



Full wwPDB EM Validation Report ⓘ

Jul 19, 2026 – 10:36 PM EDT

PDB ID : 9ZQT / pdb_00009zqt
EMDB ID : EMD-74581
Title : Composite map of the bGDH di-hexamer in liganded form
Authors : Shan, Z.; Lyumkis, D.
Deposited on : 2025-12-19
Resolution : 3.50 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:

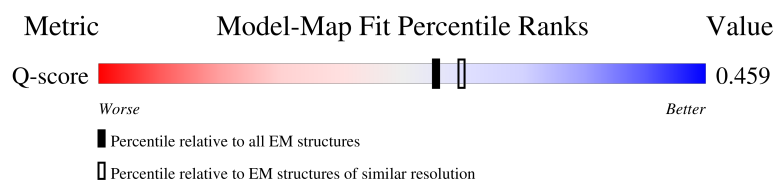
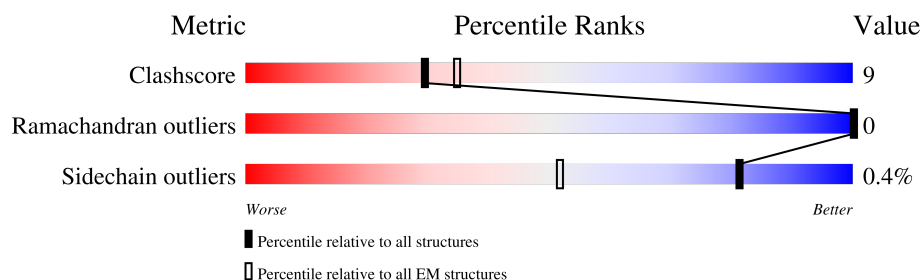
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance

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

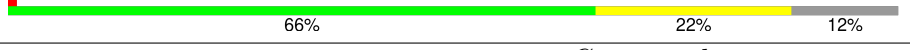
The reported resolution of this entry is 3.50 Å.

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.



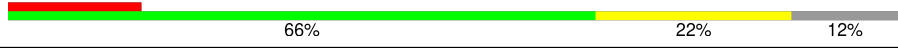
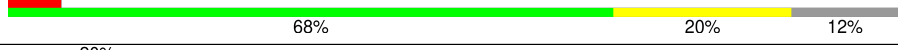
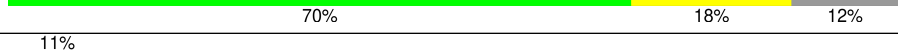
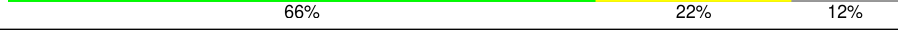
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	558	
1	B	558	
1	C	558	
1	D	558	

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Mol	Chain	Length	Quality of chain
1	E	558	 70% 18% 12%
1	F	558	 68% 20% 12%
1	G	558	 15% 66% 22% 12%
1	H	558	 6% 68% 20% 12%
1	I	558	 20% 70% 18% 12%
1	J	558	 20% 71% 18% 12%
1	K	558	 18% 70% 18% 12%
1	L	558	 11% 66% 22% 12%

2 Entry composition

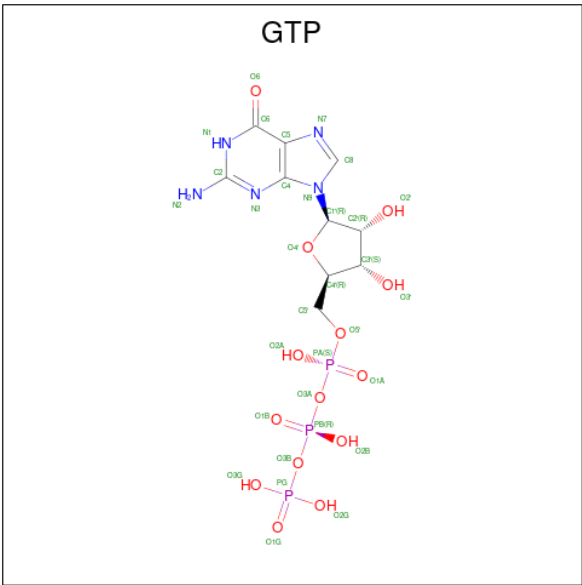
There are 4 unique types of molecules in this entry. The entry contains 47760 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutamate dehydrogenase 1, mitochondrial.

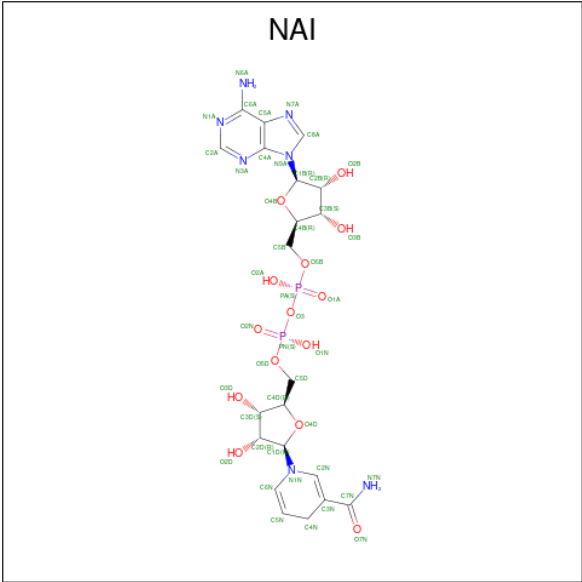
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	B	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	C	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	D	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	E	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	F	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	G	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	H	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	I	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	J	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	K	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		
1	L	493	Total	C	N	O	S	0	0
			3855	2437	676	723	19		

- 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	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	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	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	H	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	I	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	J	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	K	1	Total	C	N	O	P	0
			32	10	5	14	3	
2	L	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 3 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



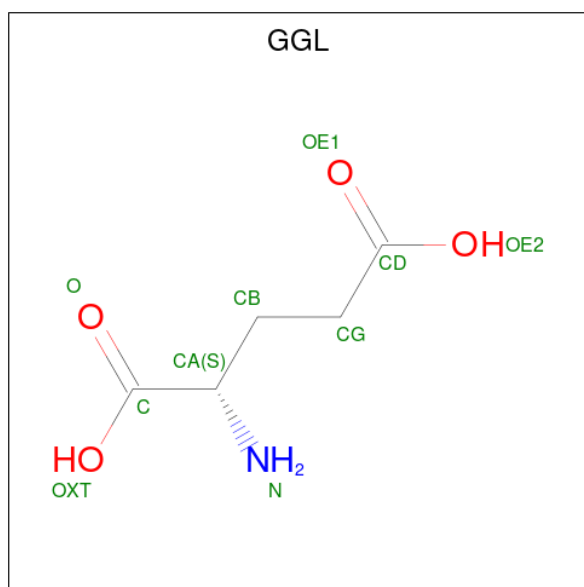
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	A	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	B	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	B	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	C	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	C	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	D	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	D	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	E	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	E	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	F	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	F	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	G	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	G	1	Total	C	N	O	P	0
			44	21	7	14	2	

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Mol	Chain	Residues	Atoms					AltConf
3	H	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	H	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	I	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	I	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	J	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	J	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	K	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	K	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	L	1	Total	C	N	O	P	0
			44	21	7	14	2	
3	L	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 4 is GAMMA-L-GLUTAMIC ACID (CCD ID: GGL) (formula: $C_5H_9NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			10	5	1	4	

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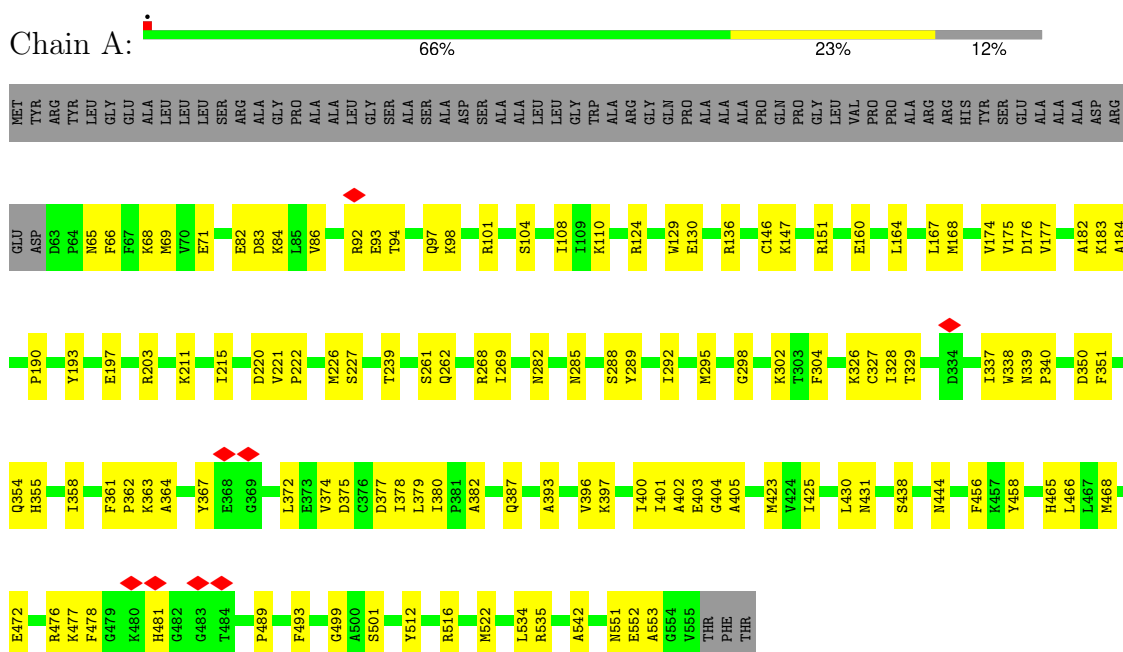
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Mol	Chain	Residues	Atoms				AltConf
4	B	1	Total 10	C 5	N 1	O 4	0
4	C	1	Total 10	C 5	N 1	O 4	0
4	D	1	Total 10	C 5	N 1	O 4	0
4	E	1	Total 10	C 5	N 1	O 4	0
4	F	1	Total 10	C 5	N 1	O 4	0

