	603	ATP	N3-C4-N9	4.09	134.13	127.17
3	B	603	ATP	N3-C4-N9	4.09	134.12	127.17
3	A	603	ATP	N3-C4-N9	4.08	134.11	127.17
2	C	602	GTP	C4'-O4'-C1'	-3.81	101.06	109.47
2	G	602	GTP	C4'-O4'-C1'	-3.80	101.08	109.47
2	D	602	GTP	C4'-O4'-C1'	-3.79	101.09	109.47
2	E	602	GTP	C4'-O4'-C1'	-3.79	101.10	109.47
2	H	602	GTP	C4'-O4'-C1'	-3.79	101.10	109.47
2	G	601	GTP	C2'-C1'-N9	-3.77	102.75	113.25
2	D	601	GTP	C2'-C1'-N9	-3.77	102.75	113.25
2	B	602	GTP	C4'-O4'-C1'	-3.77	101.15	109.47
2	A	602	GTP	C4'-O4'-C1'	-3.77	101.15	109.47
2	F	602	GTP	C4'-O4'-C1'	-3.77	101.15	109.47
2	A	601	GTP	C2'-C1'-N9	-3.76	102.78	113.25
2	E	601	GTP	C2'-C1'-N9	-3.76	102.78	113.25
2	H	601	GTP	C2'-C1'-N9	-3.76	102.79	113.25
2	B	601	GTP	C2'-C1'-N9	-3.75	102.81	113.25
2	F	601	GTP	C2'-C1'-N9	-3.75	102.81	113.25
2	C	601	GTP	C2'-C1'-N9	-3.75	102.81	113.25
2	B	602	GTP	C2-N3-C4	3.75	118.75	112.30
2	H	602	GTP	C2-N3-C4	3.73	118.72	112.30
2	G	602	GTP	C2-N3-C4	3.72	118.71	112.30
2	A	601	GTP	N9-C8-N7	-3.72	106.50	113.40
2	F	602	GTP	C2-N3-C4	3.72	118.70	112.30
2	E	601	GTP	N9-C8-N7	-3.72	106.51	113.40
2	E	602	GTP	C2-N3-C4	3.72	118.70	112.30
2	A	602	GTP	C2-N3-C4	3.71	118.70	112.30
2	C	602	GTP	C2-N3-C4	3.71	118.69	112.30
2	B	601	GTP	N9-C8-N7	-3.71	106.52	113.40
2	D	602	GTP	C2-N3-C4	3.71	118.68	112.30
2	H	601	GTP	N9-C8-N7	-3.69	106.56	113.40
2	D	601	GTP	N9-C8-N7	-3.69	106.57	113.40
2	F	601	GTP	N9-C8-N7	-3.68	106.57	113.40
2	G	601	GTP	N9-C8-N7	-3.67	106.59	113.40
2	C	601	GTP	N9-C8-N7	-3.67	106.59	113.40
2	E	601	GTP	C1'-N9-C8	-3.61	116.47	126.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	GTP	C1'-N9-C8	-3.60	116.51	126.73
2	B	601	GTP	C1'-N9-C8	-3.60	116.51	126.73
2	H	601	GTP	C1'-N9-C8	-3.60	116.52	126.73
2	F	601	GTP	C1'-N9-C8	-3.59	116.54	126.73
2	D	601	GTP	C1'-N9-C8	-3.58	116.56	126.73
2	G	601	GTP	C1'-N9-C8	-3.58	116.56	126.73
2	C	601	GTP	C1'-N9-C8	-3.58	116.56	126.73
2	E	602	GTP	N9-C8-N7	-3.42	107.07	113.40
2	G	602	GTP	N9-C8-N7	-3.41	107.08	113.40
2	D	602	GTP	N9-C8-N7	-3.40	107.09	113.40
2	C	602	GTP	N9-C8-N7	-3.40	107.09	113.40
2	F	602	GTP	N9-C8-N7	-3.40	107.09	113.40
2	B	602	GTP	N9-C8-N7	-3.40	107.10	113.40
2	H	602	GTP	N9-C8-N7	-3.39	107.11	113.40
2	A	602	GTP	N9-C8-N7	-3.38	107.13	113.40
2	D	601	GTP	C2-N1-C6	-3.36	119.02	125.11
2	F	601	GTP	C2-N1-C6	-3.35	119.03	125.11
2	A	601	GTP	C2-N1-C6	-3.35	119.04	125.11
2	B	601	GTP	C2-N1-C6	-3.34	119.06	125.11
2	G	601	GTP	C2-N1-C6	-3.33	119.06	125.11
2	E	601	GTP	C2-N1-C6	-3.32	119.09	125.11
2	C	601	GTP	C2-N1-C6	-3.32	119.09	125.11
2	H	601	GTP	C2-N1-C6	-3.32	119.10	125.11
3	E	603	ATP	C2-N3-C4	3.27	119.82	111.83
3	B	603	ATP	C2-N3-C4	3.27	119.82	111.83
3	G	603	ATP	C2-N3-C4	3.27	119.82	111.83
3	C	603	ATP	C2-N3-C4	3.26	119.79	111.83
3	D	603	ATP	C5-N7-C8	3.25	108.56	103.45
3	F	603	ATP	C2-N3-C4	3.25	119.78	111.83
3	H	603	ATP	C2-N3-C4	3.25	119.78	111.83
3	A	603	ATP	C2-N3-C4	3.25	119.77	111.83
3	D	603	ATP	C2-N3-C4	3.24	119.75	111.83
3	C	603	ATP	C5-N7-C8	3.24	108.54	103.45
3	H	603	ATP	C5-N7-C8	3.23	108.53	103.45
3	G	603	ATP	C5-N7-C8	3.23	108.53	103.45
3	F	603	ATP	C5-N7-C8	3.23	108.52	103.45
3	E	603	ATP	C5-N7-C8	3.22	108.51	103.45
3	A	603	ATP	C5-N7-C8	3.21	108.50	103.45
3	B	603	ATP	C5-N7-C8	3.20	108.48	103.45
2	E	602	GTP	C1'-N9-C8	-3.04	118.09	126.73
2	G	602	GTP	C1'-N9-C8	-3.03	118.11	126.73
2	C	602	GTP	C1'-N9-C8	-3.03	118.12	126.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	602	GTP	C1'-N9-C8	-3.02	118.14	126.73
2	D	602	GTP	C1'-N9-C8	-3.02	118.15	126.73
2	B	602	GTP	C1'-N9-C8	-3.02	118.16	126.73
2	F	602	GTP	C1'-N9-C8	-3.01	118.17	126.73
2	A	602	GTP	C1'-N9-C8	-3.01	118.18	126.73
2	D	602	GTP	C2-N1-C6	-2.90	119.85	125.11
2	E	602	GTP	C2-N1-C6	-2.89	119.87	125.11
2	C	602	GTP	C2-N1-C6	-2.89	119.88	125.11
2	F	602	GTP	C2-N1-C6	-2.88	119.88	125.11
2	H	602	GTP	C2-N1-C6	-2.88	119.89	125.11
2	A	602	GTP	C2-N1-C6	-2.88	119.89	125.11
2	G	602	GTP	C2-N1-C6	-2.87	119.91	125.11
2	B	602	GTP	C2-N1-C6	-2.85	119.94	125.11
2	A	601	GTP	C3'-C2'-C1'	2.83	106.83	101.46
2	H	601	GTP	C3'-C2'-C1'	2.83	106.82	101.46
2	E	601	GTP	C3'-C2'-C1'	2.81	106.78	101.46
2	D	601	GTP	C3'-C2'-C1'	2.80	106.77	101.46
2	C	601	GTP	C3'-C2'-C1'	2.80	106.76	101.46
2	F	601	GTP	C3'-C2'-C1'	2.79	106.75	101.46
2	B	601	GTP	C3'-C2'-C1'	2.79	106.73	101.46
2	G	601	GTP	C3'-C2'-C1'	2.77	106.70	101.46
2	A	601	GTP	C8-N7-C5	2.72	109.10	104.26
2	H	601	GTP	C1'-N9-C4	2.71	134.50	126.49
2	G	601	GTP	C1'-N9-C4	2.71	134.50	126.49
2	B	601	GTP	C1'-N9-C4	2.71	134.49	126.49
2	E	601	GTP	C1'-N9-C4	2.71	134.48	126.49
2	C	601	GTP	C1'-N9-C4	2.71	134.48	126.49
2	F	601	GTP	C1'-N9-C4	2.70	134.47	126.49
2	E	601	GTP	C8-N7-C5	2.70	109.08	104.26
2	A	601	GTP	C1'-N9-C4	2.70	134.47	126.49
2	B	601	GTP	C8-N7-C5	2.70	109.07	104.26
2	D	601	GTP	C1'-N9-C4	2.69	134.45	126.49
2	H	601	GTP	C8-N7-C5	2.69	109.06	104.26
2	D	601	GTP	C8-N7-C5	2.69	109.05	104.26
2	F	601	GTP	C8-N7-C5	2.69	109.05	104.26
2	G	601	GTP	C8-N7-C5	2.68	109.04	104.26
2	C	601	GTP	C8-N7-C5	2.67	109.02	104.26
3	B	603	ATP	C3'-C2'-C1'	2.59	106.37	101.46
3	A	603	ATP	C3'-C2'-C1'	2.58	106.35	101.46
3	C	603	ATP	C3'-C2'-C1'	2.58	106.34	101.46
3	D	603	ATP	C3'-C2'-C1'	2.58	106.34	101.46
3	E	603	ATP	C3'-C2'-C1'	2.58	106.33	101.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	603	ATP	C3'-C2'-C1'	2.57	106.32	101.46
3	G	603	ATP	C3'-C2'-C1'	2.56	106.31	101.46
3	F	603	ATP	C3'-C2'-C1'	2.56	106.31	101.46
2	E	601	GTP	N9-C4-N3	2.47	130.89	125.95
2	A	601	GTP	N9-C4-N3	2.46	130.88	125.95
2	D	601	GTP	N9-C4-N3	2.46	130.88	125.95
2	A	601	GTP	C4-C5-N7	-2.45	106.78	110.67
2	F	601	GTP	N9-C4-N3	2.45	130.85	125.95
2	H	601	GTP	N9-C4-N3	2.45	130.85	125.95
2	G	601	GTP	N9-C4-N3	2.45	130.85	125.95
2	H	601	GTP	C4-C5-N7	-2.44	106.80	110.67
2	B	601	GTP	N9-C4-N3	2.44	130.83	125.95
2	C	601	GTP	N9-C4-N3	2.44	130.83	125.95
2	B	601	GTP	C4-C5-N7	-2.43	106.81	110.67
2	E	601	GTP	C4-C5-N7	-2.43	106.81	110.67
3	A	603	ATP	C6-C5-C4	2.43	120.49	117.18
3	H	603	ATP	C6-C5-C4	2.43	120.49	117.18
2	C	601	GTP	C4-C5-N7	-2.42	106.83	110.67
2	G	601	GTP	C4-C5-N7	-2.42	106.83	110.67
2	D	601	GTP	C4-C5-N7	-2.42	106.84	110.67
2	F	601	GTP	C4-C5-N7	-2.42	106.84	110.67
3	F	603	ATP	C6-C5-C4	2.41	120.47	117.18
3	C	603	ATP	C6-C5-C4	2.41	120.47	117.18
3	B	603	ATP	C6-C5-C4	2.40	120.46	117.18
3	E	603	ATP	C6-C5-C4	2.38	120.43	117.18
3	G	603	ATP	C6-C5-C4	2.38	120.43	117.18
2	F	601	GTP	C5-C6-N1	2.38	119.31	113.25
2	D	601	GTP	C5-C6-N1	2.38	119.30	113.25
2	B	601	GTP	C5-C6-N1	2.38	119.30	113.25
2	A	601	GTP	C5-C6-N1	2.38	119.30	113.25
2	G	601	GTP	C5-C6-N1	2.37	119.28	113.25
2	C	601	GTP	C5-C6-N1	2.36	119.27	113.25
3	D	603	ATP	C6-C5-C4	2.36	120.40	117.18
2	H	601	GTP	C5-C6-N1	2.36	119.26	113.25
2	A	601	GTP	O6-C6-C5	-2.36	120.31	126.53
2	E	601	GTP	C5-C6-N1	2.36	119.25	113.25
2	B	601	GTP	O6-C6-C5	-2.35	120.32	126.53
2	C	601	GTP	O6-C6-C5	-2.35	120.32	126.53
2	H	602	GTP	N9-C4-N3	2.35	130.65	125.95
2	E	601	GTP	O6-C6-C5	-2.35	120.34	126.53
2	G	601	GTP	O6-C6-C5	-2.34	120.34	126.53
2	H	601	GTP	O6-C6-C5	-2.34	120.34	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	602	GTP	N9-C4-N3	2.34	130.64	125.95
2	C	602	GTP	N9-C4-N3	2.34	130.64	125.95
2	E	602	GTP	N9-C4-N3	2.34	130.63	125.95
2	D	601	GTP	O6-C6-C5	-2.34	120.36	126.53
2	F	601	GTP	O6-C6-C5	-2.34	120.36	126.53
2	B	602	GTP	N9-C4-N3	2.34	130.63	125.95
2	F	602	GTP	N9-C4-N3	2.33	130.62	125.95
2	A	602	GTP	N9-C4-N3	2.33	130.62	125.95
2	A	602	GTP	C5-C6-N1	2.33	119.18	113.25
2	D	602	GTP	C5-C6-N1	2.32	119.17	113.25
2	E	602	GTP	C5-C6-N1	2.32	119.16	113.25
2	C	602	GTP	C5-C6-N1	2.32	119.15	113.25
2	G	602	GTP	N9-C4-N3	2.32	130.58	125.95
2	G	602	GTP	C5-C6-N1	2.30	119.12	113.25
2	F	601	GTP	C2'-C3'-C4'	2.30	107.06	102.61
2	B	602	GTP	C5-C6-N1	2.30	119.12	113.25
2	H	602	GTP	C5-C6-N1	2.30	119.11	113.25
2	F	602	GTP	C5-C6-N1	2.30	119.11	113.25
2	B	601	GTP	C2'-C3'-C4'	2.28	107.02	102.61
2	G	602	GTP	C8-N7-C5	2.28	108.33	104.26
2	H	602	GTP	C3'-C2'-C1'	2.28	105.78	101.46
2	G	601	GTP	C2'-C3'-C4'	2.28	107.02	102.61
2	G	602	GTP	C3'-C2'-C1'	2.28	105.77	101.46
2	E	601	GTP	C2'-C3'-C4'	2.28	107.01	102.61
2	B	602	GTP	C8-N7-C5	2.28	108.32	104.26
2	C	602	GTP	C8-N7-C5	2.28	108.31	104.26
2	A	602	GTP	C3'-C2'-C1'	2.28	105.77	101.46
2	F	602	GTP	C8-N7-C5	2.27	108.31	104.26
2	A	602	GTP	C8-N7-C5	2.27	108.31	104.26
2	C	601	GTP	C2'-C3'-C4'	2.27	106.99	102.61
2	D	602	GTP	C8-N7-C5	2.27	108.30	104.26
2	B	602	GTP	C3'-C2'-C1'	2.27	105.75	101.46
2	E	602	GTP	C8-N7-C5	2.27	108.30	104.26
2	F	602	GTP	C3'-C2'-C1'	2.27	105.75	101.46
2	H	601	GTP	C2'-C3'-C4'	2.26	106.98	102.61
2	E	602	GTP	C3'-C2'-C1'	2.26	105.74	101.46
2	D	602	GTP	C3'-C2'-C1'	2.26	105.74	101.46
2	D	601	GTP	C2'-C3'-C4'	2.26	106.97	102.61
2	A	602	GTP	O6-C6-C5	-2.25	120.59	126.53
2	H	602	GTP	C8-N7-C5	2.25	108.27	104.26
2	B	602	GTP	C2'-C3'-C4'	2.25	106.96	102.61
2	C	602	GTP	C2'-C3'-C4'	2.25	106.95	102.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	602	GTP	O6-C6-C5	-2.25	120.60	126.53
2	C	602	GTP	C3'-C2'-C1'	2.25	105.71	101.46
2	G	602	GTP	O6-C6-C5	-2.24	120.61	126.53
2	A	601	GTP	C2'-C3'-C4'	2.24	106.94	102.61
2	B	602	GTP	O6-C6-C5	-2.24	120.61	126.53
2	A	602	GTP	C2'-C3'-C4'	2.24	106.94	102.61
2	D	602	GTP	C2'-C3'-C4'	2.24	106.93	102.61
2	D	602	GTP	O6-C6-C5	-2.24	120.63	126.53
2	C	602	GTP	O6-C6-C5	-2.23	120.63	126.53
2	E	602	GTP	C2'-C3'-C4'	2.23	106.92	102.61
2	G	602	GTP	C2'-C3'-C4'	2.23	106.91	102.61
2	F	602	GTP	C2'-C3'-C4'	2.22	106.90	102.61
2	H	602	GTP	C2'-C3'-C4'	2.22	106.90	102.61
2	F	602	GTP	O6-C6-C5	-2.22	120.69	126.53
2	H	602	GTP	O6-C6-C5	-2.22	120.69	126.53
2	E	601	GTP	O3G-PG-O3B	2.21	112.05	104.64
2	F	601	GTP	O3G-PG-O3B	2.21	112.03	104.64
2	C	601	GTP	O3G-PG-O3B	2.20	112.02	104.64
2	D	601	GTP	O3G-PG-O3B	2.20	112.02	104.64
2	B	601	GTP	O3G-PG-O3B	2.20	112.02	104.64
2	H	601	GTP	O3G-PG-O3B	2.20	112.01	104.64
2	A	601	GTP	O3G-PG-O3B	2.20	112.01	104.64
2	G	601	GTP	O3G-PG-O3B	2.19	111.98	104.64
2	G	602	GTP	C1'-N9-C4	2.14	132.80	126.49
2	B	602	GTP	C1'-N9-C4	2.12	132.75	126.49
2	C	602	GTP	C1'-N9-C4	2.12	132.74	126.49
2	E	602	GTP	C1'-N9-C4	2.12	132.74	126.49
2	D	602	GTP	C1'-N9-C4	2.12	132.74	126.49
2	A	602	GTP	C1'-N9-C4	2.11	132.72	126.49
2	H	602	GTP	C1'-N9-C4	2.11	132.71	126.49
2	F	602	GTP	C1'-N9-C4	2.11	132.71	126.49
2	E	601	GTP	N2-C2-N1	2.07	121.13	116.76
2	B	601	GTP	N2-C2-N1	2.06	121.11	116.76
2	C	601	GTP	N2-C2-N1	2.06	121.11	116.76
2	H	601	GTP	N2-C2-N1	2.06	121.10	116.76
2	A	601	GTP	N2-C2-N1	2.05	121.09	116.76
2	F	601	GTP	N2-C2-N1	2.05	121.08	116.76
2	G	601	GTP	N2-C2-N1	2.05	121.08	116.76
2	D	601	GTP	N2-C2-N1	2.04	121.07	116.76
3	C	603	ATP	O2G-PG-O3B	2.01	111.38	104.64
3	D	603	ATP	O2G-PG-O3B	2.01	111.36	104.64
3	B	603	ATP	O2G-PG-O3B	2.00	111.35	104.64

There are no chirality outliers.