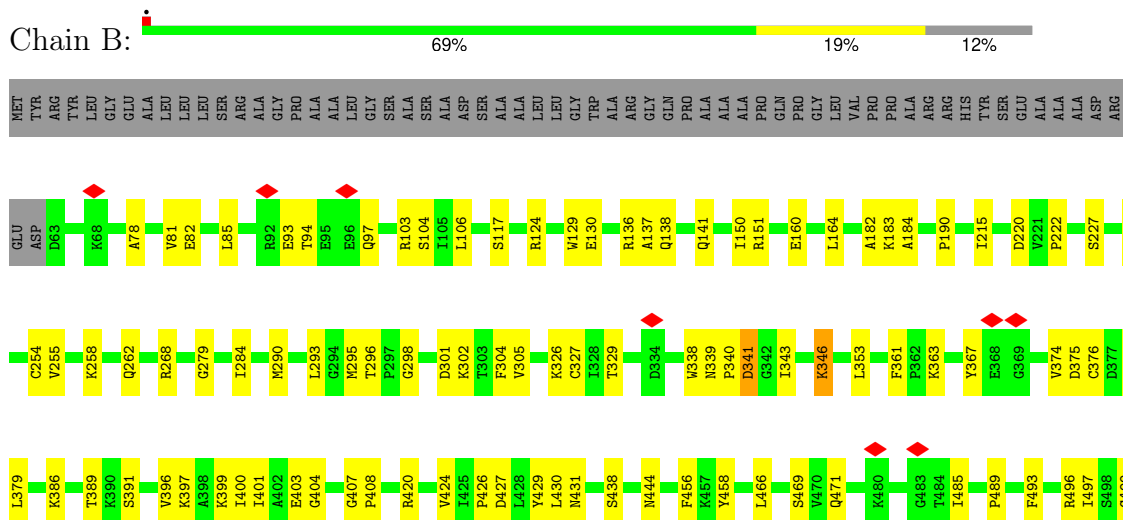
3 Residue-property plots

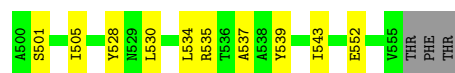
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

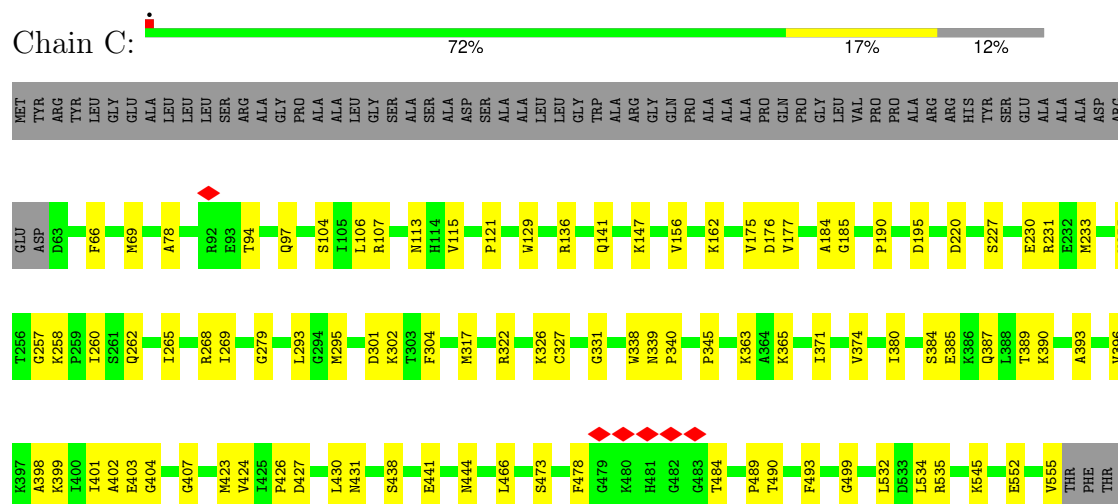


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

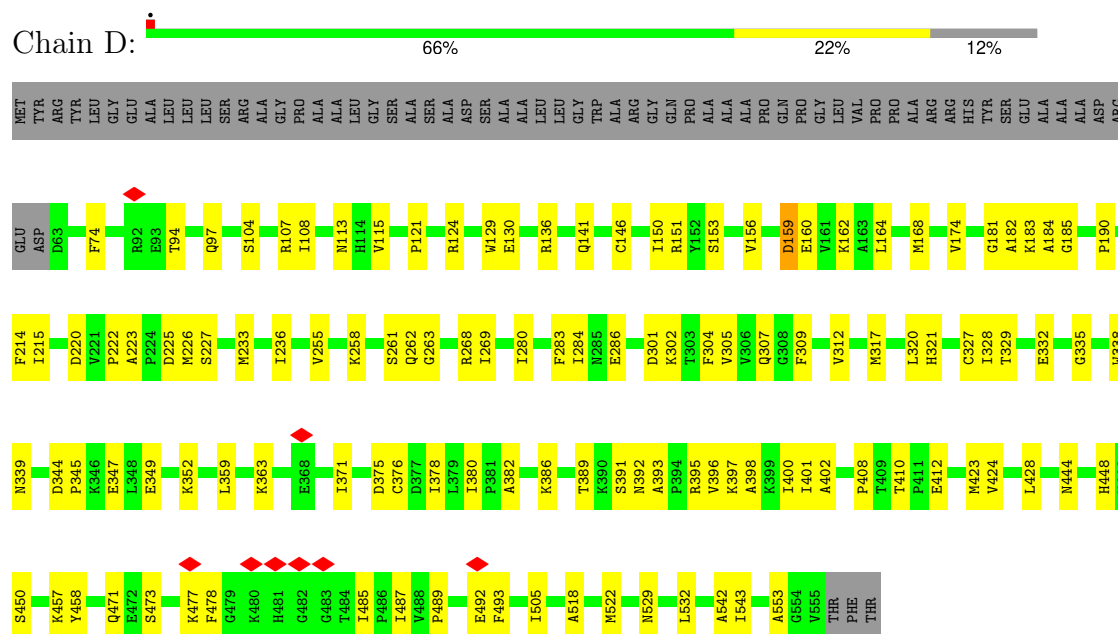




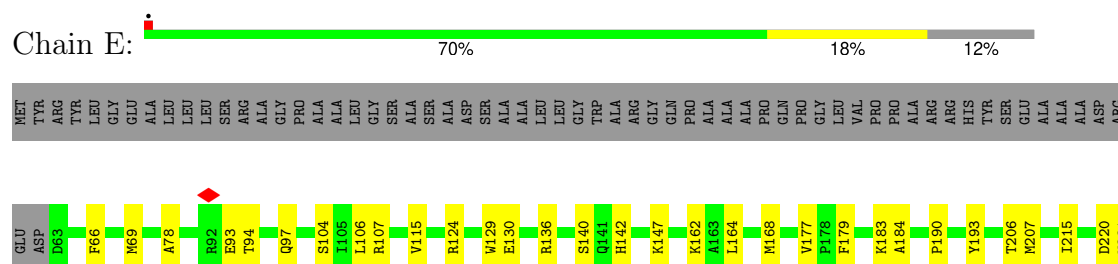
- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

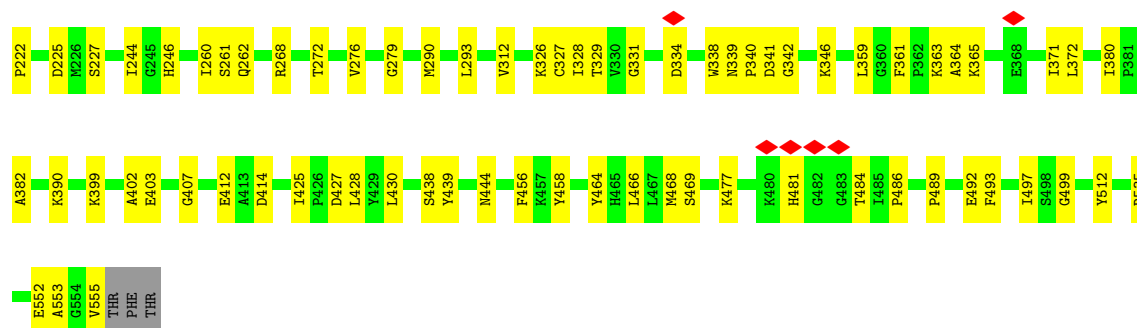


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

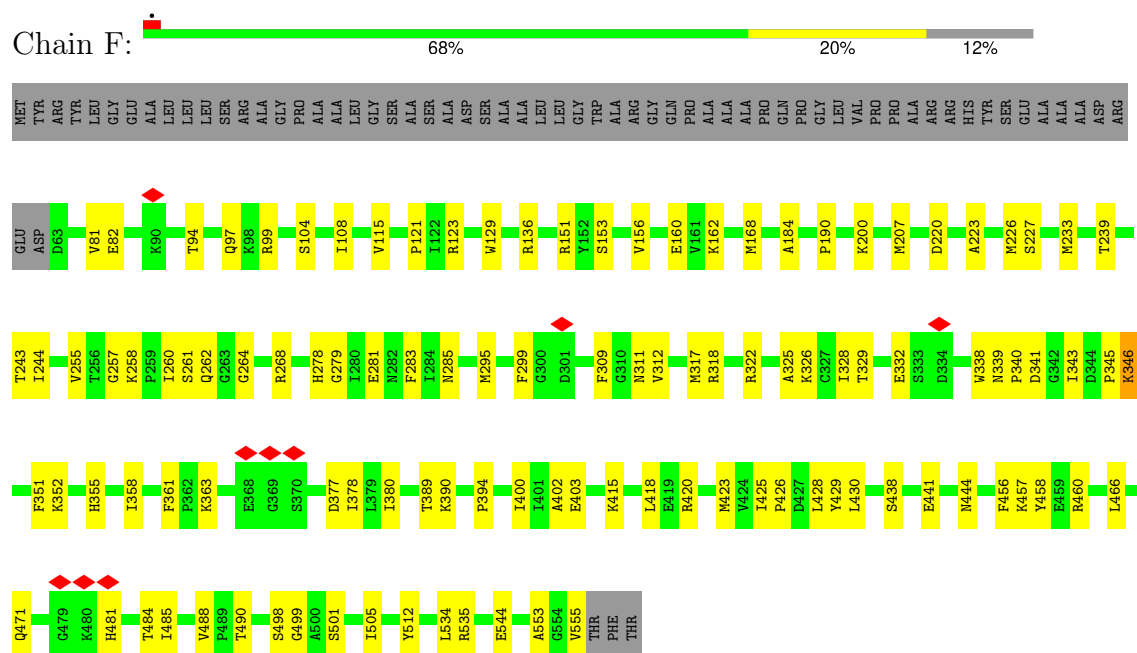


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

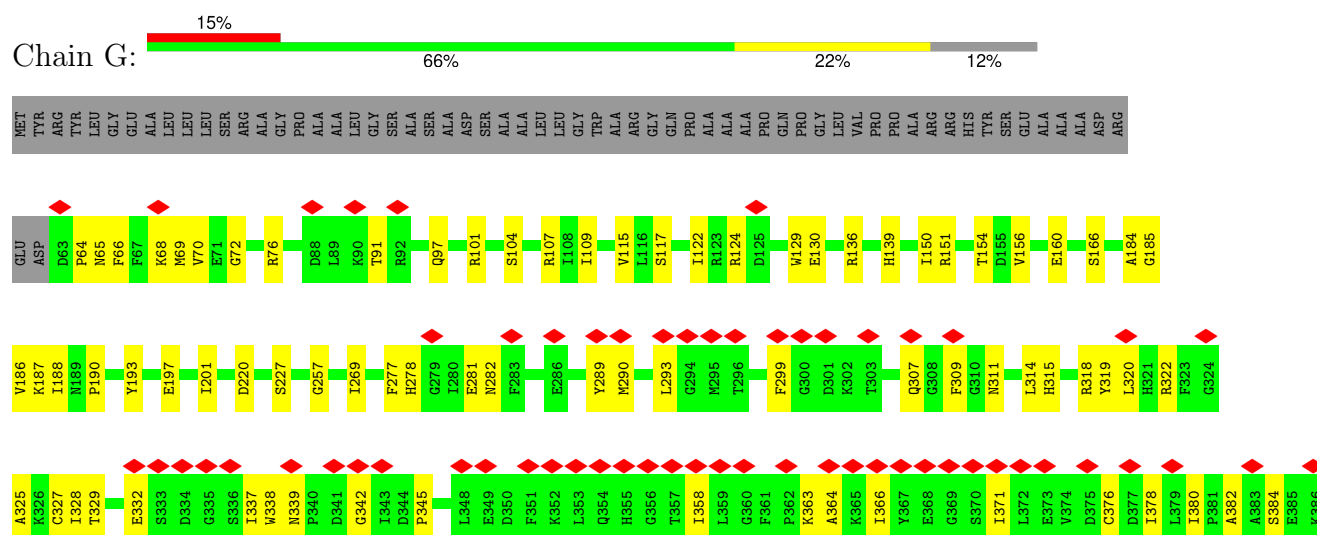


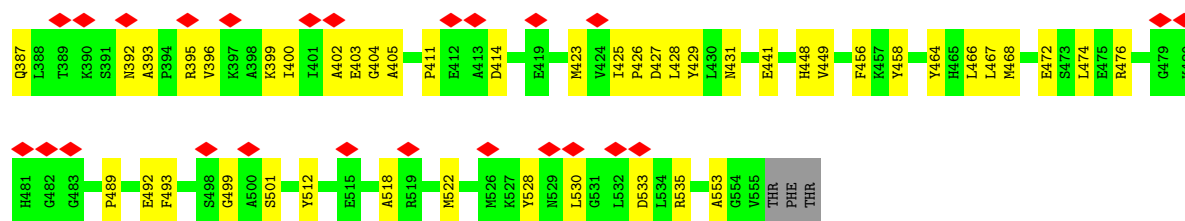


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

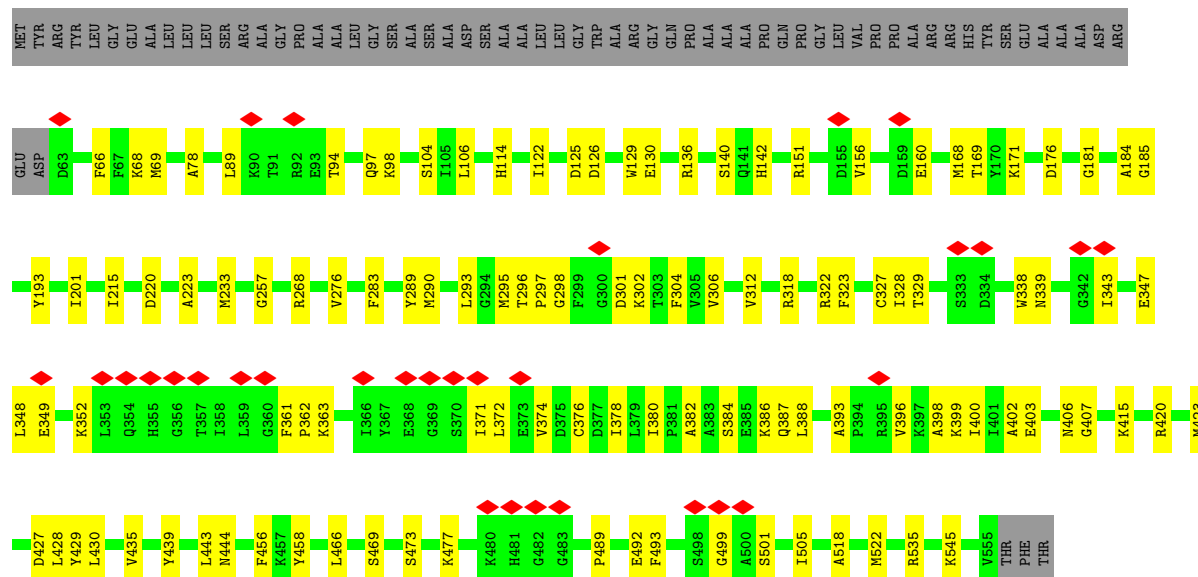


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial



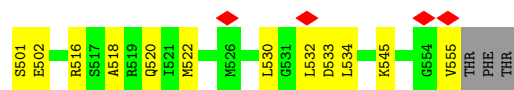


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

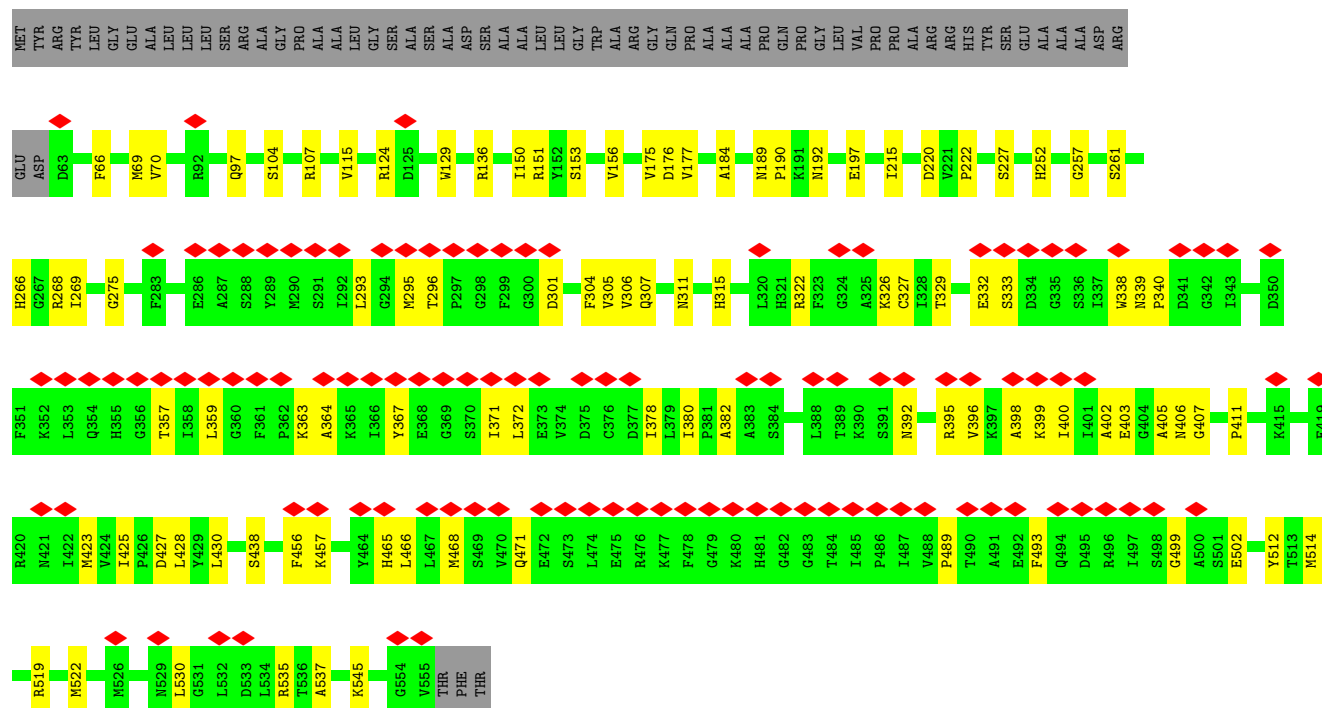


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

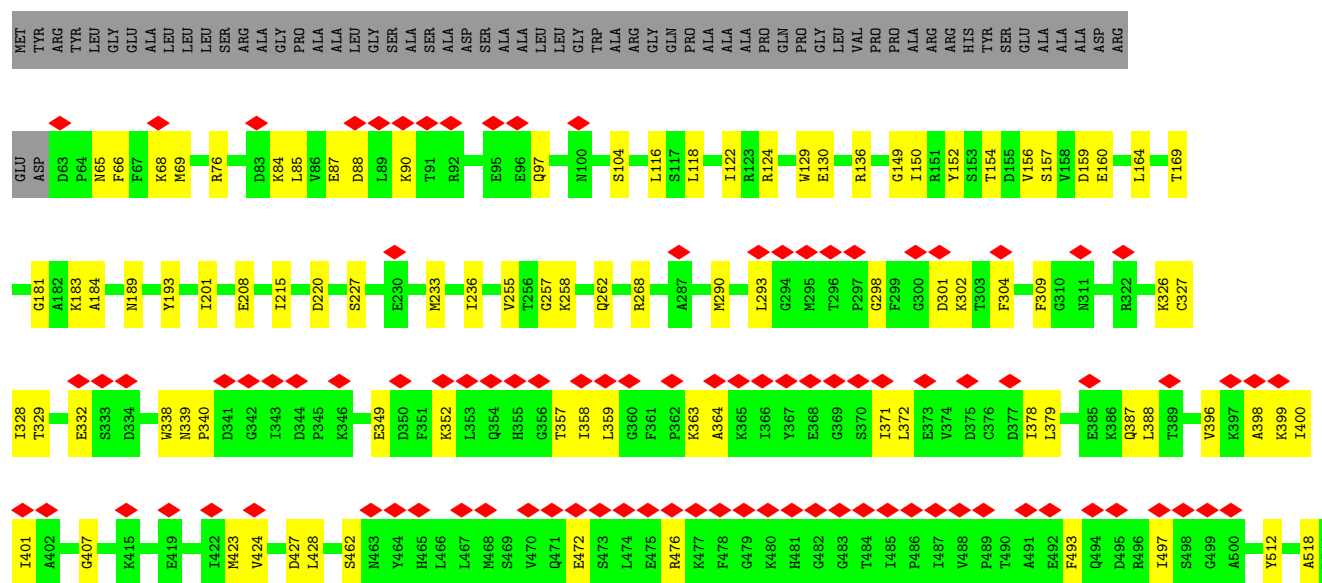


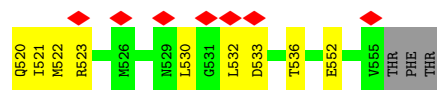


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

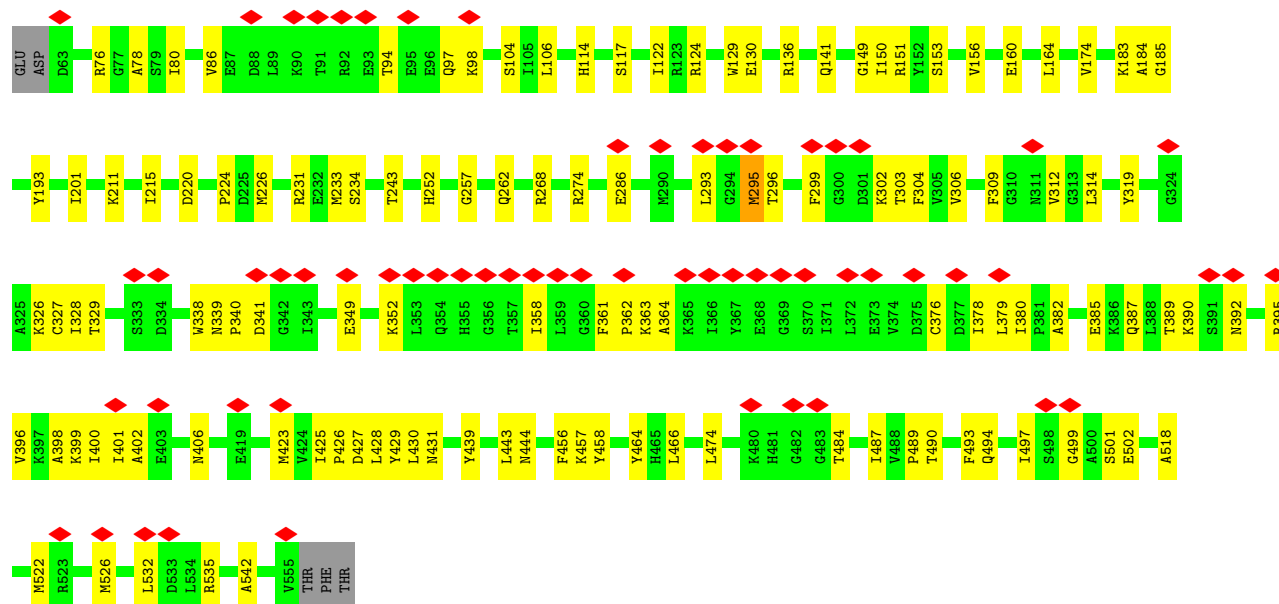
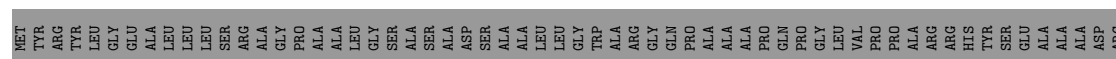


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial





- Molecule 1: Glutamate dehydrogenase 1, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97554	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.677	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.08	Depositor
Map size ($\text{\AA}$)	420.86398, 420.86398, 420.86398	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3152, 1.3152, 1.3152	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.24	0/3937	0.28	0/5315