All (139) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GTP	PB-O3B-PG-O2G
2	A	601	GTP	PB-O3B-PG-O3G
2	A	601	GTP	C5'-O5'-PA-O3A
2	A	601	GTP	C5'-O5'-PA-O1A
2	A	601	GTP	C5'-O5'-PA-O2A
2	A	602	GTP	C5'-O5'-PA-O3A
2	A	602	GTP	C5'-O5'-PA-O2A
2	B	601	GTP	PB-O3B-PG-O2G
2	B	601	GTP	PB-O3B-PG-O3G
2	B	601	GTP	C5'-O5'-PA-O3A
2	B	601	GTP	C5'-O5'-PA-O1A
2	B	601	GTP	C5'-O5'-PA-O2A
2	B	602	GTP	C5'-O5'-PA-O3A
2	B	602	GTP	C5'-O5'-PA-O2A
2	C	601	GTP	PB-O3B-PG-O2G
2	C	601	GTP	PB-O3B-PG-O3G
2	C	601	GTP	C5'-O5'-PA-O3A
2	C	601	GTP	C5'-O5'-PA-O1A
2	C	601	GTP	C5'-O5'-PA-O2A
2	C	602	GTP	C5'-O5'-PA-O3A
2	C	602	GTP	C5'-O5'-PA-O2A
2	D	601	GTP	PB-O3B-PG-O2G
2	D	601	GTP	PB-O3B-PG-O3G
2	D	601	GTP	C5'-O5'-PA-O3A
2	D	601	GTP	C5'-O5'-PA-O1A
2	D	601	GTP	C5'-O5'-PA-O2A
2	D	602	GTP	C5'-O5'-PA-O3A
2	D	602	GTP	C5'-O5'-PA-O2A
2	E	601	GTP	PB-O3B-PG-O2G
2	E	601	GTP	PB-O3B-PG-O3G
2	E	601	GTP	C5'-O5'-PA-O3A
2	E	601	GTP	C5'-O5'-PA-O1A
2	E	601	GTP	C5'-O5'-PA-O2A
2	E	602	GTP	C5'-O5'-PA-O3A
2	E	602	GTP	C5'-O5'-PA-O2A
2	F	601	GTP	PB-O3B-PG-O2G
2	F	601	GTP	PB-O3B-PG-O3G
2	F	601	GTP	C5'-O5'-PA-O3A
2	F	601	GTP	C5'-O5'-PA-O1A
2	F	601	GTP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
2	F	602	GTP	C5'-O5'-PA-O3A
2	F	602	GTP	C5'-O5'-PA-O2A
2	G	601	GTP	PB-O3B-PG-O2G
2	G	601	GTP	PB-O3B-PG-O3G
2	G	601	GTP	C5'-O5'-PA-O3A
2	G	601	GTP	C5'-O5'-PA-O1A
2	G	601	GTP	C5'-O5'-PA-O2A
2	G	602	GTP	C5'-O5'-PA-O3A
2	G	602	GTP	C5'-O5'-PA-O2A
2	H	601	GTP	PB-O3B-PG-O2G
2	H	601	GTP	PB-O3B-PG-O3G
2	H	601	GTP	C5'-O5'-PA-O3A
2	H	601	GTP	C5'-O5'-PA-O1A
2	H	601	GTP	C5'-O5'-PA-O2A
2	H	602	GTP	C5'-O5'-PA-O3A
2	H	602	GTP	C5'-O5'-PA-O2A
2	A	601	GTP	O4'-C1'-N9-C8
2	B	601	GTP	O4'-C1'-N9-C8
2	C	601	GTP	O4'-C1'-N9-C8
2	D	601	GTP	O4'-C1'-N9-C8
2	E	601	GTP	O4'-C1'-N9-C8
2	F	601	GTP	O4'-C1'-N9-C8
2	G	601	GTP	O4'-C1'-N9-C8
2	H	601	GTP	O4'-C1'-N9-C8
2	A	602	GTP	O4'-C4'-C5'-O5'
2	B	602	GTP	O4'-C4'-C5'-O5'
2	C	602	GTP	O4'-C4'-C5'-O5'
2	D	602	GTP	O4'-C4'-C5'-O5'
2	E	602	GTP	O4'-C4'-C5'-O5'
2	F	602	GTP	O4'-C4'-C5'-O5'
2	G	602	GTP	O4'-C4'-C5'-O5'
2	H	602	GTP	O4'-C4'-C5'-O5'
2	A	601	GTP	O4'-C1'-N9-C4
2	B	601	GTP	O4'-C1'-N9-C4
2	C	601	GTP	O4'-C1'-N9-C4
2	D	601	GTP	O4'-C1'-N9-C4
2	E	601	GTP	O4'-C1'-N9-C4
2	F	601	GTP	O4'-C1'-N9-C4
2	G	601	GTP	O4'-C1'-N9-C4
2	H	601	GTP	O4'-C1'-N9-C4
2	A	602	GTP	C3'-C4'-C5'-O5'
2	B	602	GTP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	C	602	GTP	C3'-C4'-C5'-O5'
2	D	602	GTP	C3'-C4'-C5'-O5'
2	E	602	GTP	C3'-C4'-C5'-O5'
2	F	602	GTP	C3'-C4'-C5'-O5'
2	G	602	GTP	C3'-C4'-C5'-O5'
2	H	602	GTP	C3'-C4'-C5'-O5'
2	A	601	GTP	C3'-C4'-C5'-O5'
2	B	601	GTP	C3'-C4'-C5'-O5'
2	C	601	GTP	C3'-C4'-C5'-O5'
2	D	601	GTP	C3'-C4'-C5'-O5'
2	E	601	GTP	C3'-C4'-C5'-O5'
2	F	601	GTP	C3'-C4'-C5'-O5'
2	G	601	GTP	C3'-C4'-C5'-O5'
2	H	601	GTP	C3'-C4'-C5'-O5'
2	G	601	GTP	O4'-C4'-C5'-O5'
2	A	601	GTP	O4'-C4'-C5'-O5'
2	B	601	GTP	O4'-C4'-C5'-O5'
2	C	601	GTP	O4'-C4'-C5'-O5'
2	D	601	GTP	O4'-C4'-C5'-O5'
2	E	601	GTP	O4'-C4'-C5'-O5'
2	F	601	GTP	O4'-C4'-C5'-O5'
2	H	601	GTP	O4'-C4'-C5'-O5'
2	A	601	GTP	PB-O3A-PA-O2A
2	B	601	GTP	PB-O3A-PA-O2A
2	C	601	GTP	PB-O3A-PA-O2A
2	D	601	GTP	PB-O3A-PA-O2A
2	E	601	GTP	PB-O3A-PA-O2A
2	F	601	GTP	PB-O3A-PA-O2A
2	G	601	GTP	PB-O3A-PA-O2A
2	H	601	GTP	PB-O3A-PA-O2A
2	A	601	GTP	C4'-C5'-O5'-PA
2	B	601	GTP	C4'-C5'-O5'-PA
2	C	601	GTP	C4'-C5'-O5'-PA
2	D	601	GTP	C4'-C5'-O5'-PA
2	E	601	GTP	C4'-C5'-O5'-PA
2	F	601	GTP	C4'-C5'-O5'-PA
2	G	601	GTP	C4'-C5'-O5'-PA
2	H	601	GTP	C4'-C5'-O5'-PA
2	A	602	GTP	PB-O3B-PG-O2G
2	B	602	GTP	PB-O3B-PG-O2G
2	C	602	GTP	PB-O3B-PG-O2G
2	D	602	GTP	PB-O3B-PG-O2G

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Mol	Chain	Res	Type	Atoms
2	E	602	GTP	PB-O3B-PG-O2G
2	F	602	GTP	PB-O3B-PG-O2G
2	G	602	GTP	PB-O3B-PG-O2G
2	H	602	GTP	PB-O3B-PG-O2G
3	A	603	ATP	C2'-C1'-N9-C8
3	B	603	ATP	C2'-C1'-N9-C8
3	C	603	ATP	C2'-C1'-N9-C8
3	D	603	ATP	C2'-C1'-N9-C8
3	E	603	ATP	C2'-C1'-N9-C8
3	F	603	ATP	C2'-C1'-N9-C8
3	G	603	ATP	C2'-C1'-N9-C8
3	H	603	ATP	C2'-C1'-N9-C8
2	A	602	GTP	PA-O3A-PB-O1B
2	D	602	GTP	PA-O3A-PB-O1B
2	F	602	GTP	PA-O3A-PB-O1B

There are no ring outliers.

24 monomers are involved in 33 short contacts:

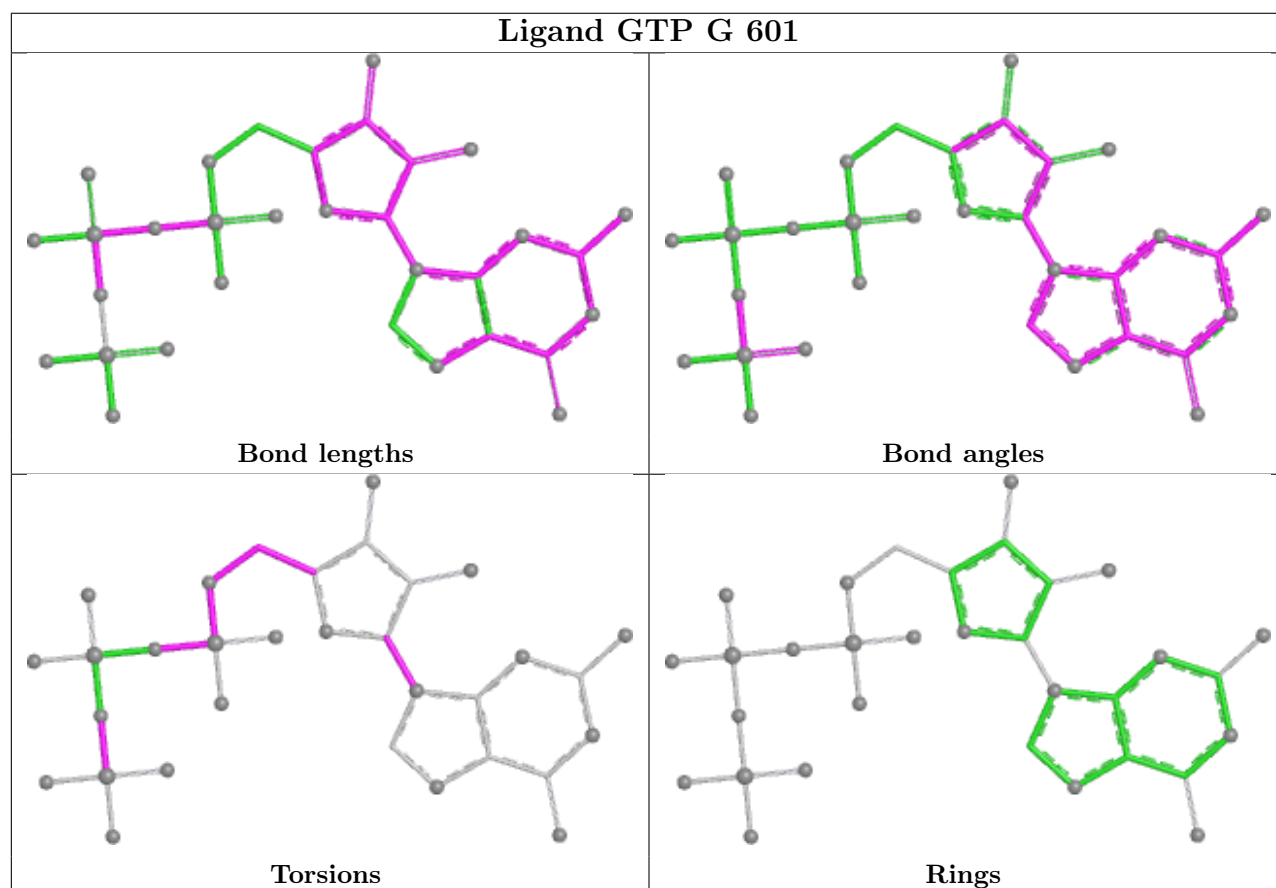
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	601	GTP	1	0
2	B	601	GTP	1	0
2	D	601	GTP	1	0
3	D	603	ATP	2	0
2	H	601	GTP	1	0
3	H	603	ATP	2	0
3	C	603	ATP	2	0
2	C	601	GTP	1	0
2	D	602	GTP	1	0
2	F	601	GTP	1	0
3	F	603	ATP	2	0
2	A	602	GTP	1	0
2	C	602	GTP	1	0
2	E	602	GTP	1	0
2	F	602	GTP	1	0
3	E	603	ATP	2	0
2	A	601	GTP	1	0
2	G	602	GTP	1	0
3	G	603	ATP	2	0
2	H	602	GTP	1	0
2	B	602	GTP	1	0
3	B	603	ATP	2	0

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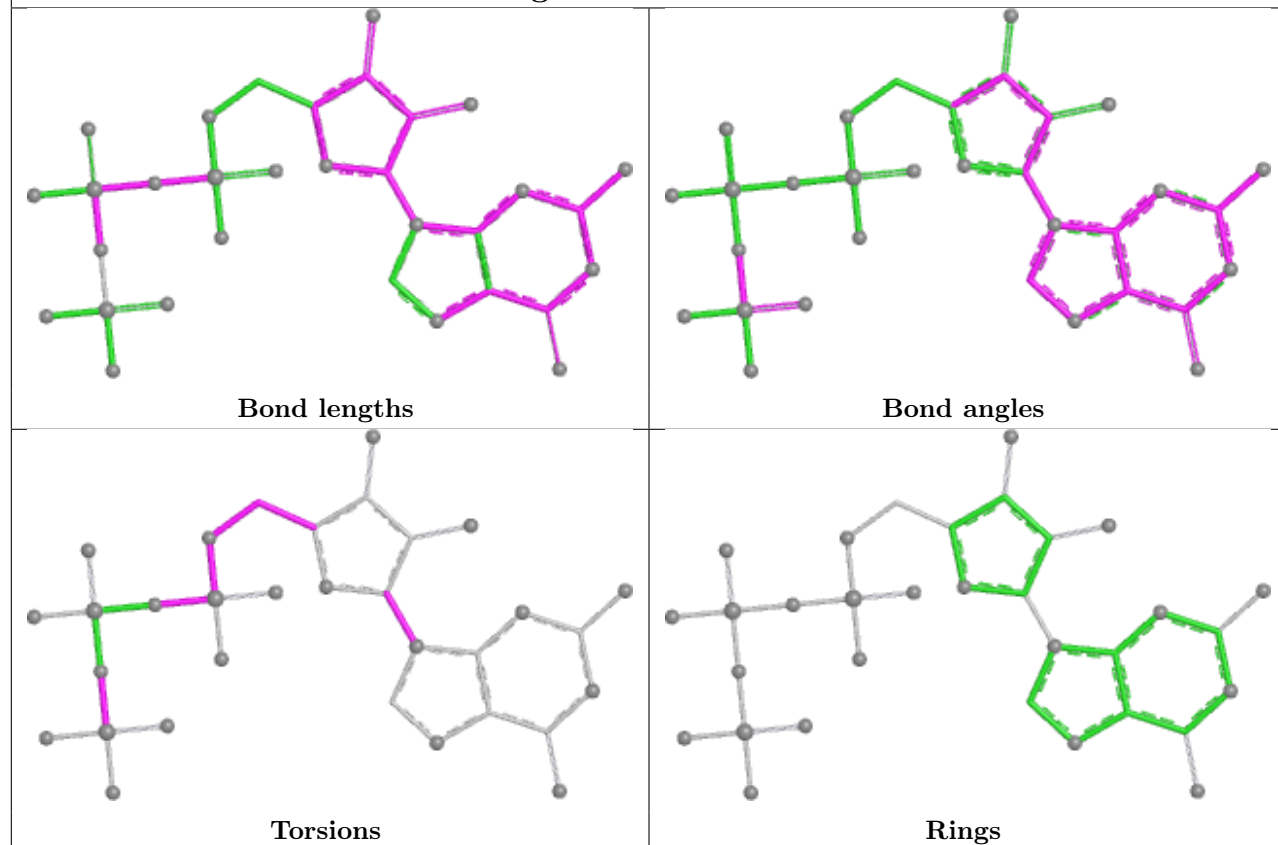
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	603	ATP	3	0
2	E	601	GTP	1	0

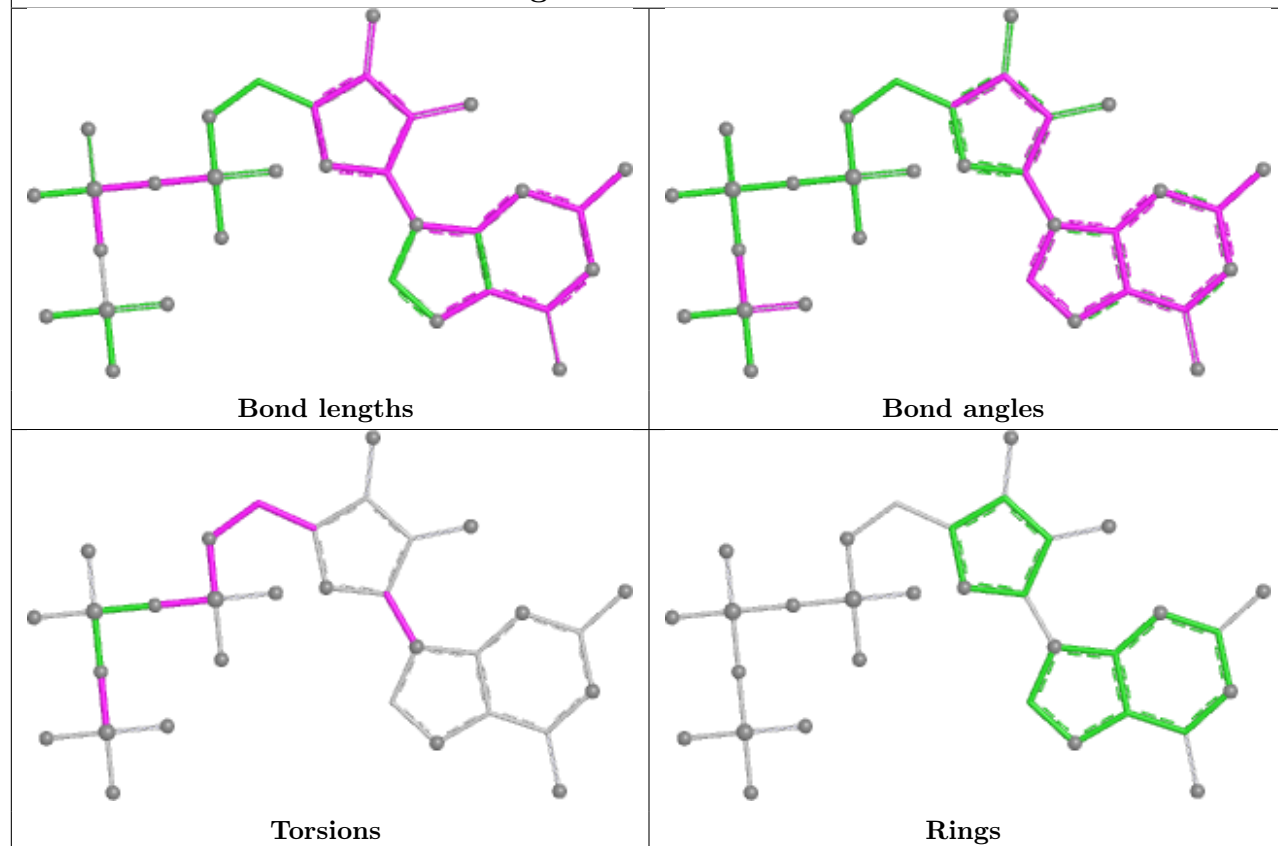
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