1	B	0.25	0/3937	0.29	0/5315
1	C	0.25	0/3937	0.27	0/5315
1	D	0.25	0/3937	0.27	0/5315
1	E	0.24	0/3937	0.28	0/5315
1	F	0.24	0/3937	0.28	0/5315
1	G	0.15	0/3937	0.24	0/5315
1	H	0.16	0/3937	0.26	0/5315
1	I	0.12	0/3937	0.24	0/5315
1	J	0.11	0/3937	0.22	0/5315
1	K	0.12	0/3937	0.23	0/5315
1	L	0.14	0/3937	0.24	0/5315
All	All	0.20	0/47244	0.26	0/63780

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	3855	0	3823	89	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3855	0	3823	79	0
1	C	3855	0	3823	64	0
1	D	3855	0	3823	87	0
1	E	3855	0	3823	78	0
1	F	3855	0	3823	82	0
1	G	3855	0	3823	89	0
1	H	3855	0	3823	82	0
1	I	3855	0	3823	72	0
1	J	3855	0	3823	67	0
1	K	3855	0	3823	68	0
1	L	3855	0	3823	89	0
2	A	32	0	12	0	0
2	B	32	0	12	0	0
2	C	32	0	12	1	0
2	D	32	0	12	1	0
2	E	32	0	12	0	0
2	F	32	0	12	1	0
2	G	32	0	12	1	0
2	H	32	0	12	3	0
2	I	32	0	12	1	0
2	J	32	0	12	1	0
2	K	32	0	12	1	0
2	L	32	0	12	1	0
3	A	88	0	53	1	0
3	B	88	0	53	1	0
3	C	88	0	53	2	0
3	D	88	0	53	3	0
3	E	88	0	53	3	0
3	F	88	0	53	4	0
3	G	88	0	53	1	0
3	H	88	0	53	3	0
3	I	88	0	53	1	0
3	J	88	0	53	8	0
3	K	88	0	53	2	0
3	L	88	0	53	4	0
4	A	10	0	7	2	0
4	B	10	0	7	0	0
4	C	10	0	7	1	0
4	D	10	0	7	1	0
4	E	10	0	7	3	0
4	F	10	0	7	1	0
All	All	47760	0	46698	869	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 9.

All (869) 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:G:66:PHE:HA	1:G:69:MET:HE3	1.58	0.86
1:K:66:PHE:HA	1:K:69:MET:HE2	1.56	0.85
1:I:465:HIS:HA	1:I:468:MET:HE2	1.58	0.83
1:A:351:PHE:HA	1:A:354:GLN:HE21	1.45	0.81
1:A:326:LYS:NZ	1:A:340:PRO:O	2.17	0.77
1:B:389:THR:HG22	1:B:391:SER:H	1.50	0.77
1:D:104:SER:HB3	1:F:129:TRP:HB2	1.67	0.77
1:K:293:LEU:HD11	1:K:399:LYS:HB3	1.67	0.76
1:D:317:MET:HG2	1:D:345:PRO:HG3	1.68	0.76
1:B:339:ASN:ND2	1:B:363:LYS:O	2.19	0.75
1:C:293:LEU:HD11	1:C:399:LYS:HB3	1.69	0.75
1:F:136:ARG:HH11	1:F:184:ALA:HB2	1.51	0.75
1:F:326:LYS:NZ	1:F:340:PRO:O	2.21	0.74
1:F:415:LYS:HA	1:F:415:LYS:HE2	1.70	0.74
1:C:147:LYS:NZ	4:C:603:GGL:OE2	2.21	0.73
1:I:339:ASN:ND2	1:I:363:LYS:O	2.21	0.73
1:F:339:ASN:ND2	1:F:363:LYS:O	2.20	0.73
1:B:458:TYR:OH	1:F:499:GLY:O	2.06	0.73
1:E:293:LEU:HD21	1:E:399:LYS:HB3	1.71	0.73
1:B:104:SER:HB3	1:E:129:TRP:HB2	1.69	0.72
1:D:129:TRP:HB2	1:F:104:SER:HB3	1.70	0.72
1:D:339:ASN:ND2	1:D:363:LYS:O	2.21	0.72
1:G:129:TRP:HB2	1:I:104:SER:HB3	1.70	0.72
1:H:136:ARG:HH11	1:H:184:ALA:HB2	1.55	0.72
1:J:519:ARG:HA	1:J:522:MET:HE3	1.70	0.72
1:B:151:ARG:NH1	1:B:160:GLU:OE2	2.23	0.72
1:D:477:LYS:NZ	1:E:484:THR:O	2.22	0.71
1:G:403:GLU:HB3	1:G:427:ASP:HB3	1.73	0.71
1:H:129:TRP:HB2	1:K:104:SER:HB3	1.70	0.71
1:D:347:GLU:OE1	1:D:363:LYS:NZ	2.20	0.71
1:K:339:ASN:ND2	1:K:363:LYS:O	2.23	0.71
1:F:425:ILE:HG21	1:F:430:LEU:HD13	1.73	0.70
1:A:129:TRP:HB2	1:C:104:SER:HB3	1.74	0.70
1:F:151:ARG:NH1	1:F:160:GLU:OE2	2.23	0.70
1:C:339:ASN:ND2	1:C:363:LYS:O	2.23	0.70
1:E:492:GLU:OE1	1:E:492:GLU:N	2.19	0.70
1:H:293:LEU:HD11	1:H:399:LYS:HG3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:372:LEU:HD11	1:H:387:GLN:HB3	1.73	0.69
1:L:339:ASN:ND2	1:L:363:LYS:O	2.24	0.69
1:H:298:GLY:O	1:H:302:LYS:NZ	2.25	0.69
1:L:392:ASN:HA	1:L:395:ARG:HE	1.57	0.69
1:F:380:ILE:HG12	1:F:402:ALA:HB3	1.74	0.69
1:J:339:ASN:ND2	1:J:363:LYS:O	2.25	0.69
1:C:255:VAL:O	1:C:258:LYS:NZ	2.26	0.69
1:H:306:VAL:HG12	1:H:380:ILE:HB	1.75	0.69
1:L:427:ASP:O	1:L:431:ASN:ND2	2.26	0.69
1:G:269:ILE:HG23	1:G:315:HIS:HE1	1.58	0.68
1:K:136:ARG:HH11	1:K:184:ALA:HB2	1.58	0.68
1:I:457:LYS:HB2	1:J:512:TYR:HB2	1.74	0.68
1:A:380:ILE:HG12	1:A:402:ALA:HB3	1.76	0.67
1:J:326:LYS:NZ	1:J:340:PRO:O	2.26	0.67
1:D:301:ASP:OD1	1:D:302:LYS:NZ	2.26	0.67
1:G:136:ARG:HH11	1:G:184:ALA:HB2	1.59	0.67
1:B:305:VAL:HG22	1:B:329:THR:H	1.60	0.67
1:F:281:GLU:O	1:F:285:ASN:ND2	2.28	0.67
1:H:104:SER:HB3	1:K:129:TRP:HB2	1.76	0.67
1:D:473:SER:OG	1:E:486:PRO:O	2.13	0.67
1:H:403:GLU:OE2	1:H:535:ARG:NH2	2.26	0.67
1:G:115:VAL:HB	1:I:117:SER:HB2	1.76	0.67
1:H:458:TYR:OH	1:L:499:GLY:O	2.13	0.66
1:H:477:LYS:NZ	1:L:484:THR:O	2.27	0.66
1:I:96:GLU:N	1:I:96:GLU:OE1	2.27	0.66
1:A:289:TYR:HE2	1:A:522:MET:HG2	1.62	0.65
1:D:225:ASP:OD1	4:D:603:GGL:N	2.28	0.65
1:L:303:THR:HB	1:L:328:ILE:HD13	1.78	0.65
1:L:326:LYS:NZ	1:L:340:PRO:O	2.29	0.65
1:C:136:ARG:HH11	1:C:184:ALA:HB2	1.61	0.65
1:L:380:ILE:HG12	1:L:402:ALA:HB3	1.78	0.65
1:B:284:ILE:HG12	1:B:290:MET:HE2	1.77	0.65
1:H:492:GLU:N	1:H:492:GLU:OE1	2.30	0.65
1:D:136:ARG:HH11	1:D:184:ALA:HB2	1.61	0.65
1:H:89:LEU:O	1:H:98:LYS:NZ	2.30	0.65
1:I:136:ARG:HH11	1:I:184:ALA:HB2	1.61	0.65
1:L:136:ARG:HH11	1:L:184:ALA:HB2	1.62	0.64
1:F:378:ILE:HG12	1:F:400:ILE:HB	1.78	0.64
1:J:307:GLN:HG3	1:J:371:ILE:HG21	1.78	0.64
1:B:129:TRP:HB2	1:E:104:SER:HB3	1.78	0.64
1:L:489:PRO:HB3	1:L:493:PHE:HD2	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:444:ASN:O	3:B:604:NAI:O3D	2.17	0.63
1:J:104:SER:HB3	1:L:129:TRP:HB2	1.81	0.63
1:A:423:MET:HE2	1:A:534:LEU:HD11	1.80	0.63
1:C:499:GLY:O	1:E:458:TYR:OH	2.12	0.63
1:D:151:ARG:NH1	1:D:160:GLU:OE2	2.32	0.63
1:A:104:SER:HB3	1:C:129:TRP:HB2	1.81	0.62
1:E:225:ASP:OD1	4:E:604:GGL:N	2.32	0.62
1:G:553:ALA:HB2	1:L:262:GLN:HE22	1.64	0.62
1:G:311:ASN:ND2	3:G:602:NAI:O1N	2.31	0.62
1:H:94:THR:HG22	1:H:97:GLN:HE22	1.63	0.62
1:L:124:ARG:NH1	1:L:130:GLU:OE1	2.32	0.62
1:D:262:GLN:HE22	1:E:553:ALA:HB2	1.64	0.62
1:I:257:GLY:N	1:I:441:GLU:OE2	2.32	0.62
1:K:157:SER:H	1:K:160:GLU:HG2	1.65	0.62
1:K:76:ARG:NH2	1:K:536:THR:OG1	2.32	0.62
1:E:136:ARG:HH11	1:E:184:ALA:HB2	1.64	0.62
1:G:293:LEU:HD11	1:G:399:LYS:HB3	1.82	0.61
1:C:268:ARG:NE	1:C:438:SER:OG	2.33	0.61
1:L:425:ILE:HG21	1:L:430:LEU:HD13	1.82	0.61
1:K:372:LEU:HD21	1:K:387:GLN:HB3	1.81	0.61
1:L:293:LEU:HD11	1:L:399:LYS:HB3	1.81	0.61
1:D:444:ASN:O	3:D:604:NAI:O3D	2.18	0.61
1:A:499:GLY:O	1:F:458:TYR:OH	2.15	0.61
1:B:456:PHE:HZ	1:B:501:SER:HA	1.66	0.61
1:C:484:THR:O	1:E:477:LYS:NZ	2.34	0.61
1:A:136:ARG:HH11	1:A:184:ALA:HB2	1.66	0.61
1:B:190:PRO:HG3	1:B:227:SER:HB3	1.82	0.61
1:B:426:PRO:HD3	1:B:534:LEU:HB2	1.83	0.61
1:C:317:MET:HG2	1:C:345:PRO:HG3	1.82	0.60
1:H:489:PRO:HB3	1:H:493:PHE:HD2	1.67	0.60
1:A:65:ASN:HB3	1:A:68:LYS:HG2	1.84	0.60
1:F:311:ASN:HD21	3:F:603:NAI:H72N	1.50	0.60
1:G:65:ASN:HD22	1:G:68:LYS:NZ	2.00	0.60
1:L:295:MET:HG2	1:L:302:LYS:HE3	1.82	0.59
1:A:151:ARG:HG3	1:A:226:MET:HB2	1.82	0.59
1:L:156:VAL:HG11	1:L:185:GLY:HA3	1.84	0.59
1:F:136:ARG:NE	1:F:220:ASP:OD2	2.32	0.59
1:D:136:ARG:HH21	1:D:220:ASP:CG	2.11	0.59