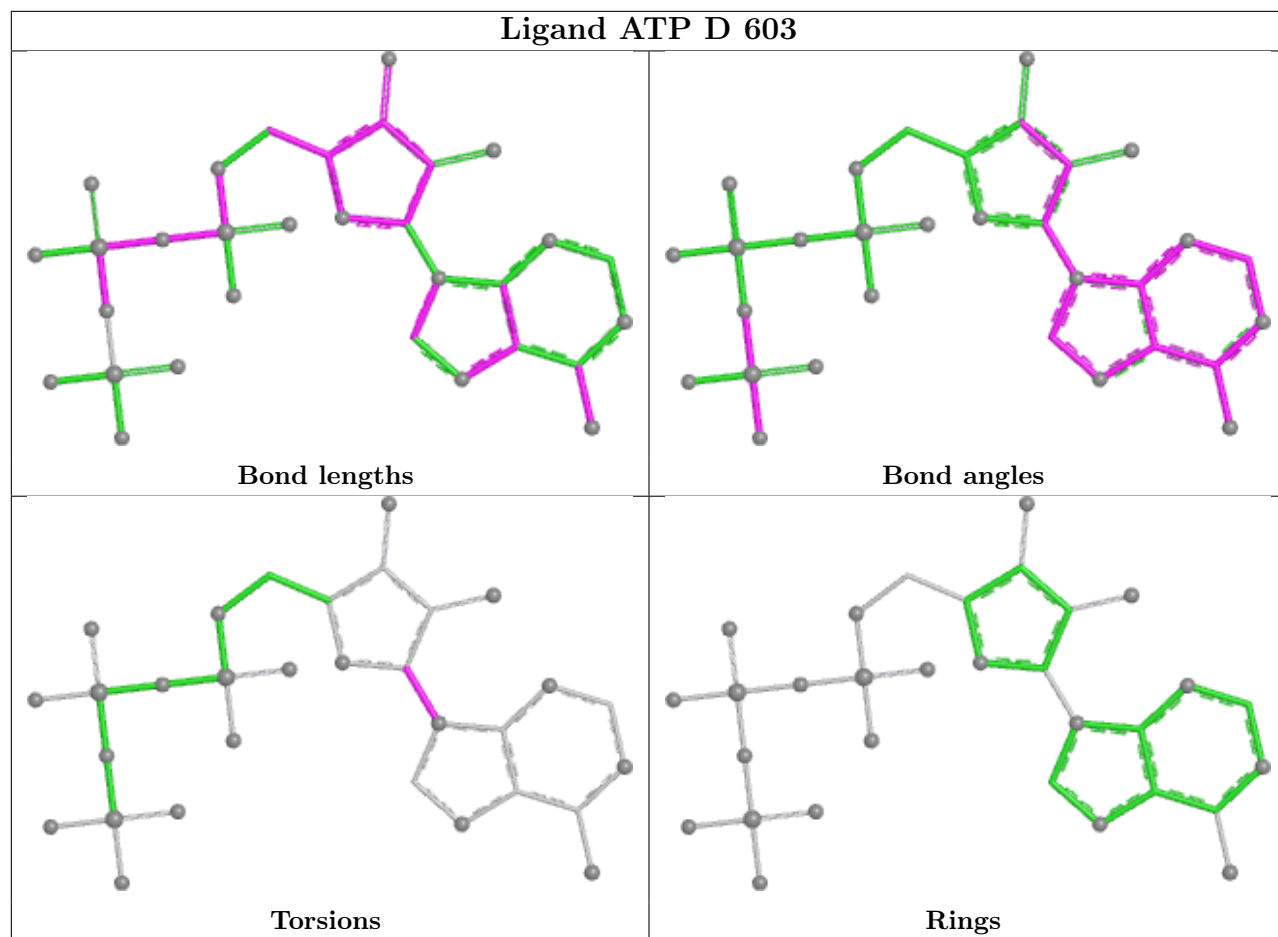


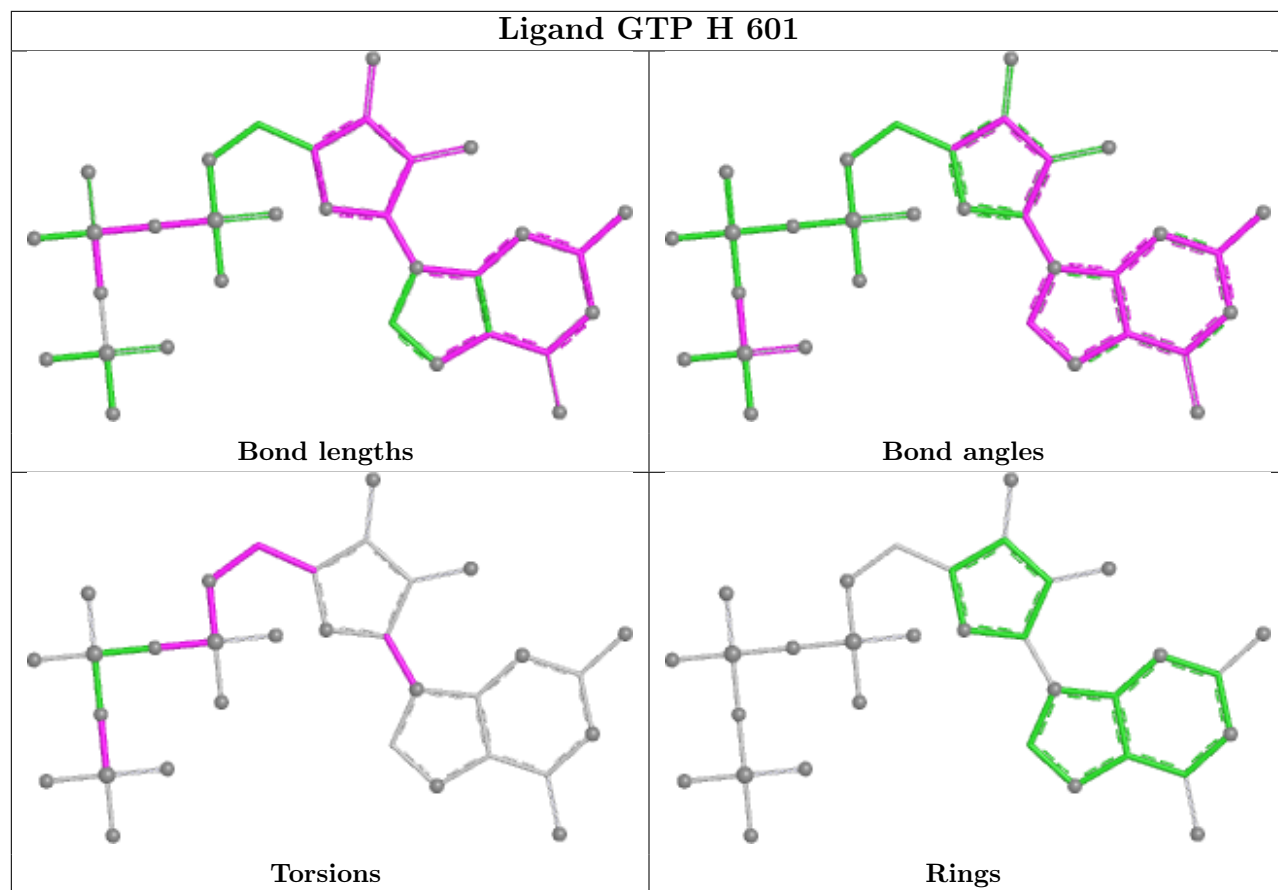
Ligand GTP B 601

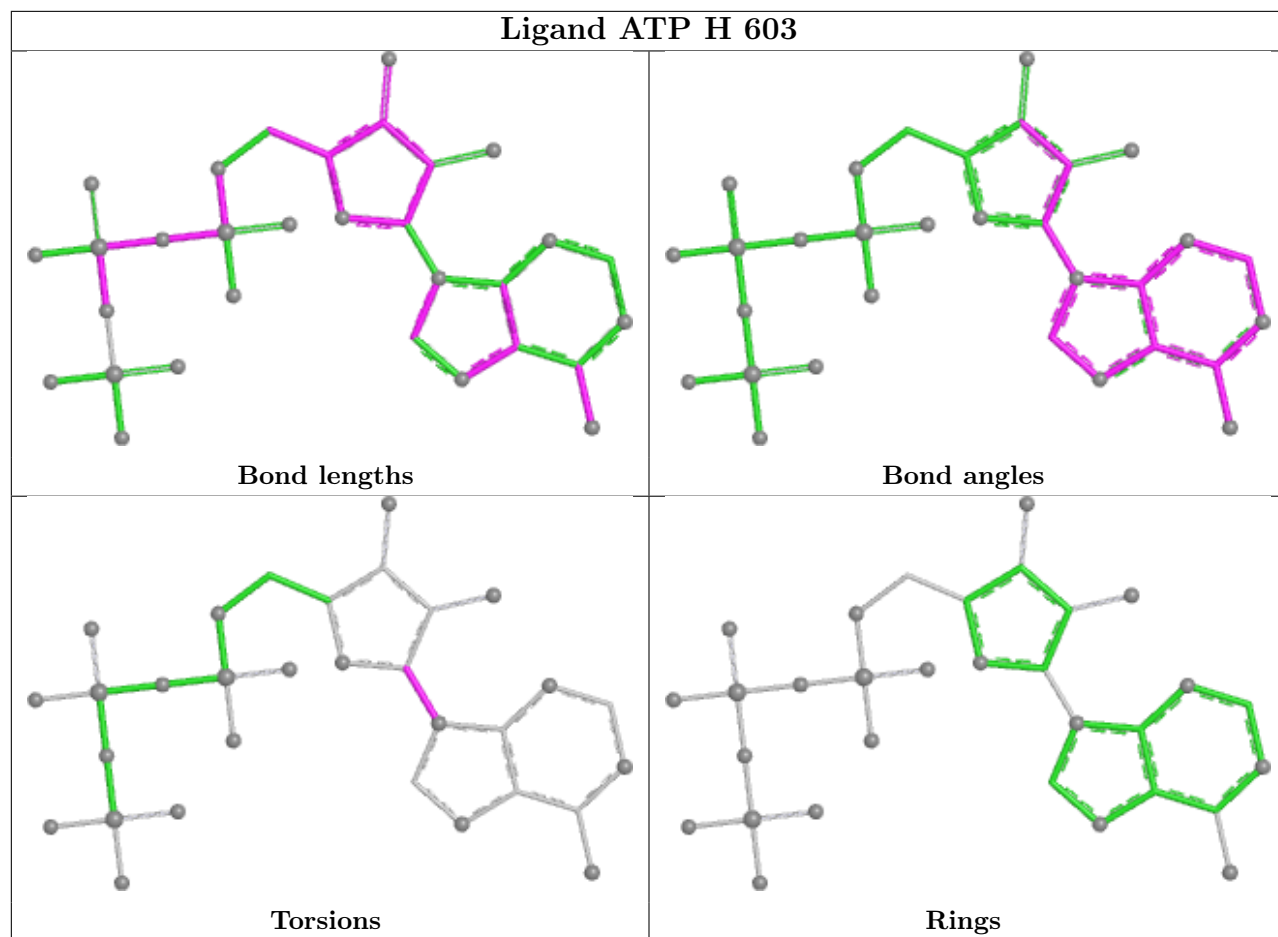


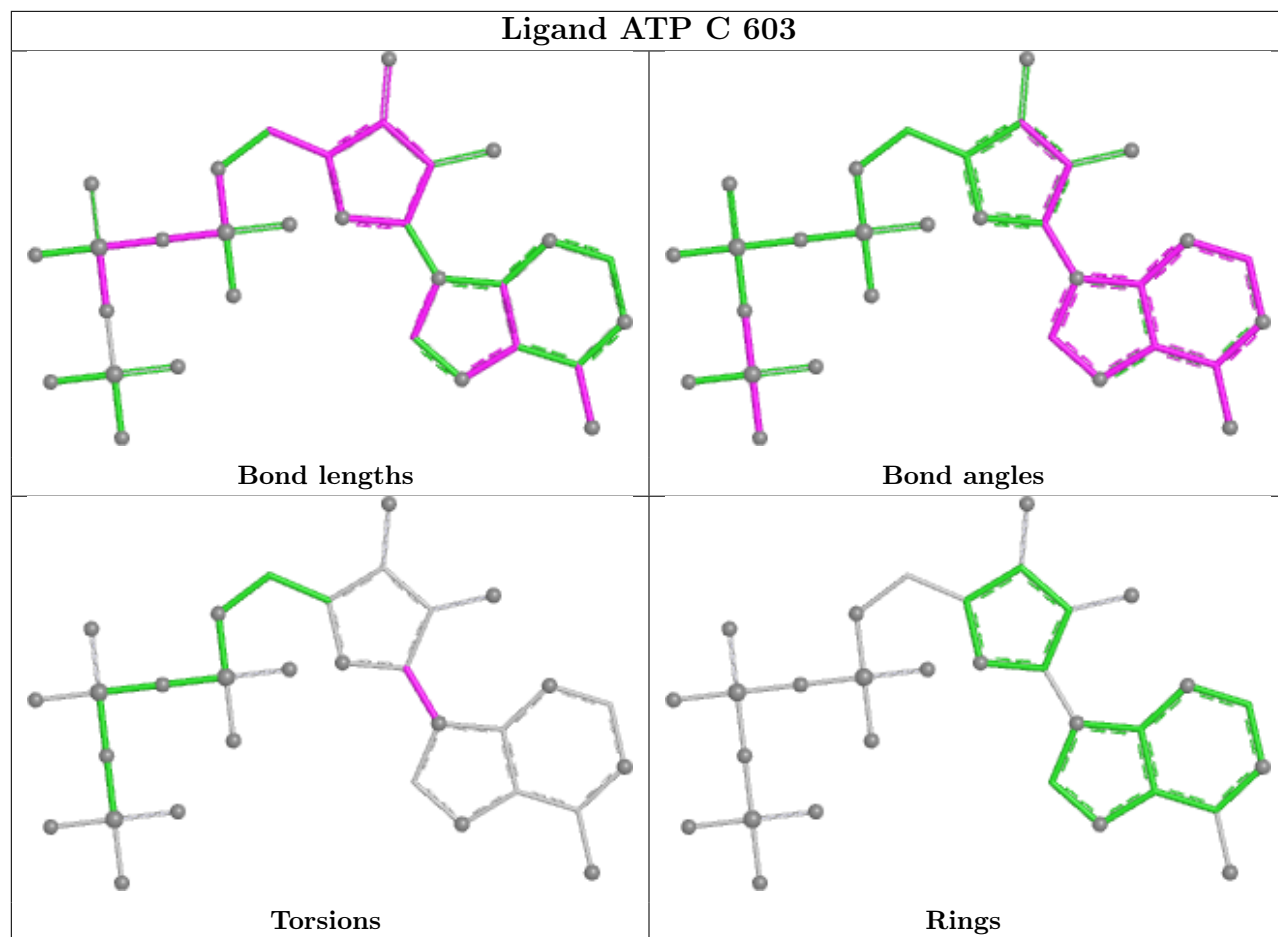
Ligand GTP D 601



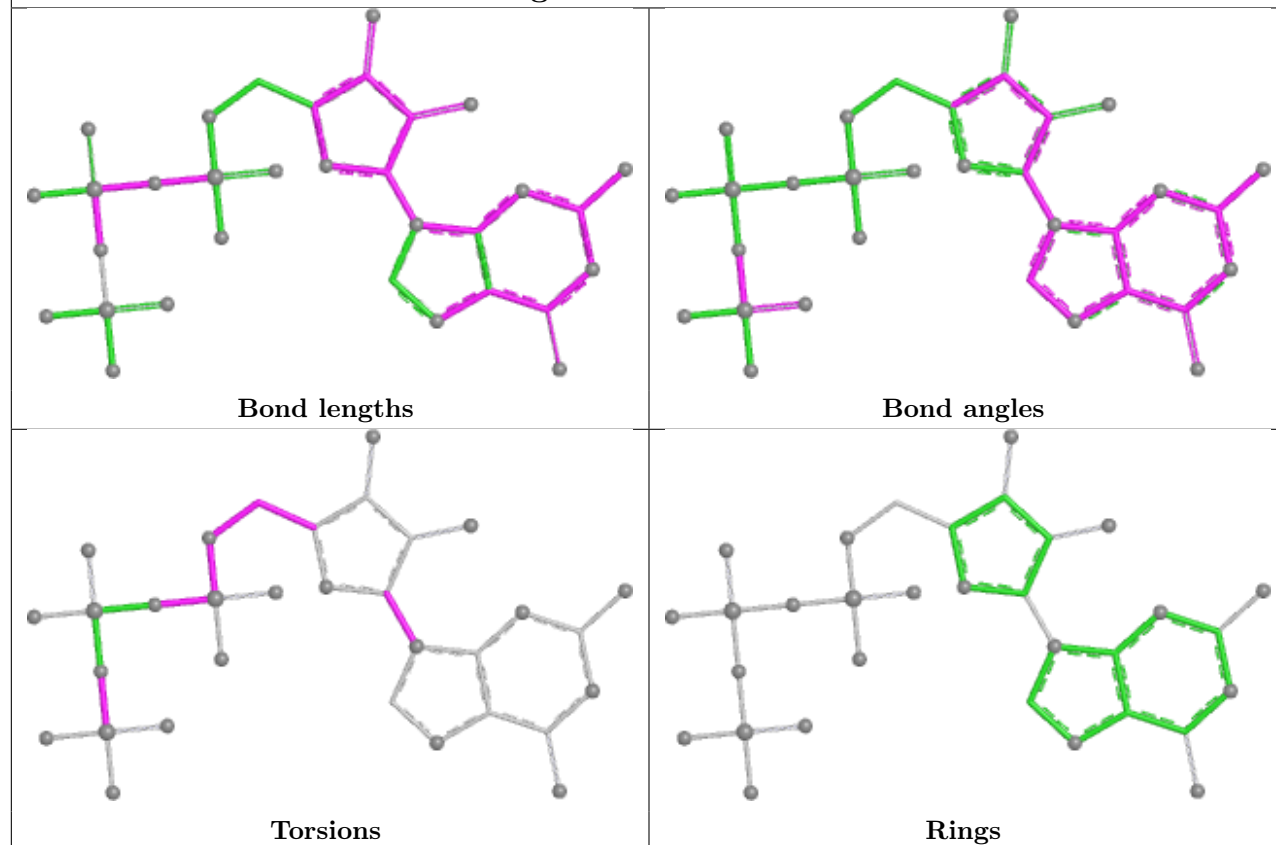