1:E:390:LYS:HB3	1:E:412:GLU:HG3	1.84	0.59
1:I:347:GLU:CD	1:I:347:GLU:H	2.10	0.59
1:A:458:TYR:OH	1:B:499:GLY:O	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:ALA:HB2	1:F:262:GLN:HE22	1.66	0.59
1:K:255:VAL:O	1:K:258:LYS:NZ	2.33	0.59
1:B:94:THR:HG22	1:B:97:GLN:HG2	1.83	0.59
1:B:124:ARG:NH1	1:B:130:GLU:OE1	2.35	0.59
1:J:465:HIS:HA	1:J:468:MET:HE3	1.83	0.59
1:K:76:ARG:NH2	1:K:533:ASP:OD2	2.35	0.59
1:G:104:SER:HB2	1:I:129:TRP:HB2	1.84	0.58
1:B:93:GLU:HB3	1:B:97:GLN:HB2	1.85	0.58
1:D:329:THR:HG23	1:D:338:TRP:HB2	1.83	0.58
1:H:122:ILE:HG13	1:H:201:ILE:HG12	1.83	0.58
1:I:176:ASP:OD1	1:I:545:LYS:NZ	2.35	0.58
1:A:295:MET:HE1	1:A:377:ASP:HB3	1.85	0.58
1:K:124:ARG:NH1	1:K:130:GLU:OE1	2.32	0.58
1:E:190:PRO:HG3	1:E:227:SER:HB3	1.85	0.58
1:I:423:MET:HB2	1:I:532:LEU:HD22	1.84	0.58
1:L:396:VAL:HG22	1:L:398:ALA:H	1.68	0.58
1:E:489:PRO:HB3	1:E:493:PHE:HD2	1.68	0.58
1:G:489:PRO:HB3	1:G:493:PHE:HD2	1.69	0.58
1:D:107:ARG:NH2	1:F:129:TRP:O	2.37	0.58
1:H:339:ASN:ND2	1:H:363:LYS:O	2.36	0.58
1:J:107:ARG:NH2	1:L:129:TRP:O	2.37	0.58
1:A:151:ARG:NH1	1:A:160:GLU:OE2	2.37	0.58
1:B:136:ARG:HH11	1:B:184:ALA:HB2	1.68	0.58
1:B:262:GLN:HE22	1:F:553:ALA:HB2	1.69	0.57
1:B:293:LEU:HD11	1:B:399:LYS:HB3	1.86	0.57
1:E:339:ASN:ND2	1:E:363:LYS:O	2.37	0.57
1:K:423:MET:HB3	1:K:532:LEU:HD22	1.86	0.57
1:B:129:TRP:O	1:E:107:ARG:NH2	2.37	0.57
1:J:296:THR:OG1	1:J:301:ASP:OD2	2.21	0.57
1:B:403:GLU:OE2	1:B:535:ARG:NH2	2.27	0.57
1:H:156:VAL:HG11	1:H:185:GLY:HA3	1.86	0.57
1:L:378:ILE:HG12	1:L:400:ILE:HB	1.86	0.57
1:K:257:GLY:HA2	1:K:268:ARG:HG2	1.87	0.57
1:E:215:ILE:HD12	1:E:222:PRO:HG2	1.85	0.57
1:G:290:MET:HA	1:G:290:MET:HE2	1.85	0.57
1:K:84:LYS:HZ1	1:K:88:ASP:HB2	1.69	0.57
1:L:400:ILE:HG12	1:L:423:MET:HB3	1.86	0.57
1:A:466:LEU:HD21	1:B:466:LEU:HD23	1.86	0.57
1:D:423:MET:HB2	1:D:532:LEU:HD22	1.86	0.57
1:G:151:ARG:NH1	1:G:160:GLU:OE2	2.38	0.57
1:D:268:ARG:O	1:D:268:ARG:NH1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:492:GLU:OE1	1:G:492:GLU:N	2.31	0.57
1:C:426:PRO:HD3	1:C:534:LEU:HB2	1.86	0.57
1:L:252:HIS:ND1	3:L:601:NAI:H42N	2.20	0.57
1:D:332:GLU:OE2	1:D:352:LYS:NZ	2.38	0.57
1:G:190:PRO:HG3	1:G:227:SER:HB3	1.86	0.57
1:G:512:TYR:HB2	1:L:457:LYS:HB2	1.85	0.57
1:J:150:ILE:HG12	1:J:184:ALA:HB3	1.87	0.57
1:J:269:ILE:HG12	1:J:315:HIS:HE2	1.70	0.57
1:G:65:ASN:HB3	1:G:68:LYS:HG2	1.87	0.56
1:H:396:VAL:O	1:H:420:ARG:NH2	2.37	0.56
1:I:243:THR:HB	1:L:243:THR:HB	1.88	0.56
1:H:257:GLY:HA2	1:H:268:ARG:HG2	1.86	0.56
1:I:150:ILE:HG12	1:I:184:ALA:HB3	1.87	0.56
1:J:136:ARG:HH11	1:J:184:ALA:HB2	1.70	0.56
1:K:472:GLU:OE1	1:K:476:ARG:NH2	2.38	0.56
1:A:147:LYS:NZ	4:A:603:GGL:OE2	2.38	0.56
1:E:94:THR:HG22	1:E:97:GLN:HG2	1.87	0.56
1:F:136:ARG:HH21	1:F:220:ASP:CG	2.13	0.56
1:I:400:ILE:HG12	1:I:423:MET:HE1	1.86	0.56
1:J:97:GLN:CD	1:J:97:GLN:H	2.14	0.56
1:A:478:PHE:HE2	1:H:297:PRO:HD3	1.71	0.56
1:G:91:THR:HG21	1:G:101:ARG:HH22	1.70	0.56
1:B:326:LYS:NZ	1:B:340:PRO:O	2.38	0.56
1:I:458:TYR:OH	1:J:499:GLY:O	2.23	0.56
1:E:136:ARG:HH21	1:E:220:ASP:CG	2.13	0.56
1:F:328:ILE:HD11	1:F:340:PRO:HA	1.89	0.55
1:K:396:VAL:HG22	1:K:398:ALA:H	1.70	0.55
1:C:262:GLN:HE22	1:D:553:ALA:HB2	1.71	0.55
1:I:496:ARG:HH12	1:K:462:SER:HA	1.71	0.55
1:E:140:SER:OG	1:E:142:HIS:ND1	2.34	0.55
1:F:351:PHE:HD2	1:F:361:PHE:HD1	1.53	0.55
1:G:277:PHE:HZ	1:G:320:LEU:HA	1.71	0.55
1:C:78:ALA:HB1	1:C:106:LEU:HD13	1.87	0.55
1:H:318:ARG:NH2	2:H:601:GTP:O1G	2.39	0.55
1:J:257:GLY:HA2	1:J:268:ARG:HG2	1.89	0.55
1:A:86:VAL:HG23	1:A:98:LYS:HB3	1.89	0.55
1:G:339:ASN:ND2	1:G:363:LYS:O	2.40	0.55
1:J:468:MET:HA	1:J:471:GLN:HB3	1.88	0.55
1:L:406:ASN:OD1	3:L:603:NAI:O2D	2.22	0.55
3:K:603:NAI:O1N	3:K:603:NAI:N7N	2.39	0.55
1:L:328:ILE:HD11	1:L:376:CYS:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:MET:HG2	1:F:345:PRO:HG3	1.88	0.55
1:G:382:ALA:HA	1:G:405:ALA:HB2	1.89	0.55
1:I:188:ILE:HD13	1:I:201:ILE:HD13	1.89	0.55
1:L:150:ILE:HG12	1:L:184:ALA:HB3	1.89	0.55
1:B:329:THR:HG22	1:B:338:TRP:HA	1.89	0.54
1:D:489:PRO:HB3	1:D:493:PHE:HD2	1.70	0.54
1:I:290:MET:HE1	1:I:297:PRO:HD3	1.89	0.54
1:H:295:MET:SD	1:H:296:THR:N	2.80	0.54
1:C:156:VAL:HG11	1:C:185:GLY:HA3	1.89	0.54
1:E:164:LEU:HB3	1:E:183:LYS:HD3	1.88	0.54
1:E:380:ILE:HG12	1:E:402:ALA:HB3	1.89	0.54
1:G:136:ARG:HH21	1:G:220:ASP:CG	2.15	0.54
1:L:114:HIS:CE1	1:L:141:GLN:HE21	2.25	0.54
1:D:375:ASP:HA	1:D:397:LYS:HB2	1.90	0.54
1:G:380:ILE:HG12	1:G:402:ALA:HB3	1.89	0.54
1:J:190:PRO:HG3	1:J:227:SER:HB2	1.89	0.54
1:C:113:ASN:ND2	1:C:141:GLN:OE1	2.37	0.54
1:G:392:ASN:HB3	1:G:395:ARG:HH21	1.73	0.54
1:J:129:TRP:HB2	1:L:104:SER:HB2	1.89	0.54
1:L:86:VAL:HG23	1:L:98:LYS:HB2	1.90	0.54
1:A:378:ILE:HG12	1:A:400:ILE:HB	1.90	0.54
1:D:153:SER:HB3	1:D:156:VAL:HG23	1.90	0.54
1:G:130:GLU:OE2	1:G:193:TYR:OH	2.26	0.54
1:J:392:ASN:HA	1:J:395:ARG:HE	1.73	0.54
1:K:326:LYS:NZ	1:K:340:PRO:O	2.40	0.54
1:H:328:ILE:HD11	1:H:376:CYS:HB3	1.89	0.54
1:H:428:LEU:HD23	1:H:428:LEU:H	1.72	0.54
1:A:361:PHE:HB3	1:A:364:ALA:HB3	1.89	0.54
1:I:370:SER:HB3	1:I:373:GLU:HB2	1.90	0.54
1:H:125:ASP:OD1	1:H:126:ASP:N	2.41	0.54