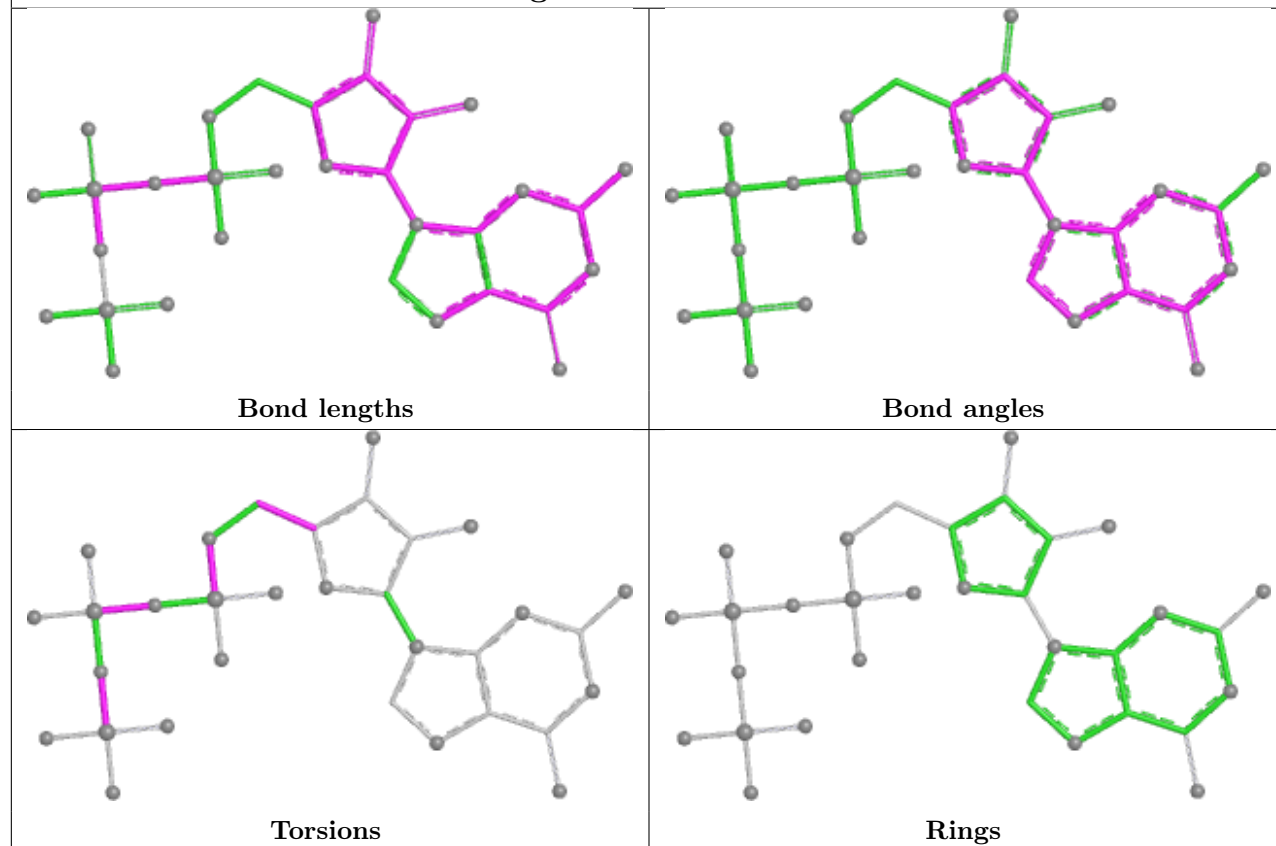


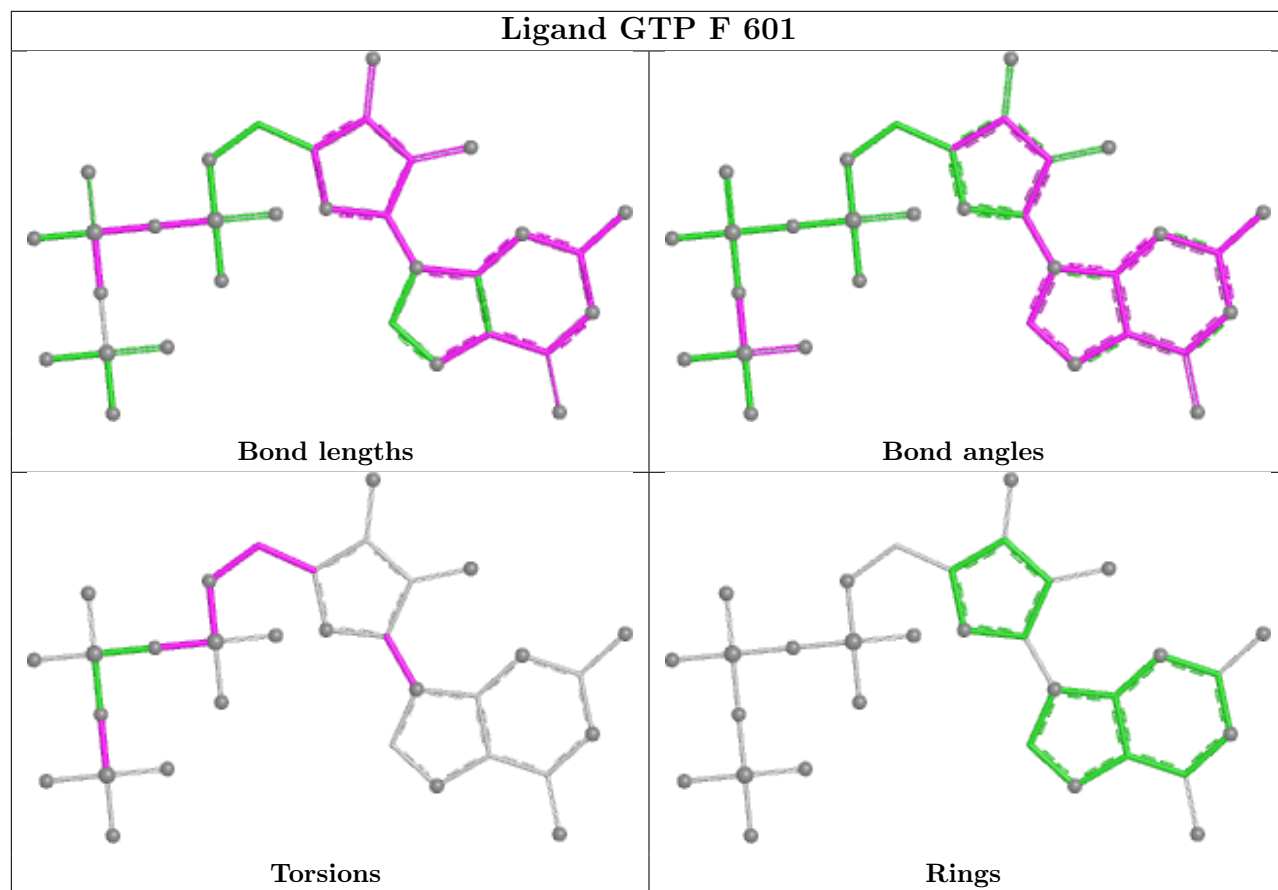


Ligand GTP C 601

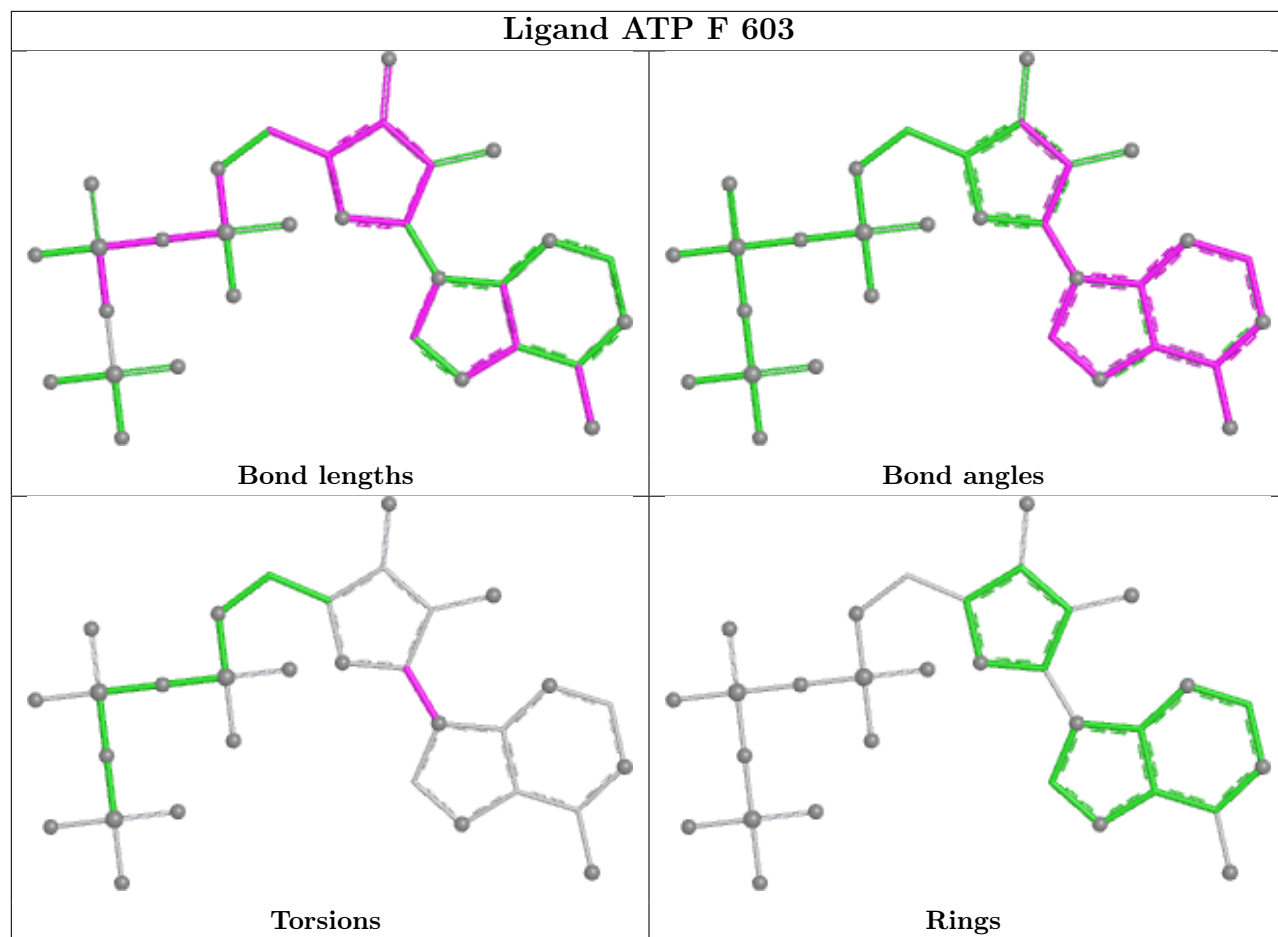


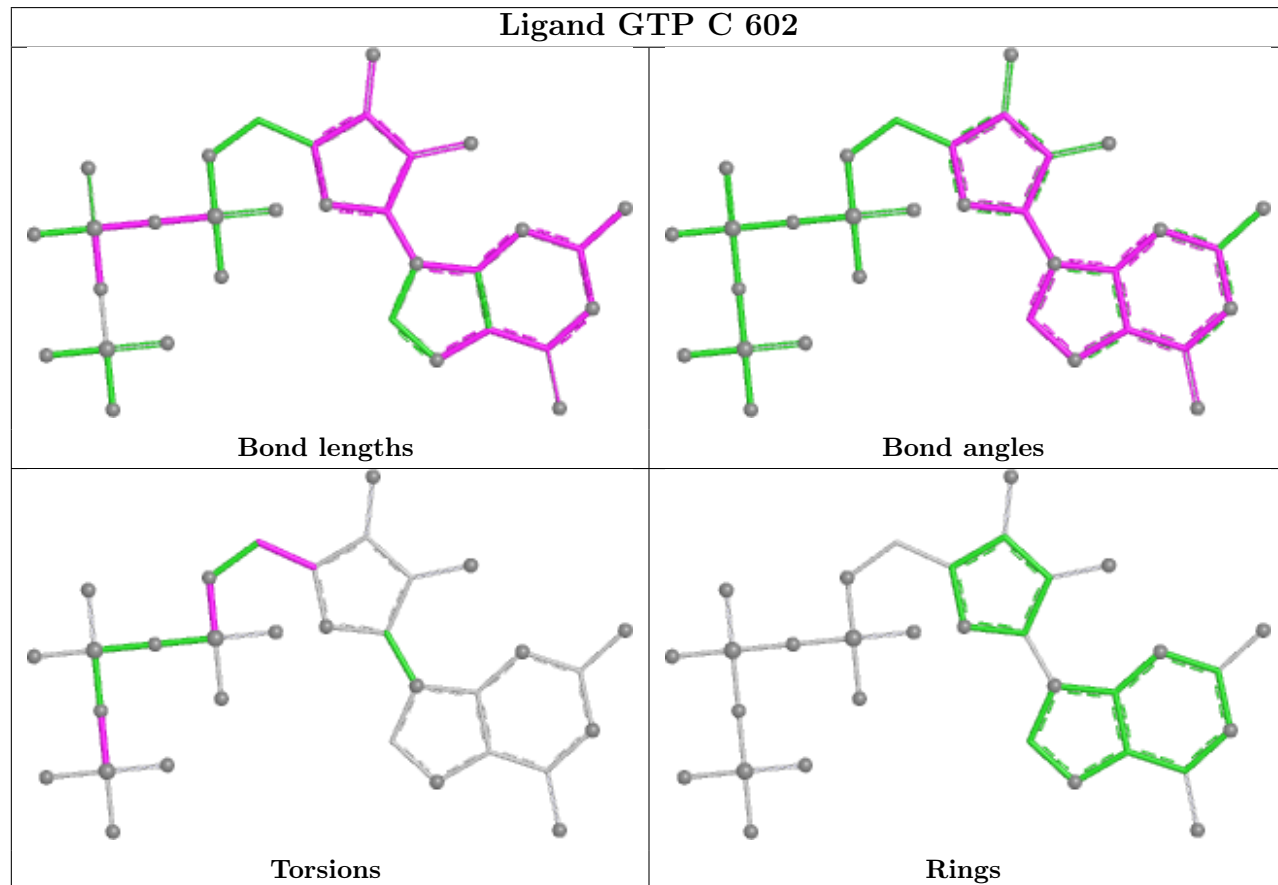
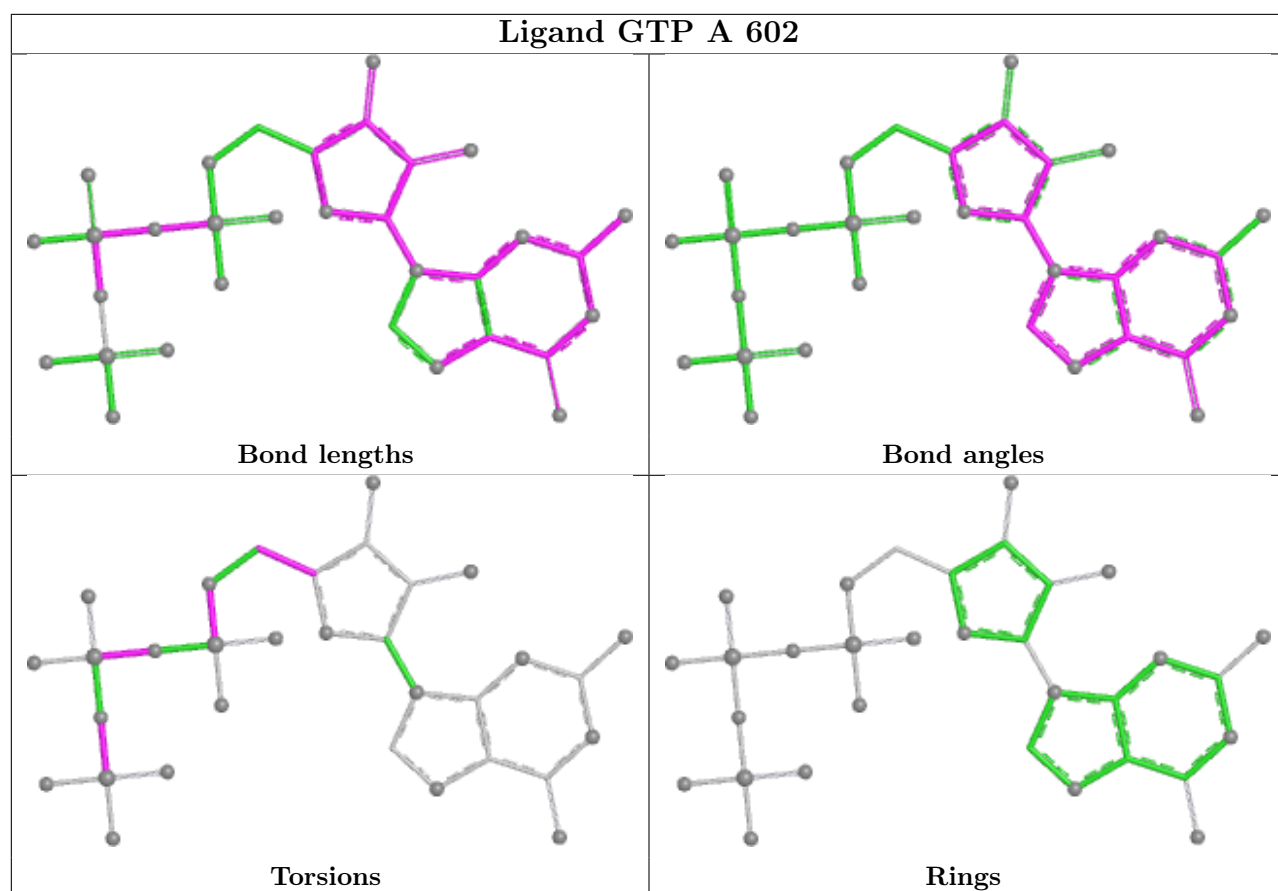
Ligand GTP D 602