1:K:357:THR:HG22	1:K:359:LEU:H	1.72	0.54
1:A:83:ASP:OD1	1:A:84:LYS:N	2.41	0.54
1:A:379:LEU:HB3	1:A:401:ILE:HD13	1.89	0.54
1:A:472:GLU:OE1	1:A:476:ARG:NH2	2.40	0.54
1:B:426:PRO:HB3	1:B:535:ARG:HA	1.90	0.53
1:H:343:ILE:HG22	1:H:348:LEU:HD21	1.89	0.53
1:J:378:ILE:HG12	1:J:400:ILE:HB	1.90	0.53
1:A:350:ASP:OD1	1:A:354:GLN:NE2	2.41	0.53
3:H:602:NAI:N7N	3:H:602:NAI:O1N	2.37	0.53
1:C:404:GLY:O	1:C:431:ASN:ND2	2.39	0.53
1:G:428:LEU:H	1:G:428:LEU:HD23	1.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:277:PHE:CE1	1:G:320:LEU:HD22	2.43	0.53
1:H:304:PHE:CZ	1:H:327:CYS:HB2	2.43	0.53
1:H:406:ASN:OD1	3:H:602:NAI:O2D	2.24	0.53
1:K:122:ILE:HG21	1:K:201:ILE:HG12	1.90	0.53
1:H:473:SER:HB3	1:L:487:ILE:HA	1.90	0.53
1:I:86:VAL:HG21	1:I:99:ARG:HD2	1.90	0.53
1:I:90:LYS:O	1:I:92:ARG:NH2	2.41	0.53
1:B:466:LEU:HD21	1:F:466:LEU:HD23	1.91	0.53
1:L:151:ARG:NH1	1:L:160:GLU:OE2	2.41	0.53
1:A:372:LEU:HD11	1:A:387:GLN:HB3	1.89	0.53
1:H:136:ARG:HH21	1:H:220:ASP:CG	2.17	0.53
1:F:223:ALA:HB3	4:F:604:GGL:HB3	1.90	0.53
1:G:277:PHE:CZ	1:G:320:LEU:HA	2.44	0.53
1:G:466:LEU:HD23	1:L:466:LEU:HD21	1.91	0.53
1:C:401:ILE:HB	1:C:424:VAL:HG22	1.91	0.53
1:E:407:GLY:N	1:E:427:ASP:OD2	2.39	0.53
3:C:602:NAI:N7N	3:C:602:NAI:O1N	2.39	0.52
1:E:136:ARG:NE	1:E:220:ASP:OD2	2.32	0.52
1:F:299:PHE:HD2	1:F:325:ALA:HB2	1.74	0.52
1:B:396:VAL:O	1:B:420:ARG:NH2	2.36	0.52
1:F:389:THR:HG22	1:F:390:LYS:H	1.74	0.52
1:D:223:ALA:C	1:D:233:MET:HE2	2.34	0.52
1:F:428:LEU:HD23	1:F:428:LEU:H	1.75	0.52
1:G:339:ASN:HD22	1:G:364:ALA:HA	1.74	0.52
1:C:136:ARG:NE	1:C:220:ASP:OD2	2.33	0.52
1:D:349:GLU:OE2	2:D:601:GTP:N2	2.34	0.52
1:E:326:LYS:NZ	1:E:340:PRO:O	2.43	0.52
1:E:346:LYS:H	1:E:346:LYS:HD2	1.74	0.52
1:J:176:ASP:OD1	1:J:545:LYS:NZ	2.29	0.52
1:F:309:PHE:HD2	1:F:352:LYS:HD2	1.74	0.52
1:J:457:LYS:HB2	1:K:512:TYR:HB2	1.91	0.52
1:C:322:ARG:NH2	2:C:601:GTP:O2G	2.42	0.52
1:F:94:THR:HG23	1:F:97:GLN:H	1.75	0.52
1:F:207:MET:HE1	1:F:244:ILE:HG12	1.91	0.52
1:E:312:VAL:HG13	1:E:382:ALA:HB1	1.91	0.52
1:I:380:ILE:HG12	1:I:402:ALA:HB3	1.90	0.52
1:K:84:LYS:NZ	1:K:88:ASP:HB2	2.24	0.52
1:A:339:ASN:ND2	1:A:363:LYS:O	2.42	0.52
1:I:389:THR:OG1	1:I:392:ASN:ND2	2.43	0.52
1:L:94:THR:HG22	1:L:97:GLN:OE1	2.10	0.52
1:D:380:ILE:HG12	1:D:402:ALA:HB3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:322:ARG:NH1	2:F:602:GTP:O3G	2.39	0.52
1:I:379:LEU:HG	1:I:381:PRO:HD3	1.91	0.52
1:L:136:ARG:HH21	1:L:220:ASP:CG	2.18	0.52
1:B:489:PRO:HB3	1:B:493:PHE:HD2	1.74	0.52
1:F:317:MET:HE3	1:F:345:PRO:HA	1.92	0.52
1:A:101:ARG:NH1	1:A:551:ASN:OD1	2.43	0.51
1:A:268:ARG:NE	1:A:438:SER:OG	2.43	0.51
1:B:404:GLY:O	1:B:431:ASN:ND2	2.35	0.51
1:A:136:ARG:HH21	1:A:220:ASP:CG	2.18	0.51
1:G:107:ARG:NH2	1:I:129:TRP:O	2.41	0.51
1:H:176:ASP:OD1	1:H:545:LYS:NZ	2.36	0.51
1:H:347:GLU:HB3	1:H:361:PHE:HZ	1.73	0.51
1:H:444:ASN:O	3:H:603:NAI:O3D	2.29	0.51
1:A:190:PRO:HG3	1:A:227:SER:HB3	1.91	0.51
1:E:331:GLY:HA3	1:E:371:ILE:HG12	1.93	0.51
1:J:69:MET:HG2	1:J:411:PRO:HD3	1.92	0.51
1:K:372:LEU:HD23	1:K:388:LEU:HD23	1.92	0.51
1:A:94:THR:HG22	1:A:97:GLN:HG3	1.93	0.51
1:A:468:MET:HE2	1:A:468:MET:HA	1.93	0.51
1:H:348:LEU:O	1:H:352:LYS:N	2.30	0.51
1:I:372:LEU:HD13	1:I:388:LEU:HD23	1.93	0.51
1:J:489:PRO:HB3	1:J:493:PHE:HD2	1.75	0.51
1:L:94:THR:N	1:L:97:GLN:OE1	2.38	0.51
1:A:146:CYS:HB3	1:A:182:ALA:HB2	1.92	0.51
1:B:539:TYR:O	1:B:543:ILE:HG13	2.09	0.51
1:C:403:GLU:OE2	1:C:535:ARG:NH2	2.31	0.51
1:F:403:GLU:OE2	1:F:535:ARG:NH2	2.28	0.51
1:G:456:PHE:CZ	1:G:501:SER:HA	2.45	0.51
1:C:490:THR:HG23	1:E:469:SER:HA	1.92	0.51
1:E:492:GLU:H	1:E:492:GLU:CD	2.15	0.51
1:I:69:MET:HE3	1:I:411:PRO:HD3	1.93	0.51
1:I:231:ARG:O	1:I:234:SER:OG	2.27	0.51
1:I:344:ASP:HB3	1:I:347:GLU:OE1	2.11	0.51
1:B:407:GLY:N	1:B:427:ASP:OD2	2.43	0.51
1:G:456:PHE:HZ	1:G:501:SER:HA	1.76	0.51
1:H:387:GLN:OE1	1:H:387:GLN:N	2.43	0.51
1:A:215:ILE:HD12	1:A:222:PRO:HG2	1.93	0.51
1:A:329:THR:HG21	1:A:374:VAL:HG11	1.92	0.51
1:C:426:PRO:HB3	1:C:535:ARG:HA	1.93	0.51
1:C:326:LYS:NZ	1:C:340:PRO:O	2.44	0.51
1:G:156:VAL:HG11	1:G:185:GLY:HA3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:186:VAL:HG12	1:G:188:ILE:HG23	1.93	0.51
1:F:332:GLU:HB2	1:F:358:ILE:HD11	1.93	0.50
1:K:301:ASP:OD1	1:K:302:LYS:NZ	2.39	0.50
1:G:449:VAL:HB	1:H:443:LEU:HD21	1.93	0.50
1:L:385:GLU:O	1:L:387:GLN:NE2	2.45	0.50
1:G:309:PHE:CZ	1:G:314:LEU:HD13	2.47	0.50
1:B:255:VAL:O	1:B:258:LYS:NZ	2.40	0.50
1:A:93:GLU:HB3	1:A:97:GLN:HB2	1.93	0.50
1:A:375:ASP:HA	1:A:397:LYS:HG2	1.93	0.50
1:C:257:GLY:HA2	1:C:268:ARG:HG2	1.93	0.50
1:H:349:GLU:OE2	2:H:601:GTP:N2	2.27	0.50
1:J:403:GLU:OE2	1:J:535:ARG:NH2	2.39	0.50
1:A:176:ASP:OD2	1:A:516:ARG:NH2	2.44	0.50
1:B:82:GLU:OE2	1:B:103:ARG:NE	2.45	0.50
1:C:338:TRP:O	1:C:365:LYS:NZ	2.43	0.50
1:G:448:HIS:O	1:H:439:TYR:OH	2.26	0.50
1:B:78:ALA:HB1	1:B:106:LEU:HD13	1.92	0.50
1:C:407:GLY:N	1:C:427:ASP:OD2	2.44	0.50
1:C:478:PHE:HZ	1:D:478:PHE:HE2	1.59	0.50
1:J:306:VAL:HG12	1:J:380:ILE:HB	1.92	0.50
1:K:349:GLU:OE2	2:K:602:GTP:N2	2.42	0.50
1:L:428:LEU:H	1:L:428:LEU:HD23	1.77	0.50
1:D:124:ARG:NH1	1:D:130:GLU:OE1	2.39	0.50
1:J:252:HIS:ND1	3:J:603:NAI:H42N	2.27	0.50