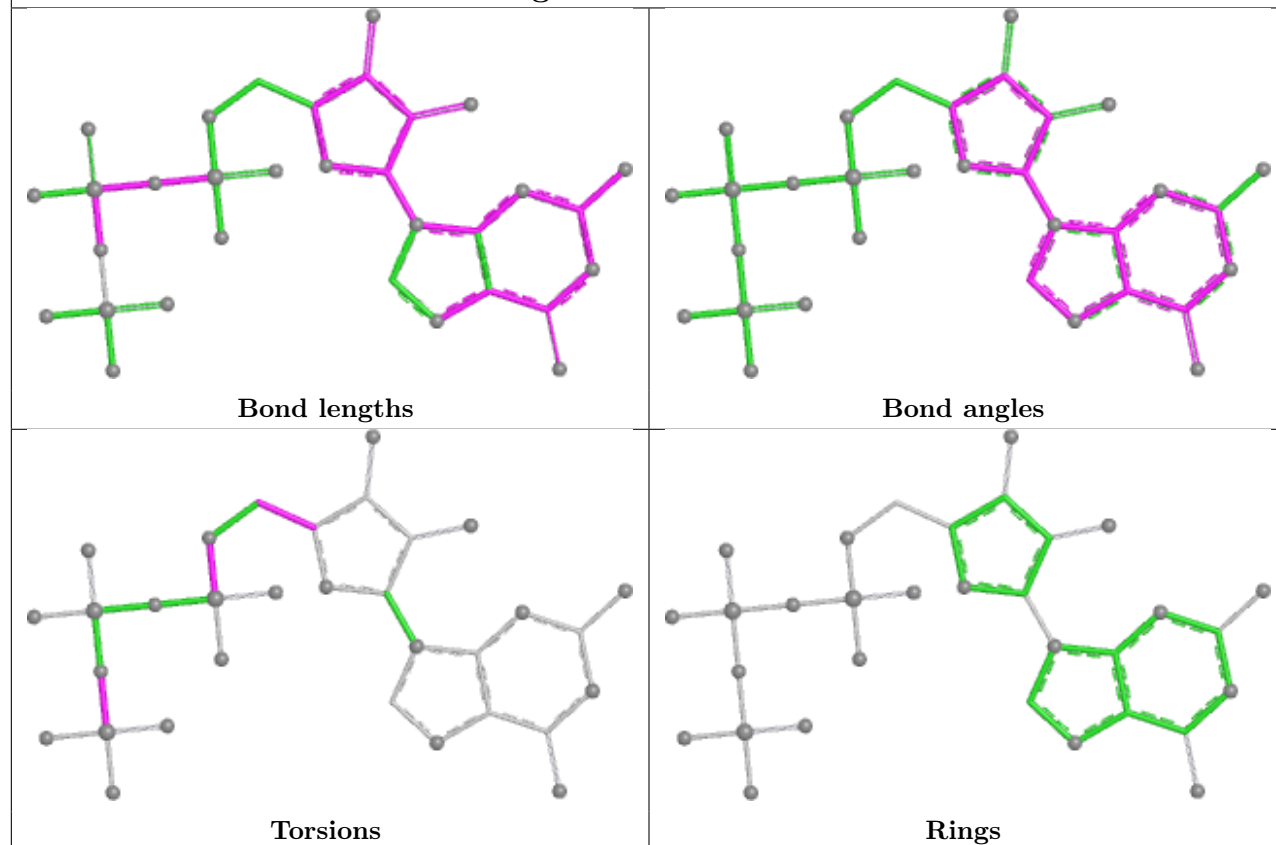


Ligand ATP F 603

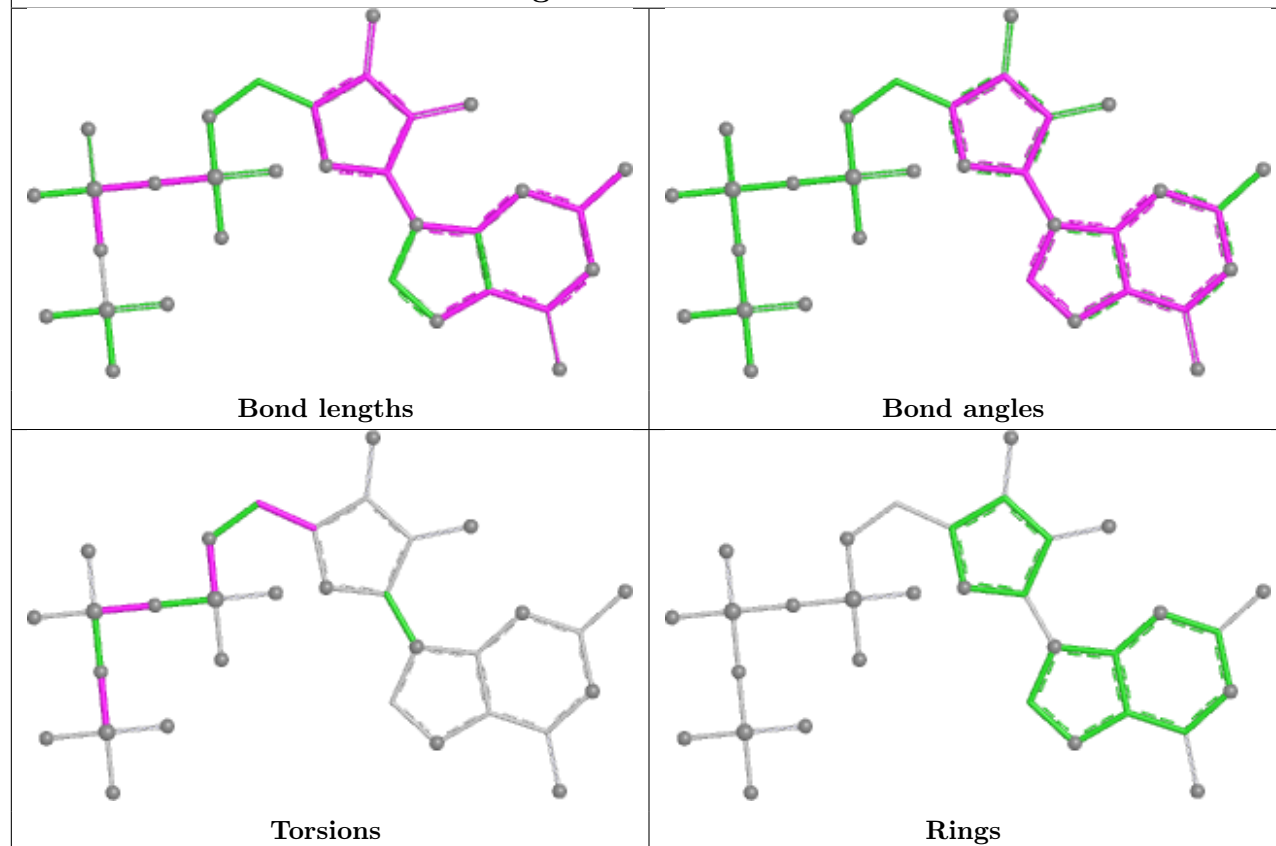


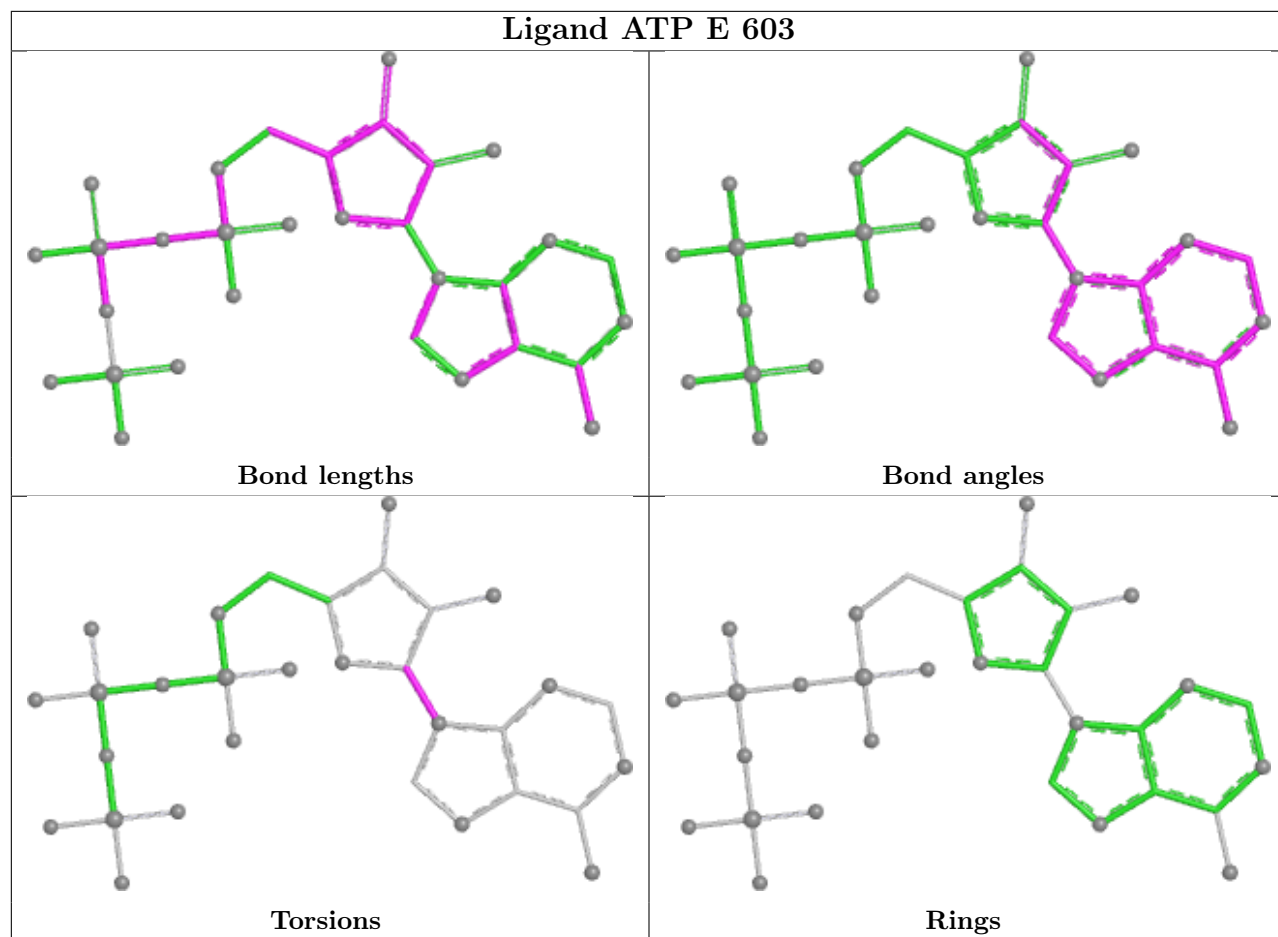


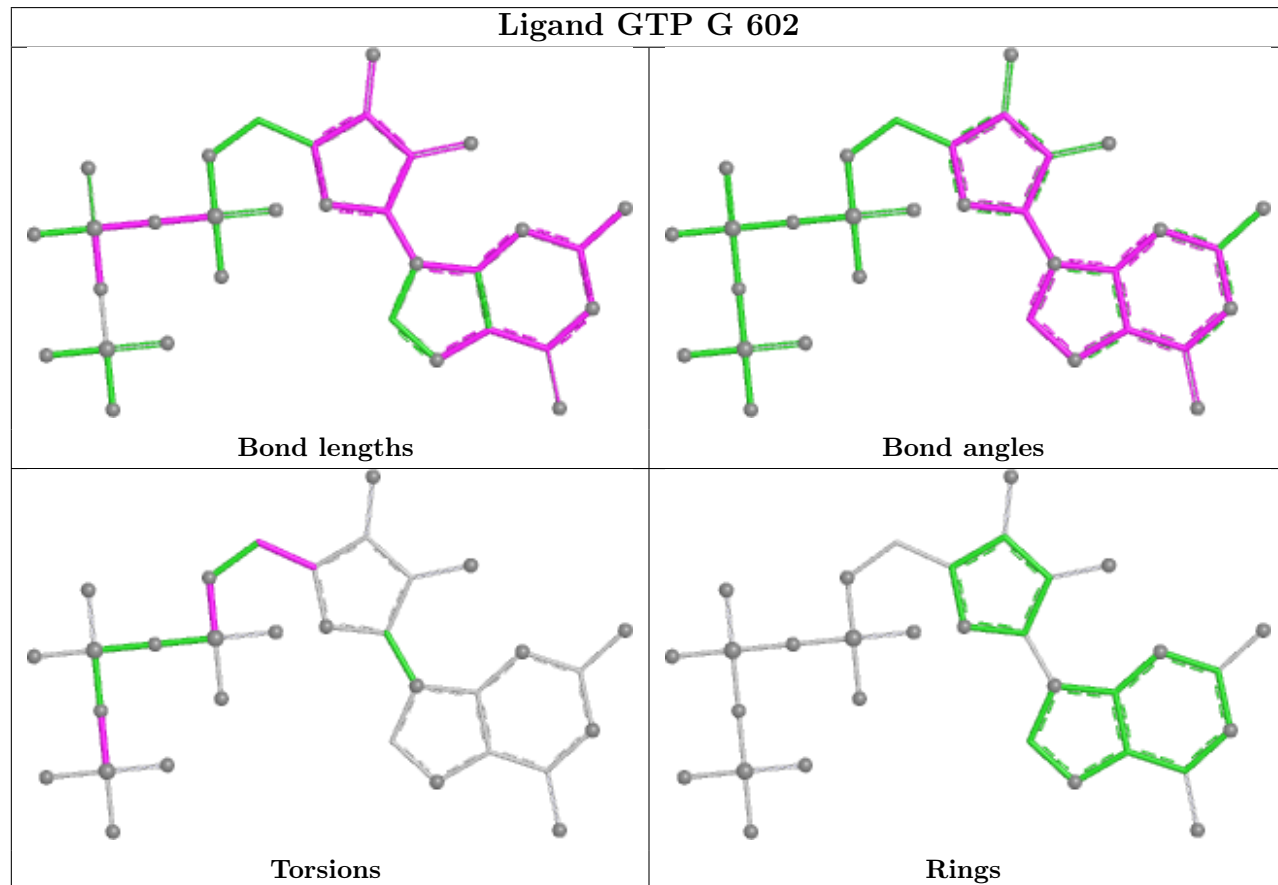
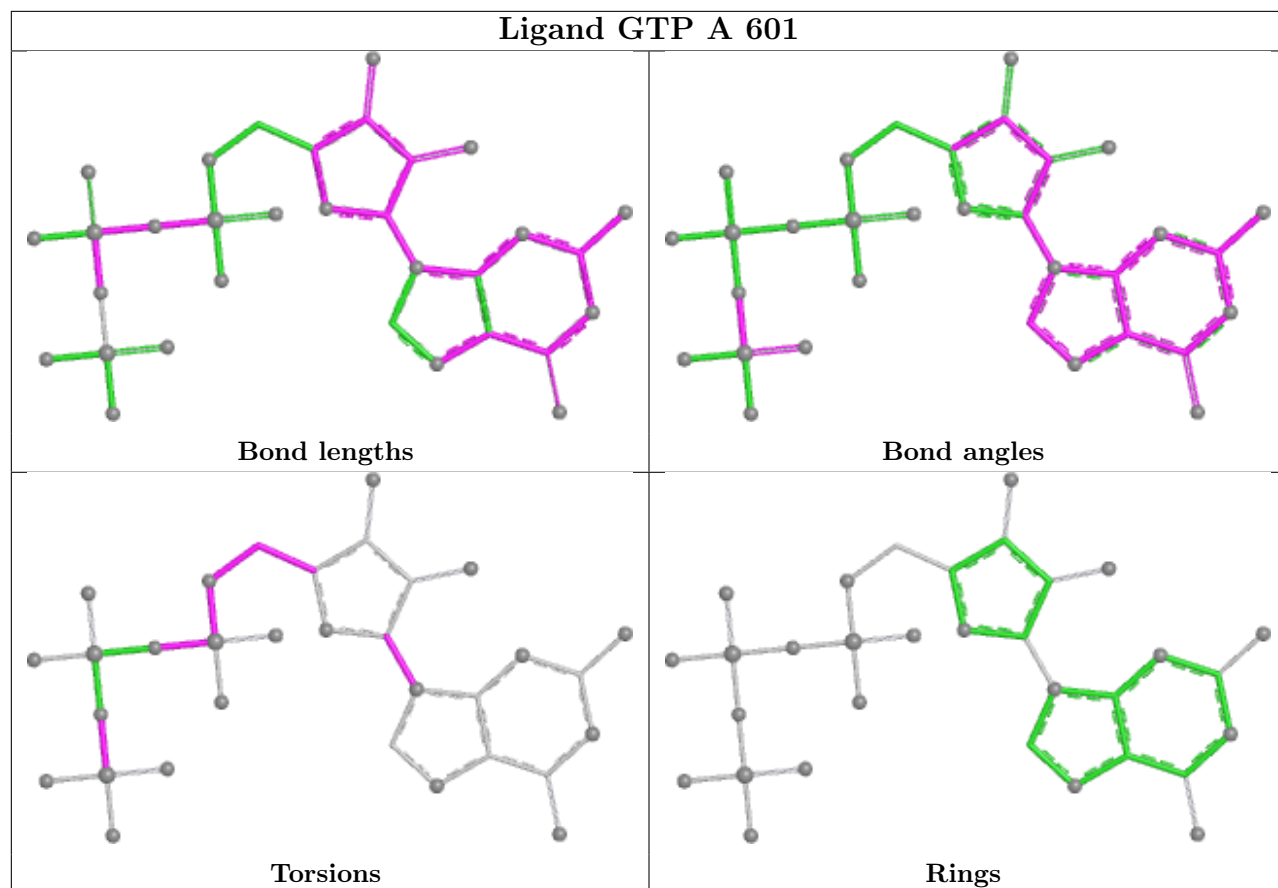
Ligand GTP E 602

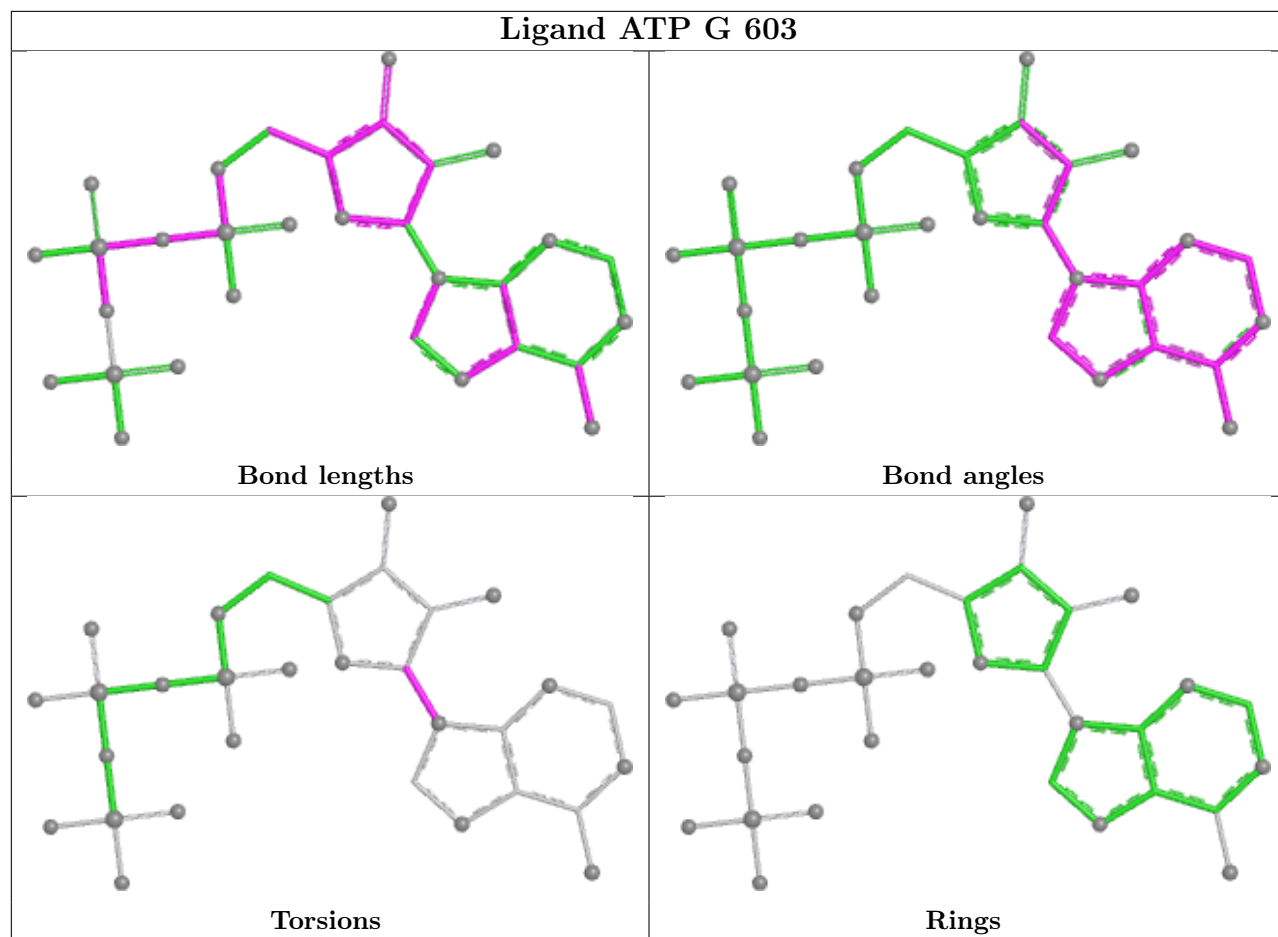


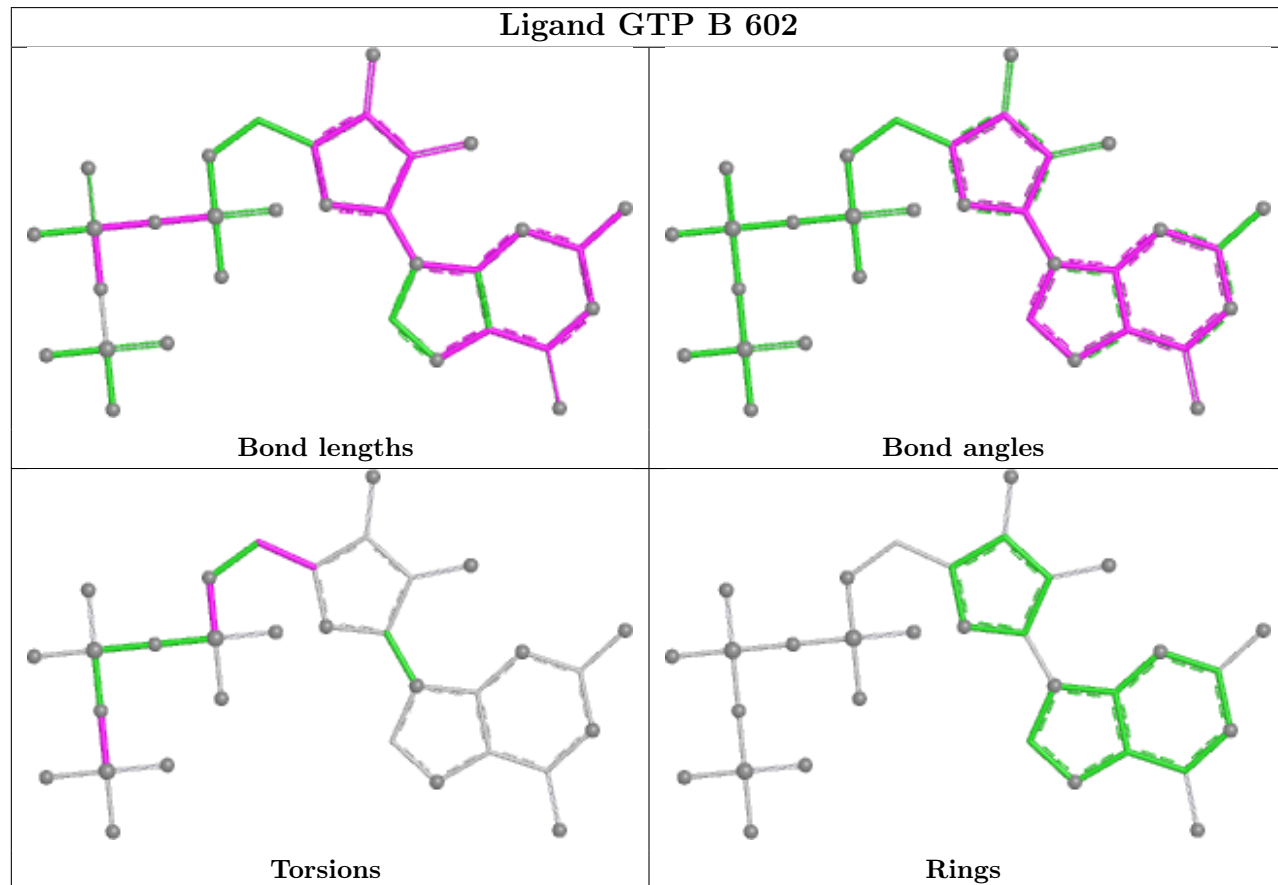
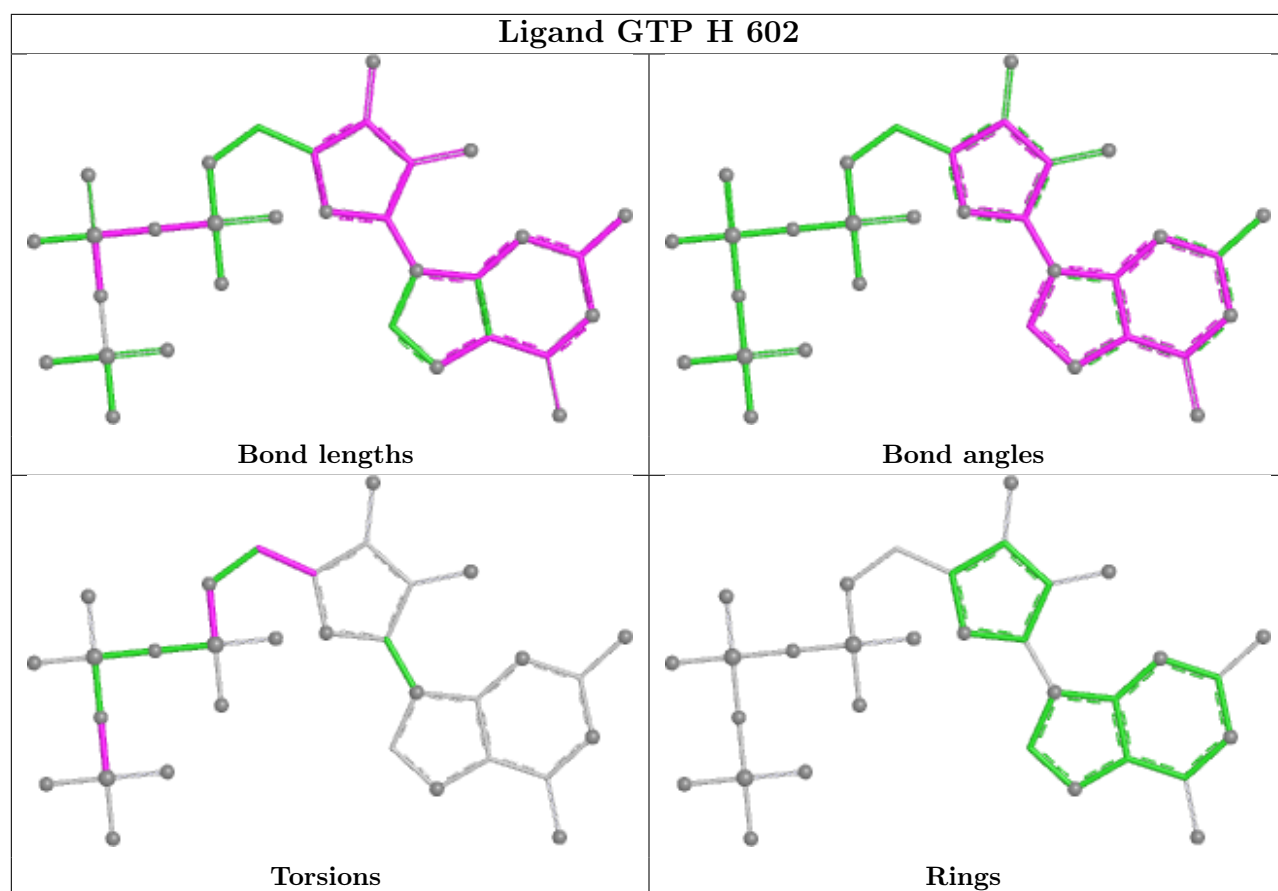
Ligand GTP F 602

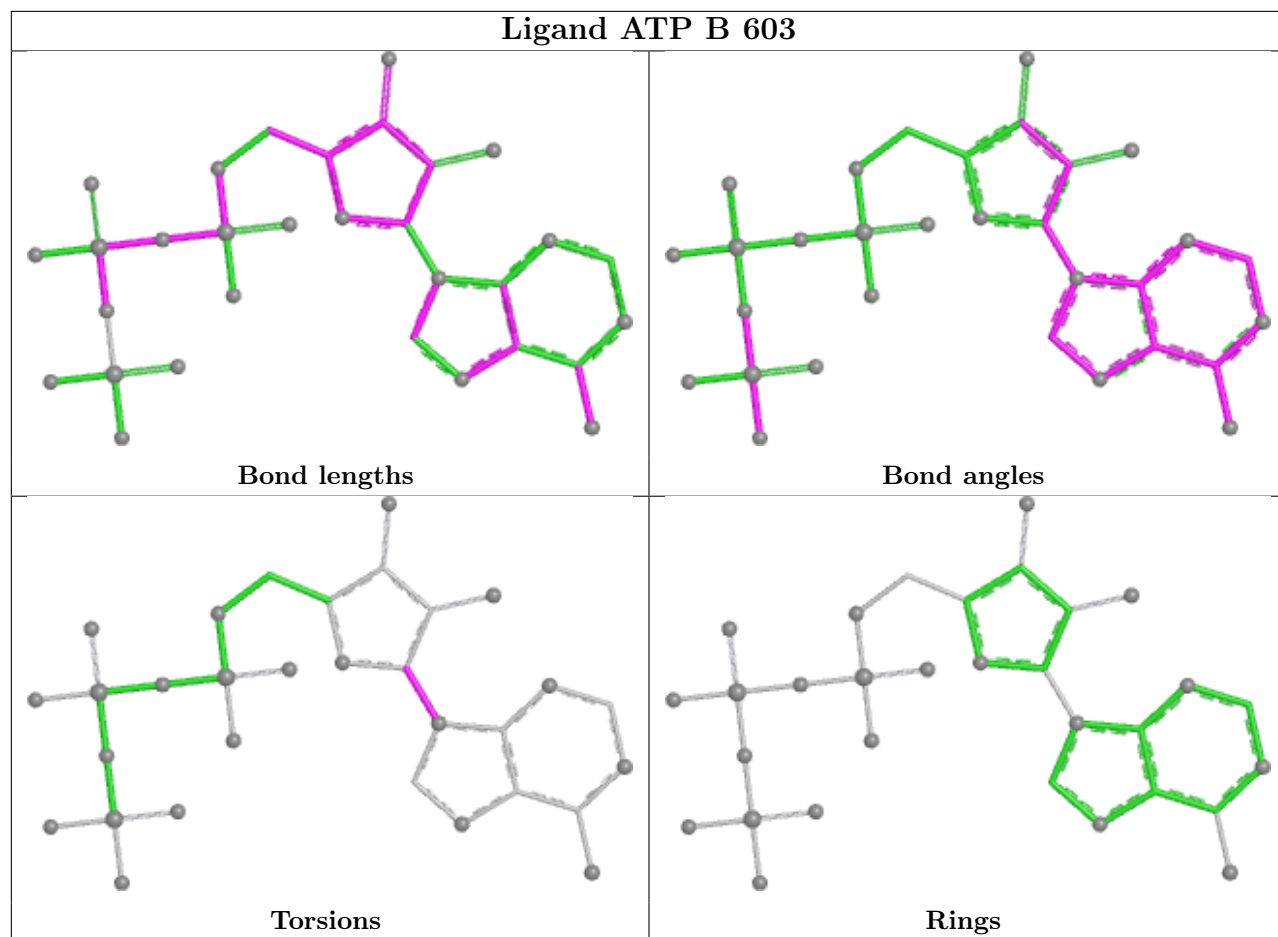


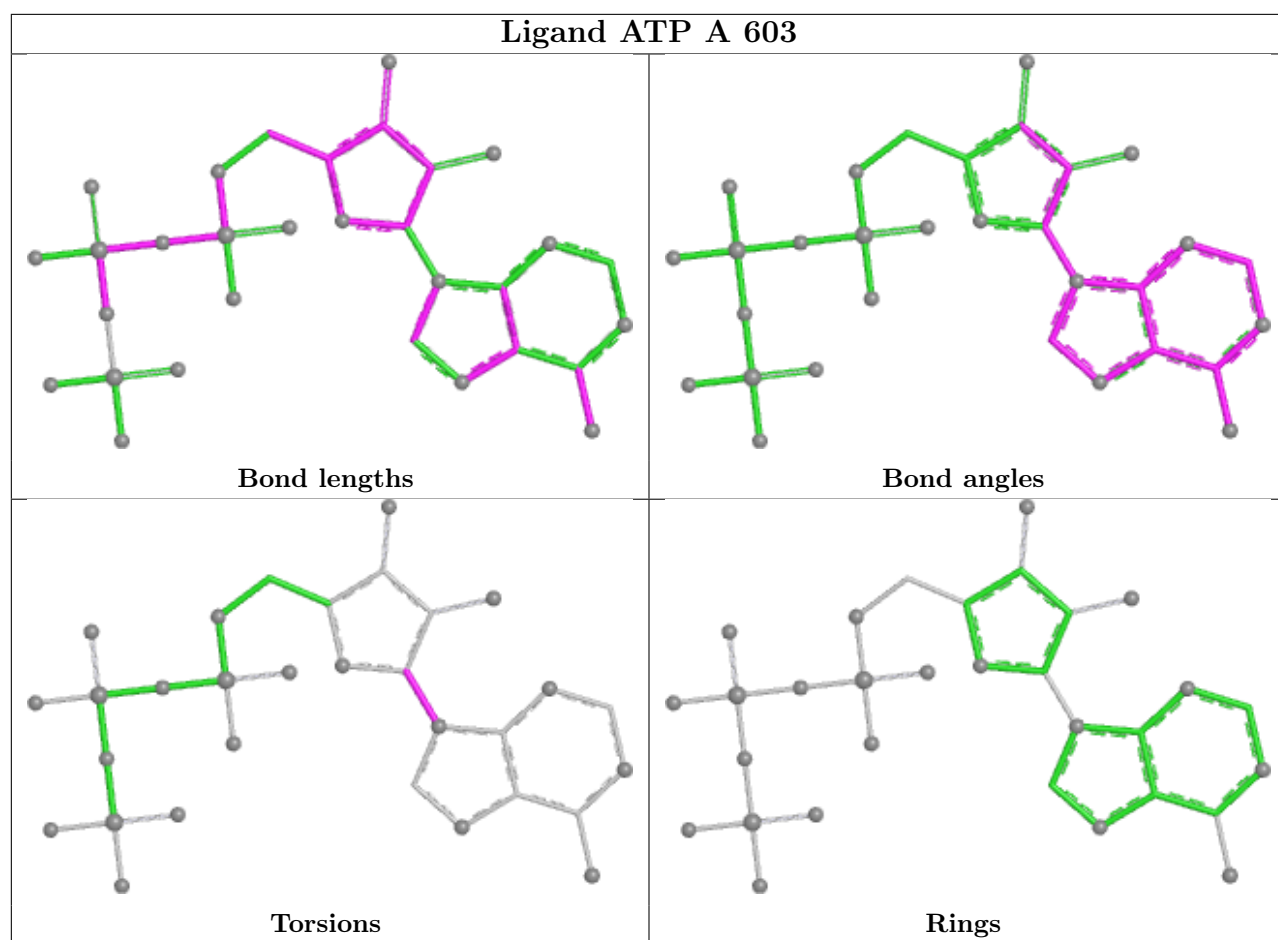


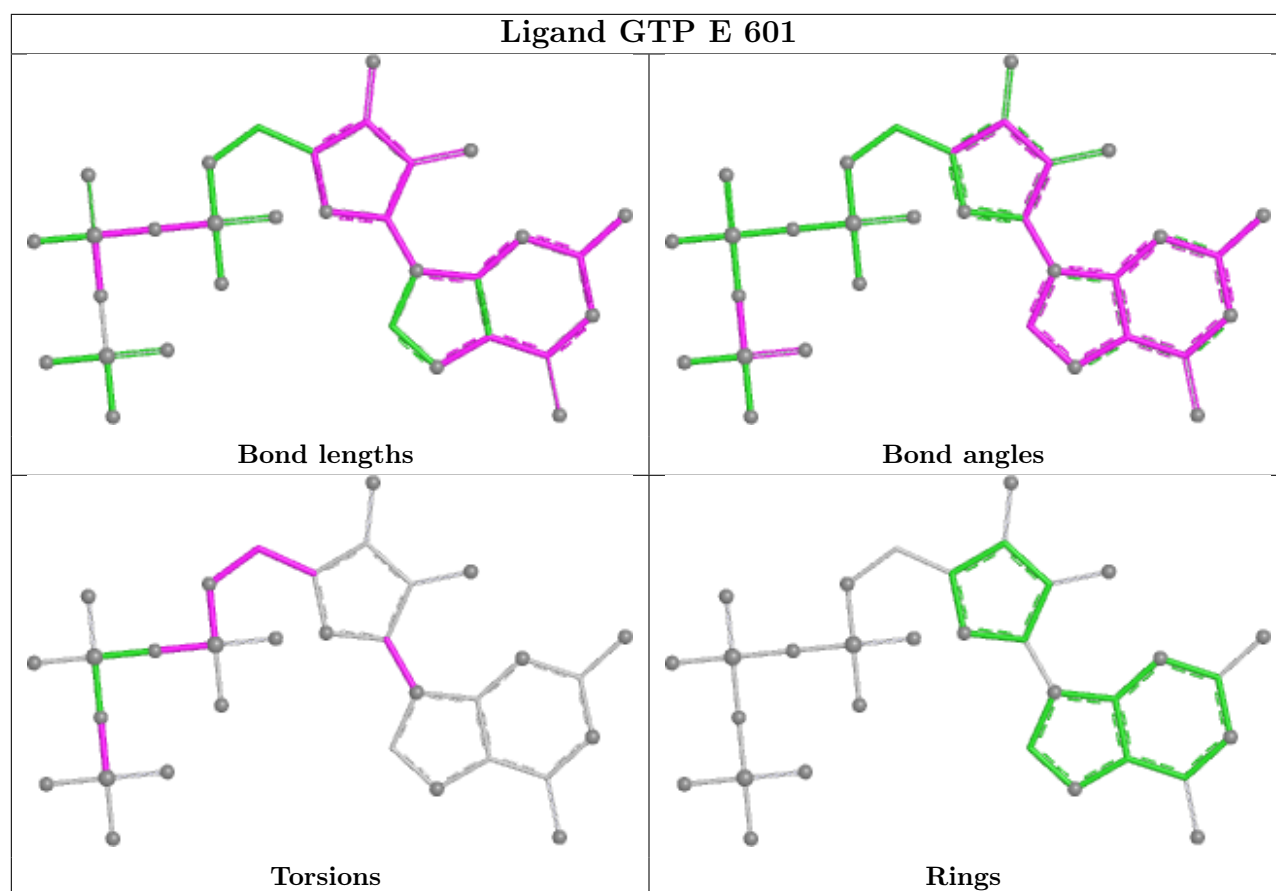












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

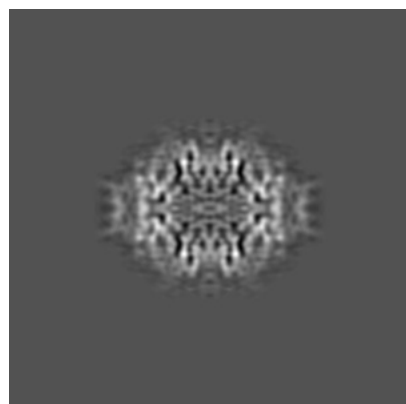
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20725. These allow visual inspection of the internal detail of the map and identification of artifacts.

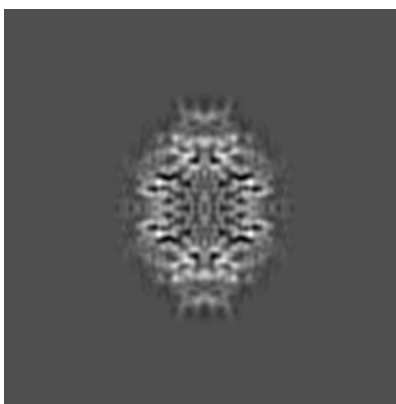
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

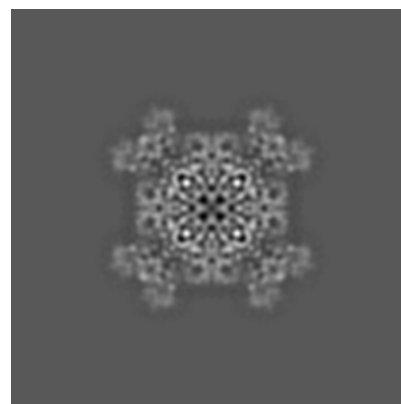
6.1.1 Primary map



X

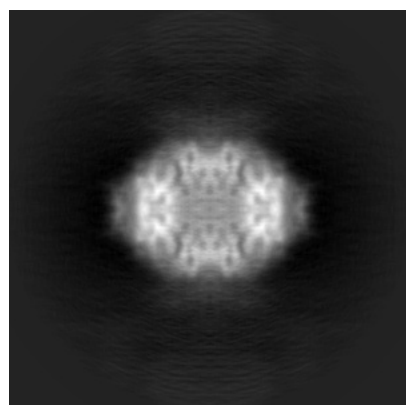


Y

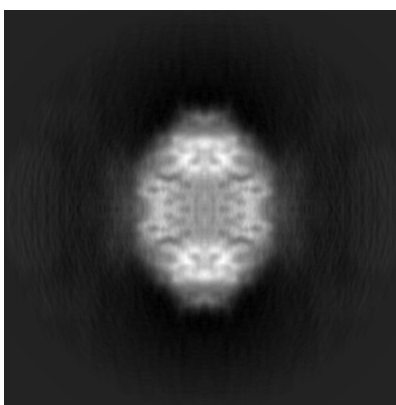


Z

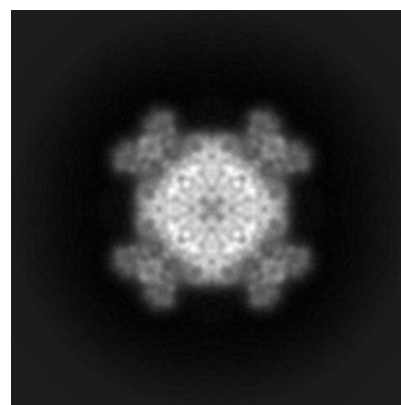
6.1.2 Raw map



X



Y

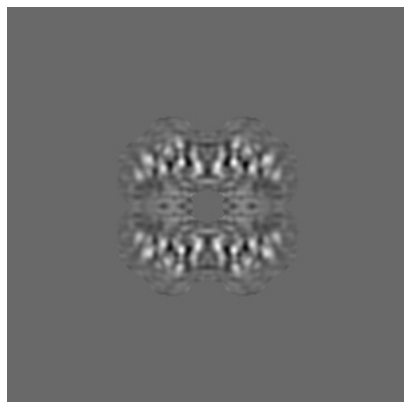


Z

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

6.2 Central slices [i](#)

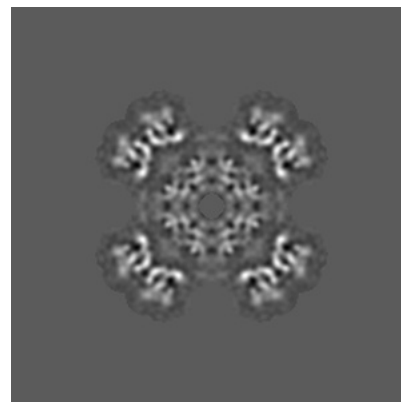
6.2.1 Primary map



X Index: 128

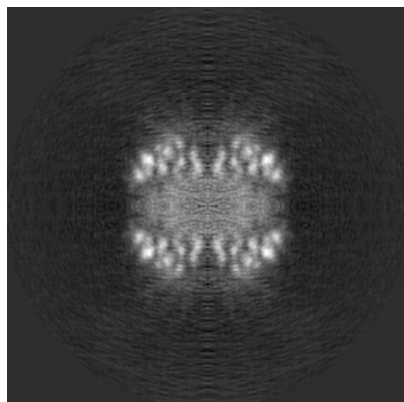


Y Index: 128

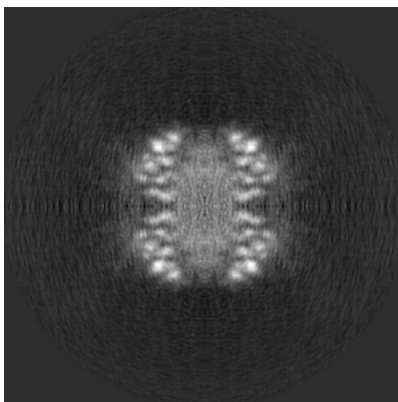


Z Index: 128

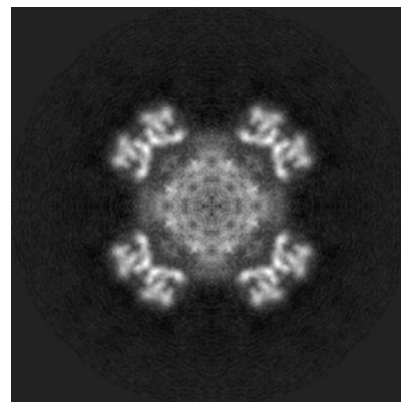
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

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

6.3 Largest variance slices [i](#)

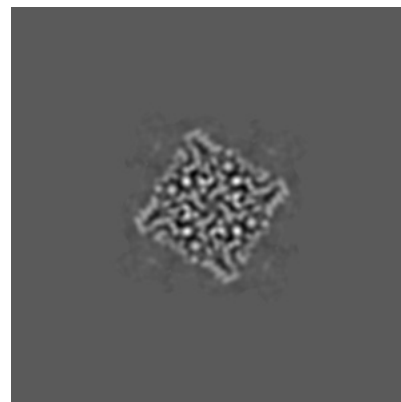
6.3.1 Primary map



X Index: 144

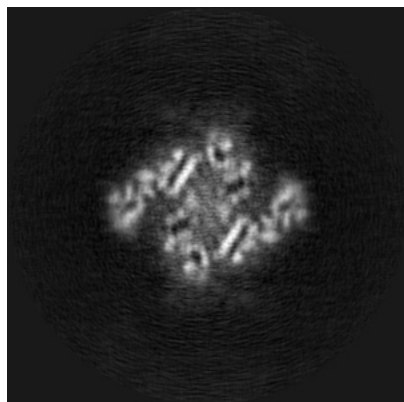


Y Index: 144

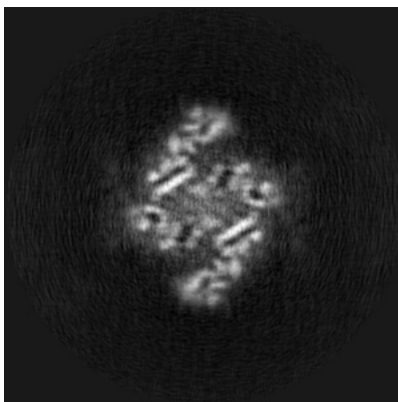


Z Index: 156

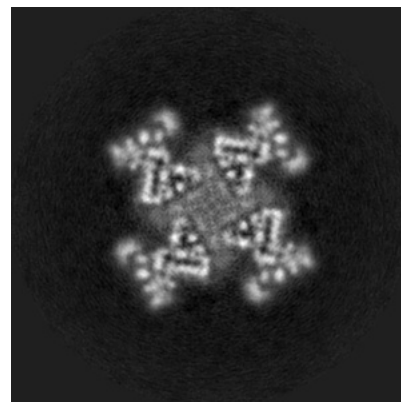
6.3.2 Raw map



X Index: 153



Y Index: 103

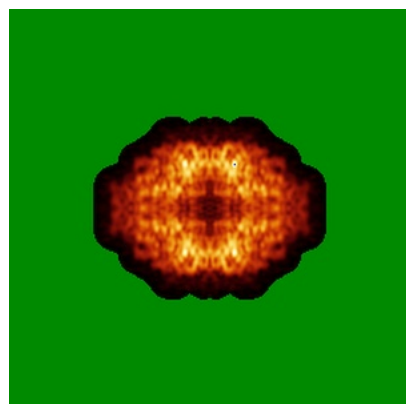


Z Index: 117

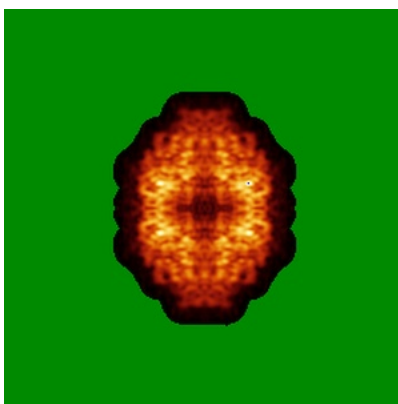
The images above show the largest variance slices of the map in three orthogonal directions.

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

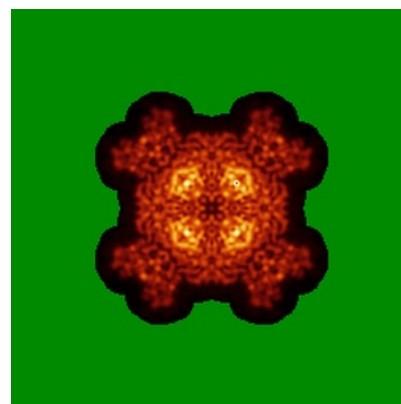
6.4.1 Primary map



X

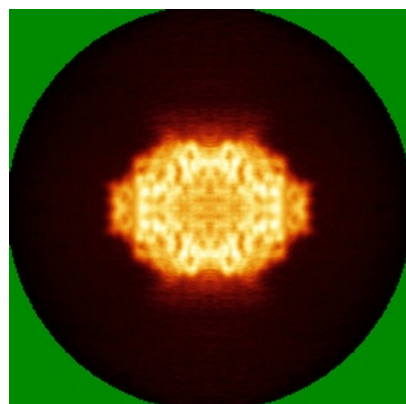


Y

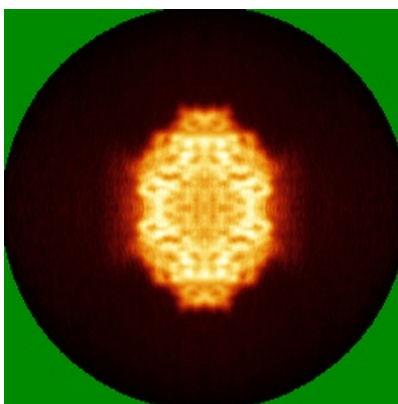


Z

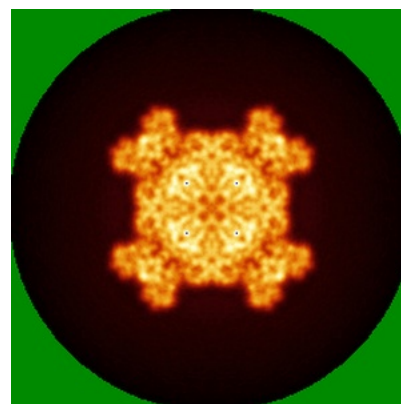
6.4.2 Raw map



X



Y



Z

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

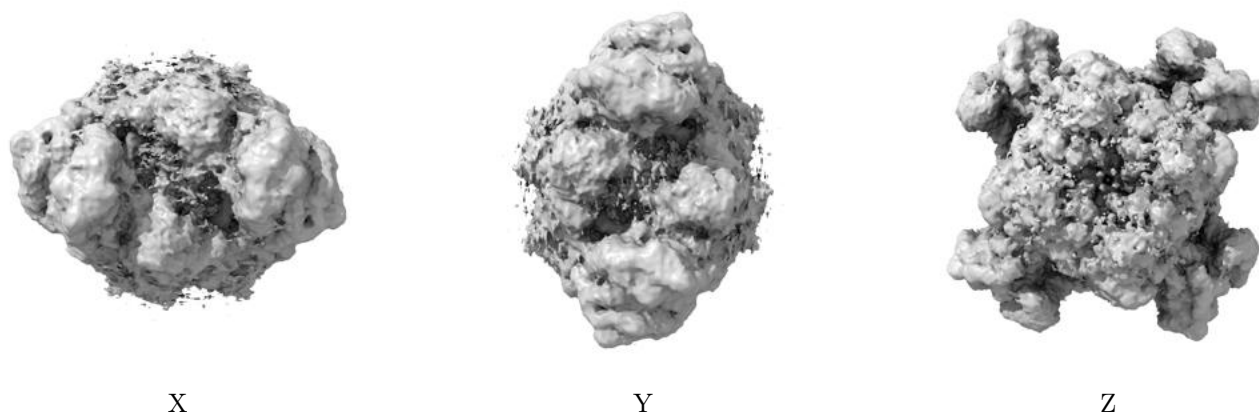
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

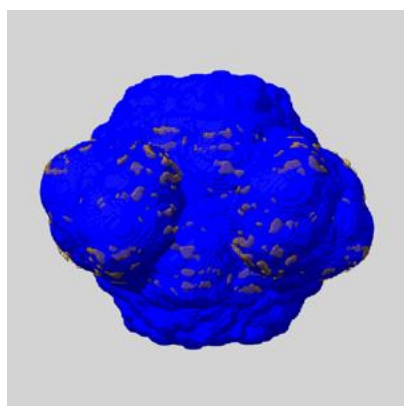
6.6 Mask visualisation [i](#)

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

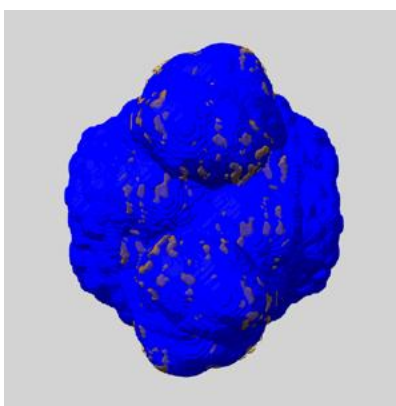
A mask typically either:

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

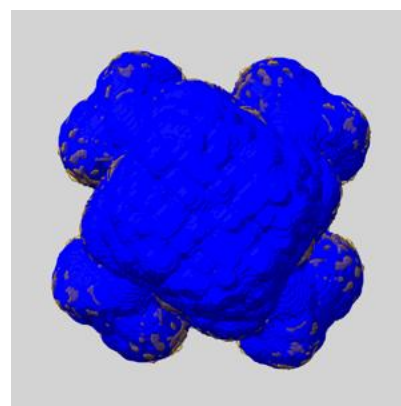
6.6.1 emd_20725_msk_1.map [i](#)



X



Y

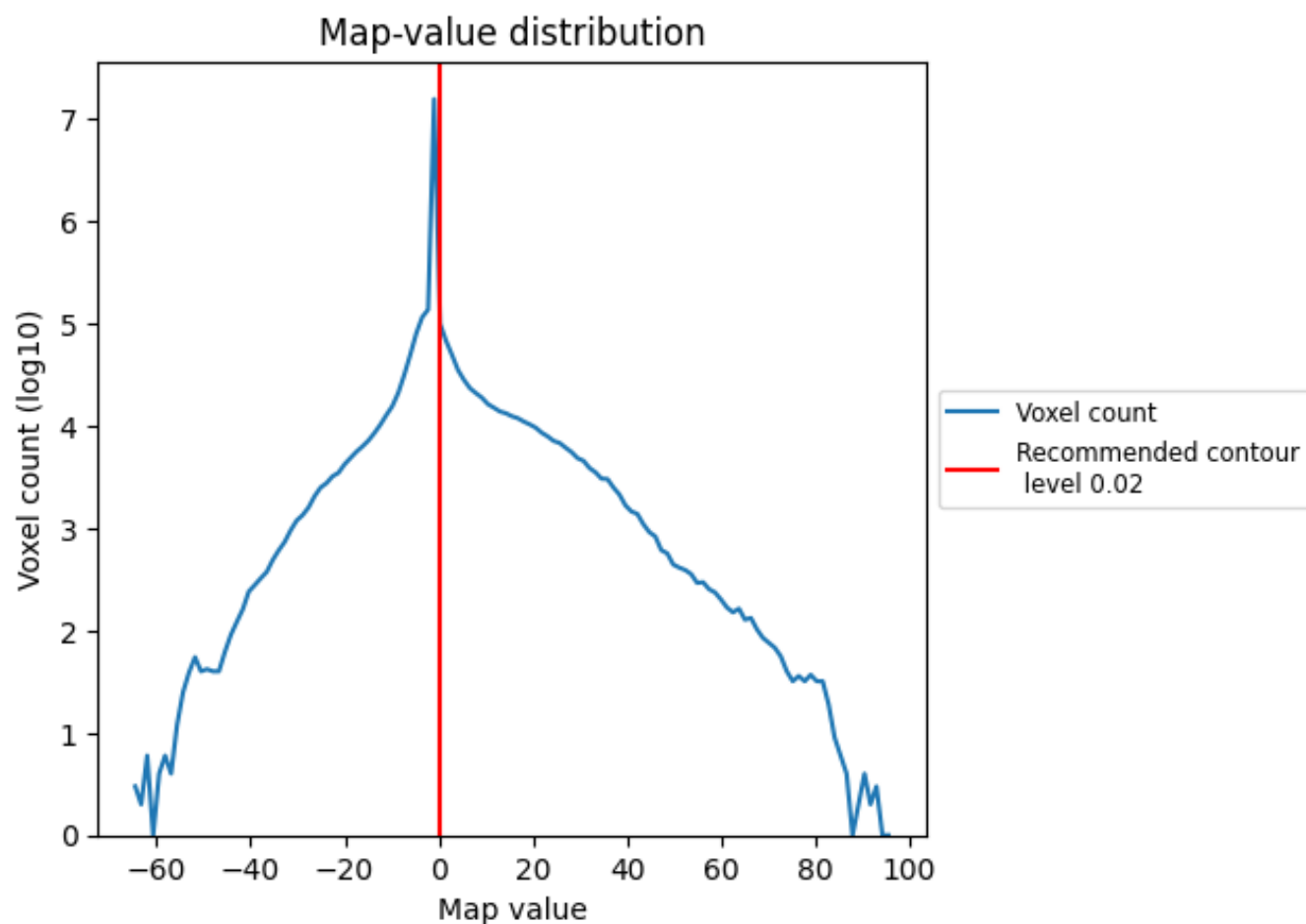


Z

7 Map analysis [i](#)

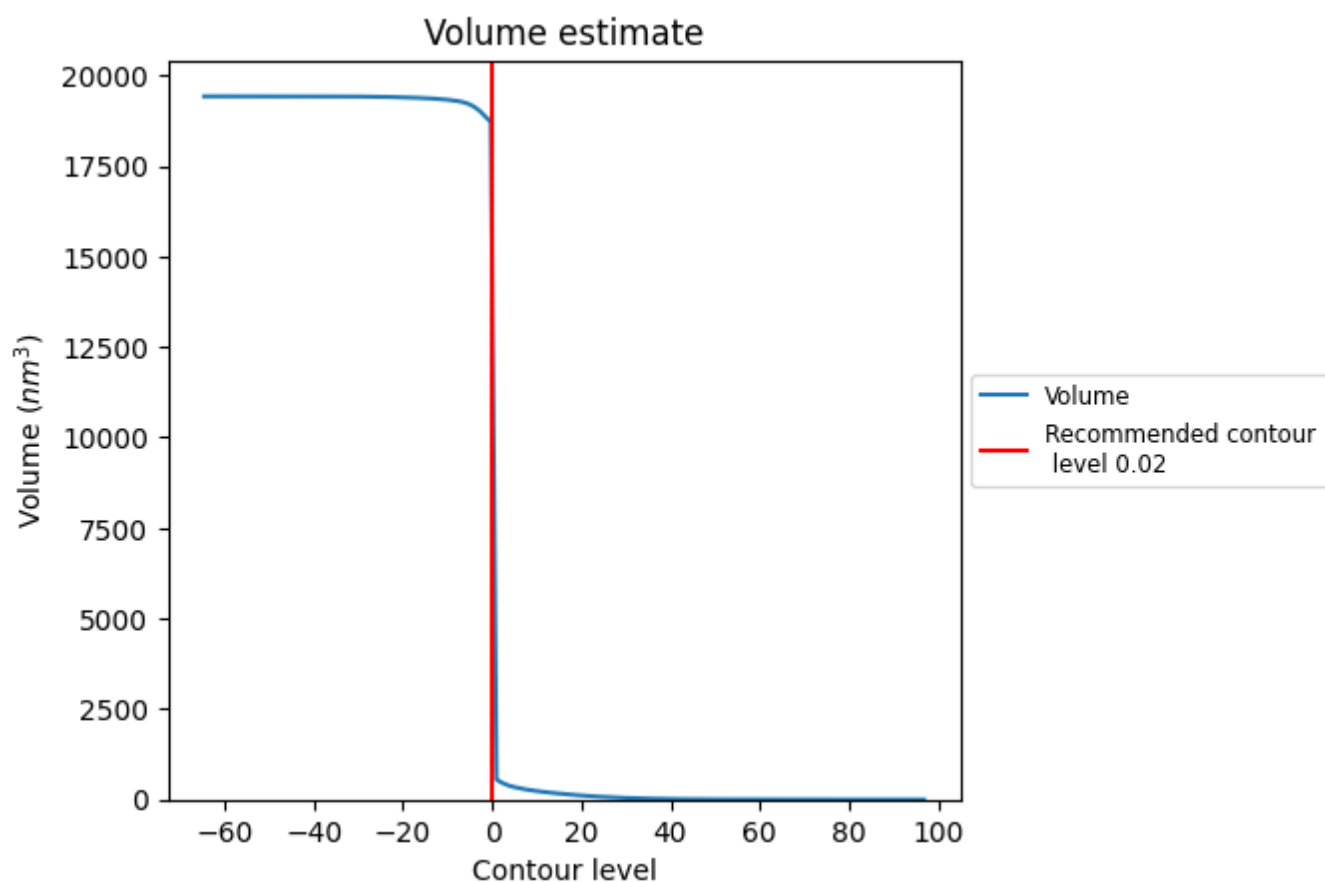
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

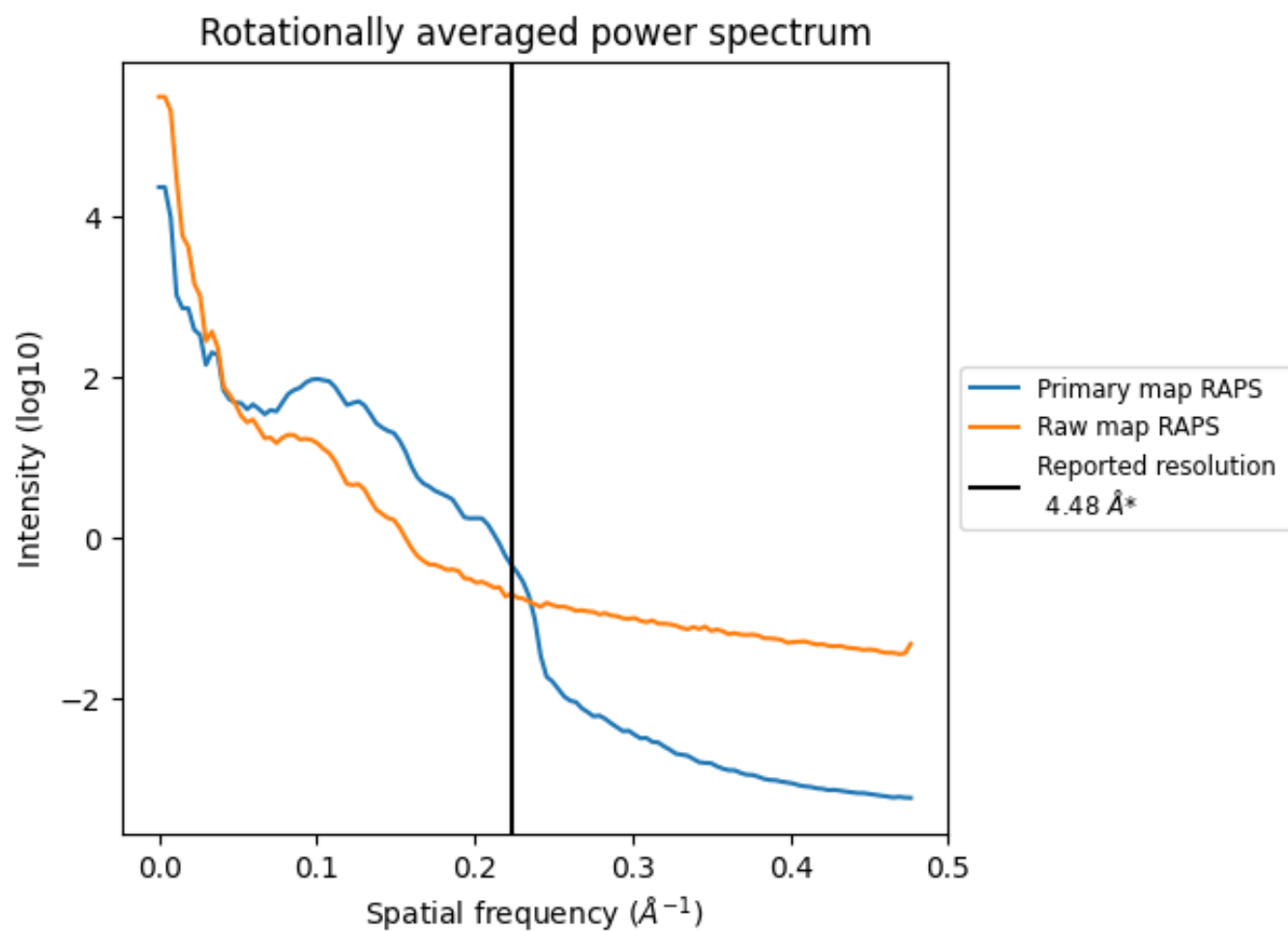
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 14672 nm³; this corresponds to an approximate mass of 13254 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

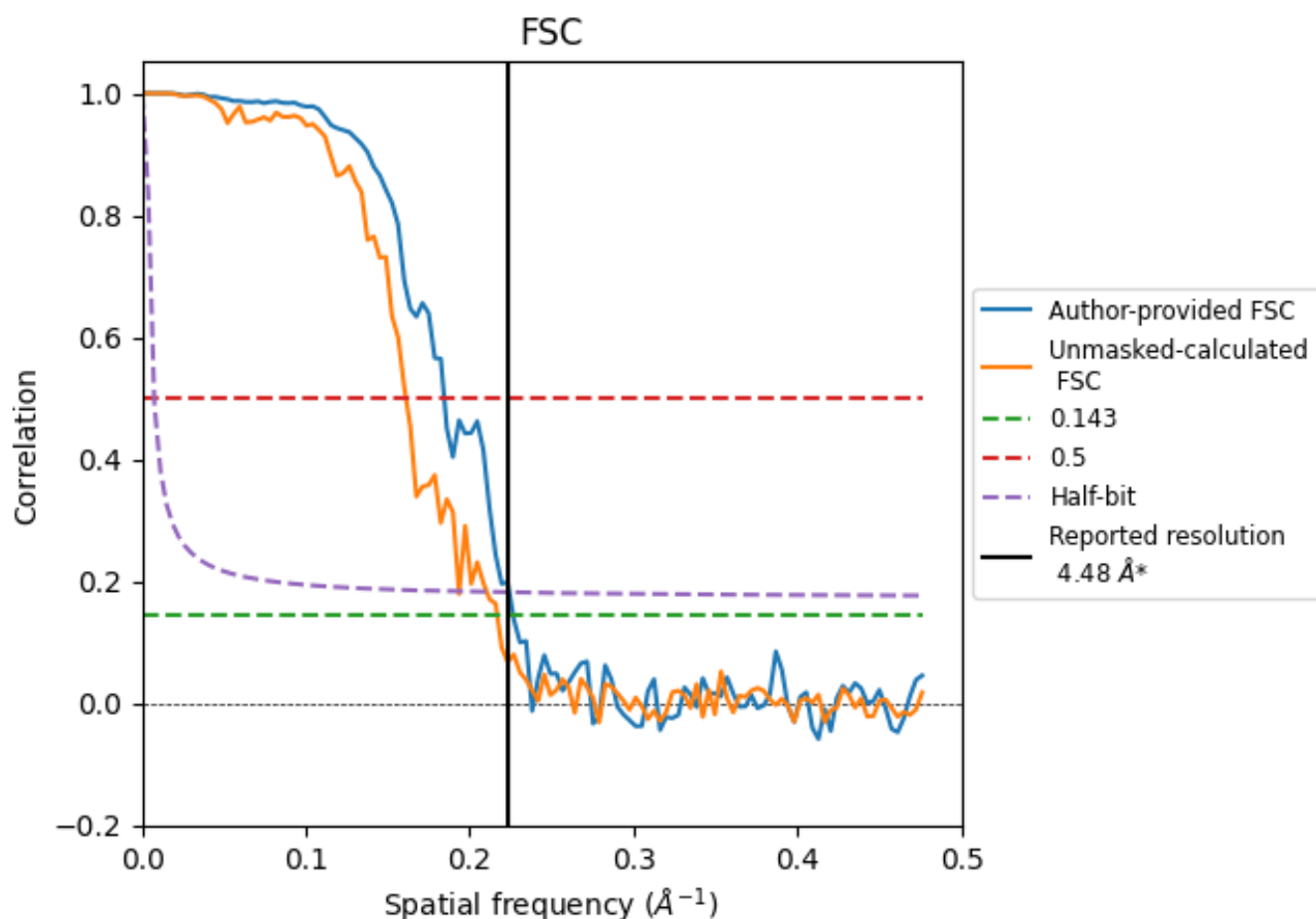


*Reported resolution corresponds to spatial frequency of 0.223 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.223 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

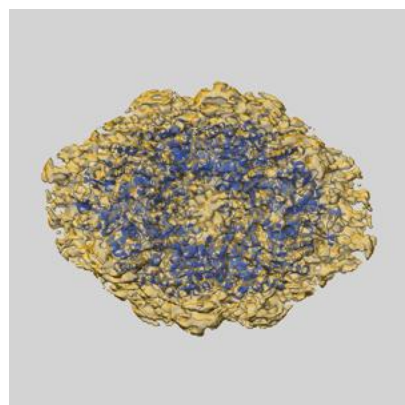
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.48	-	-
Author-provided FSC curve	4.41	5.42	4.46
Unmasked-calculated*	4.61	6.21	5.17

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

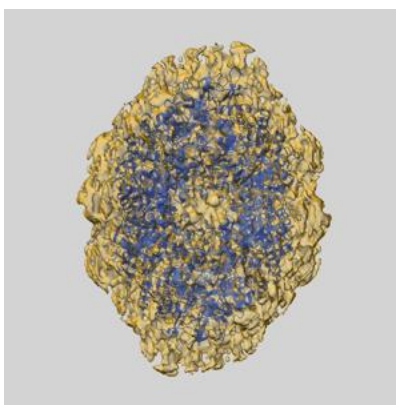
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20725 and PDB model 6UC2. Per-residue inclusion information can be found in section [3](#) on page [8](#).

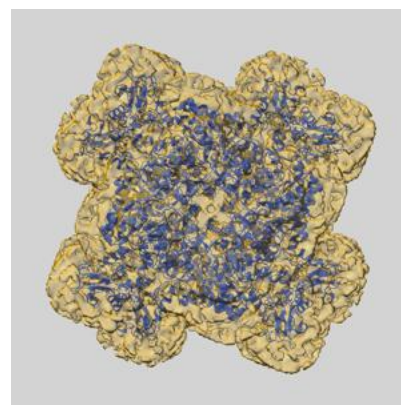
9.1 Map-model overlay [i](#)



X



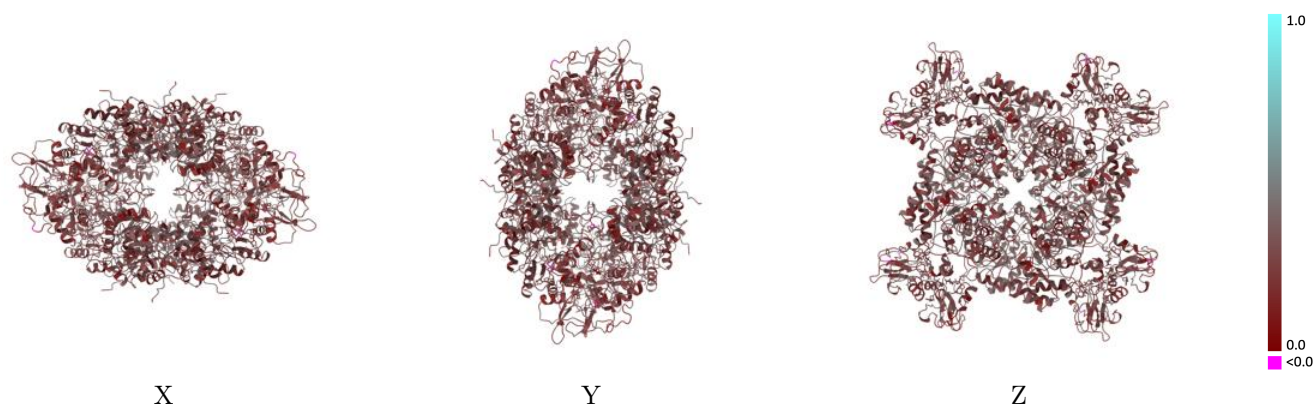
Y



Z

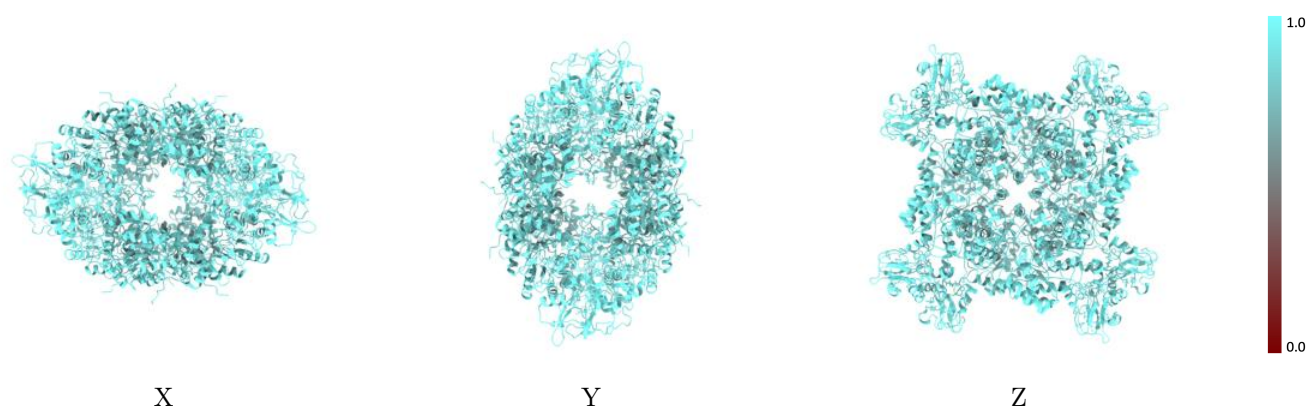
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



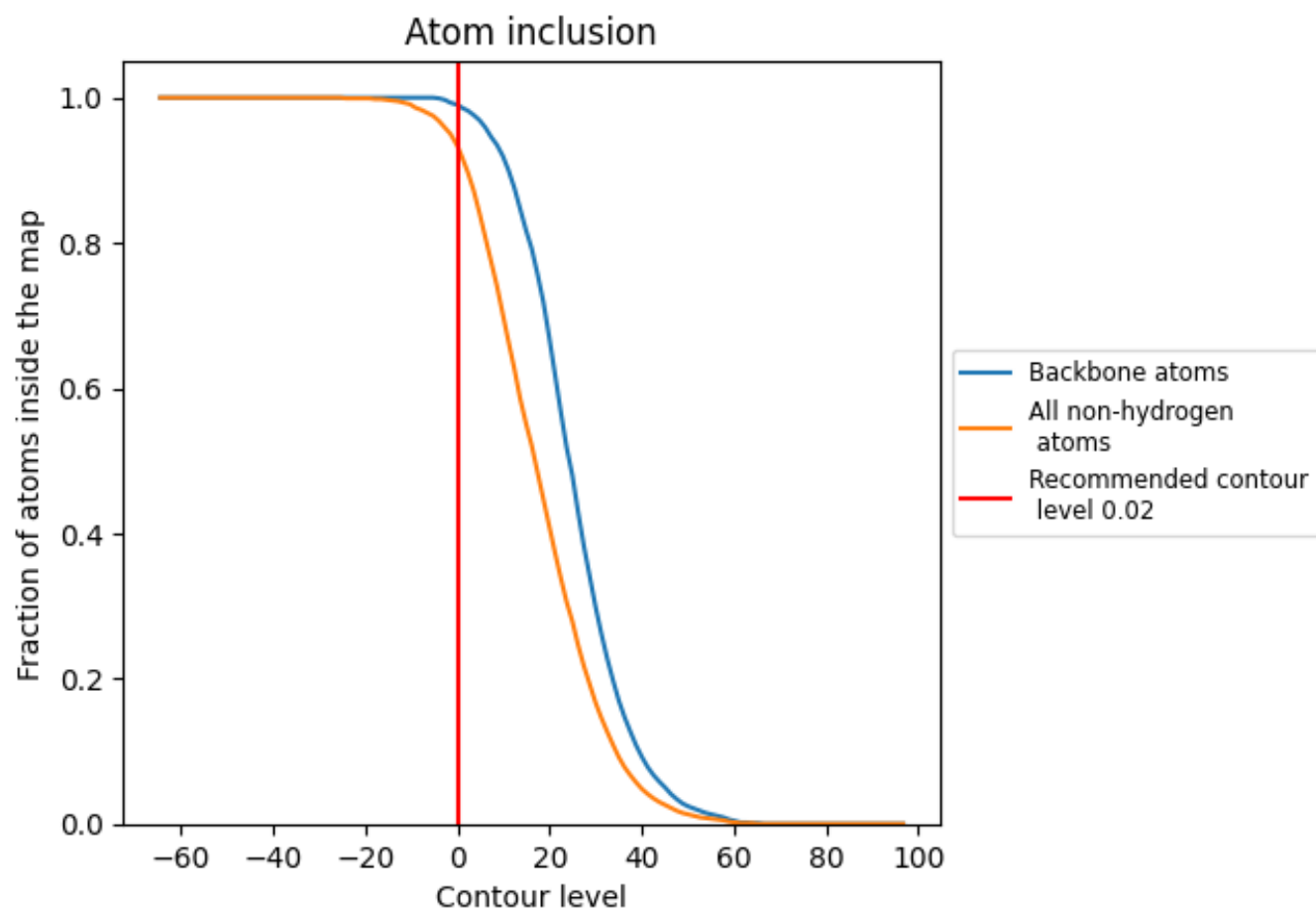
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9330	0.2740
A	0.9320	0.2740
B	0.9310	0.2740
C	0.9310	0.2740
D	0.9340	0.2760
E	0.9320	0.2740
F	0.9340	0.2730
G	0.9330	0.2740
H	0.9370	0.2750

1.0

0.0

<0.0