1:K:164:LEU:HD13	1:K:183:LYS:HE3	1.93	0.50
1:A:129:TRP:O	1:C:107:ARG:NH2	2.44	0.50
1:A:175:VAL:HG23	1:A:177:VAL:HG23	1.92	0.50
1:A:403:GLU:OE2	1:A:535:ARG:NH2	2.26	0.50
1:B:401:ILE:HB	1:B:424:VAL:HG22	1.94	0.50
1:C:176:ASP:OD1	1:C:545:LYS:NZ	2.31	0.50
1:D:328:ILE:HD11	1:D:376:CYS:HB3	1.93	0.50
1:I:426:PRO:HD3	1:I:534:LEU:HB2	1.95	0.49
1:I:428:LEU:H	1:I:428:LEU:HD23	1.77	0.49
1:J:189:ASN:ND2	1:J:192:ASN:OD1	2.45	0.49
1:K:268:ARG:O	1:K:268:ARG:NH1	2.45	0.49
1:L:78:ALA:HB1	1:L:106:LEU:HD13	1.93	0.49
1:C:136:ARG:HH21	1:C:220:ASP:CG	2.20	0.49
1:E:328:ILE:HG23	1:E:340:PRO:HA	1.94	0.49
1:G:65:ASN:HD22	1:G:68:LYS:HZ2	1.59	0.49
1:G:269:ILE:HG23	1:G:315:HIS:CE1	2.44	0.49
1:G:425:ILE:HG13	1:G:426:PRO:HD2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:466:LEU:HD21	1:L:466:LEU:HD23	1.93	0.49
1:J:396:VAL:HG22	1:J:398:ALA:H	1.77	0.49
1:K:150:ILE:HG12	1:K:184:ALA:HB3	1.93	0.49
1:E:147:LYS:NZ	4:E:604:GGL:OE1	2.43	0.49
1:E:268:ARG:NE	1:E:438:SER:OG	2.45	0.49
1:F:311:ASN:OD1	1:F:312:VAL:N	2.45	0.49
1:B:150:ILE:HG12	1:B:184:ALA:HB3	1.94	0.49
1:H:69:MET:HE1	1:H:386:LYS:HG2	1.94	0.49
1:F:255:VAL:O	1:F:258:LYS:NZ	2.37	0.49
1:G:337:ILE:HG22	1:G:366:ILE:HA	1.95	0.49
1:J:151:ARG:NH2	3:J:602:NAI:O2D	2.46	0.49
1:B:129:TRP:CH2	1:E:555:VAL:HB	2.48	0.49
1:D:136:ARG:NH1	1:D:184:ALA:HB2	2.27	0.49
1:K:65:ASN:HD22	1:K:68:LYS:HG2	1.78	0.49
1:A:382:ALA:HA	1:A:405:ALA:HB2	1.95	0.49
1:A:481:HIS:O	1:A:481:HIS:ND1	2.43	0.49
1:B:164:LEU:HB3	1:B:183:LYS:HD3	1.95	0.49
1:D:458:TYR:OH	1:E:499:GLY:O	2.25	0.49
1:J:428:LEU:HD23	1:J:428:LEU:H	1.78	0.49
1:L:153:SER:HB3	1:L:156:VAL:HG23	1.95	0.49
1:B:268:ARG:NE	1:B:438:SER:OG	2.46	0.49
1:E:339:ASN:HD22	1:E:364:ALA:HA	1.77	0.49
1:K:530:LEU:HD12	1:K:533:ASP:HB3	1.95	0.49
1:D:115:VAL:HG21	1:D:162:LYS:HD3	1.94	0.49
1:G:277:PHE:O	1:G:281:GLU:N	2.31	0.49
1:I:266:HIS:N	1:I:502:GLU:OE2	2.42	0.49
1:K:493:PHE:O	1:K:497:ILE:N	2.46	0.49
1:L:136:ARG:NE	1:L:220:ASP:OD2	2.43	0.49
1:A:329:THR:HG23	1:A:338:TRP:HB2	1.94	0.48
1:E:425:ILE:HG21	1:E:430:LEU:HD13	1.95	0.48
1:F:190:PRO:HG3	1:F:227:SER:HB3	1.94	0.48
1:G:117:SER:HB2	1:I:115:VAL:HB	1.95	0.48
1:I:378:ILE:HG12	1:I:400:ILE:HB	1.94	0.48
1:G:472:GLU:OE2	1:G:476:ARG:NH2	2.46	0.48
1:K:149:GLY:H	1:K:183:LYS:HD2	1.78	0.48
1:L:215:ILE:HA	1:L:220:ASP:HB3	1.95	0.48
1:A:304:PHE:HA	1:A:378:ILE:O	2.14	0.48
1:A:552:GLU:HG3	1:F:261:SER:OG	2.14	0.48
1:D:159:ASP:OD1	1:D:159:ASP:N	2.45	0.48
1:B:284:ILE:HD11	1:B:378:ILE:HD11	1.95	0.48
1:G:458:TYR:OH	1:H:499:GLY:O	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:151:ARG:NH1	1:H:160:GLU:OE2	2.46	0.48
1:H:290:MET:HB3	1:H:295:MET:O	2.14	0.48
1:H:312:VAL:HG13	1:H:382:ALA:HB1	1.95	0.48
1:A:129:TRP:CH2	1:C:555:VAL:HB	2.48	0.48
1:G:328:ILE:HD11	1:G:376:CYS:HB3	1.95	0.48
1:L:339:ASN:HD22	1:L:364:ALA:HA	1.78	0.48
1:J:338:TRP:CE2	1:J:340:PRO:HD3	2.48	0.48
1:C:396:VAL:HG22	1:C:398:ALA:H	1.79	0.48
3:E:603:NAI:H4N	4:E:604:GGL:HA	1.95	0.48
1:F:426:PRO:HG2	1:F:429:TYR:HB3	1.96	0.48
1:J:357:THR:HG22	1:J:359:LEU:H	1.78	0.48
1:L:522:MET:O	1:L:526:MET:HG2	2.14	0.48
1:B:403:GLU:HB3	1:B:427:ASP:HB3	1.96	0.48
1:D:401:ILE:HB	1:D:424:VAL:HG22	1.96	0.48
1:G:70:VAL:HG11	1:G:166:SER:HB2	1.96	0.48
1:I:349:GLU:OE2	2:I:601:GTP:N2	2.37	0.48
1:L:226:MET:HE2	3:L:603:NAI:H3D	1.95	0.48
1:A:327:CYS:C	1:A:328:ILE:HD13	2.38	0.48
1:J:268:ARG:NE	1:J:438:SER:OG	2.47	0.48
1:K:304:PHE:CZ	1:K:327:CYS:HB2	2.49	0.48
1:A:456:PHE:HZ	1:A:501:SER:HA	1.79	0.47
1:F:481:HIS:CE1	1:H:323:PHE:HD2	2.31	0.47
1:G:277:PHE:HE1	1:G:320:LEU:HD22	1.79	0.47
1:G:329:THR:HG23	1:G:338:TRP:HB2	1.95	0.47
1:L:329:THR:HG1	1:L:338:TRP:CD1	2.32	0.47
1:D:150:ILE:HG12	1:D:184:ALA:HB3	1.96	0.47
1:D:386:LYS:H	1:D:408:PRO:HA	1.79	0.47
1:F:123:ARG:O	1:F:200:LYS:NZ	2.30	0.47
1:A:425:ILE:HG21	1:A:430:LEU:HD13	1.96	0.47
1:B:469:SER:HA	1:F:490:THR:HG23	1.97	0.47
1:C:295:MET:HG2	1:C:302:LYS:HE3	1.95	0.47
1:C:444:ASN:O	3:C:604:NAI:O3D	2.32	0.47
1:D:94:THR:HG23	1:D:97:GLN:H	1.79	0.47
1:D:389:THR:HG23	1:D:391:SER:H	1.80	0.47
1:E:403:GLU:OE2	1:E:535:ARG:NH2	2.29	0.47
1:J:305:VAL:HG22	1:J:329:THR:HB	1.96	0.47
1:K:428:LEU:HD23	1:K:428:LEU:H	1.78	0.47
1:L:312:VAL:HG13	1:L:382:ALA:HB1	1.96	0.47
1:B:136:ARG:HH21	1:B:220:ASP:CG	2.21	0.47
1:F:456:PHE:HZ	1:F:501:SER:HA	1.79	0.47
1:G:154:THR:O	1:G:187:LYS:NZ	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:474:LEU:HD13	1:L:474:LEU:HD21	1.97	0.47
1:I:132:ILE:HG21	1:I:201:ILE:HD11	1.95	0.47
1:K:136:ARG:HH21	1:K:220:ASP:CG	2.23	0.47
1:A:66:PHE:CD1	1:A:69:MET:HE3	2.49	0.47
1:G:322:ARG:NH1	2:G:601:GTP:O3G	2.37	0.47
1:A:136:ARG:NE	1:A:220:ASP:OD2	2.32	0.47
1:B:374:VAL:HG23	1:B:376:CYS:SG	2.54	0.47
1:B:375:ASP:HA	1:B:397:LYS:HD2	1.96	0.47
1:F:346:LYS:HB2	1:F:346:LYS:HE2	1.62	0.47
1:H:290:MET:SD	1:H:290:MET:N	2.88	0.47
1:I:156:VAL:HA	1:I:160:GLU:OE2	2.15	0.47
1:C:265:ILE:HB	1:C:441:GLU:HB2	1.96	0.47
1:D:471:GLN:HG3	1:D:485:ILE:O	2.14	0.47
1:E:66:PHE:CE1	1:E:69:MET:HE2	2.50	0.47
1:F:423:MET:SD	1:F:534:LEU:HD11	2.55	0.47
1:G:518:ALA:O	1:G:522:MET:HG3	2.15	0.47
1:H:429:TYR:OH	1:H:518:ALA:HB2	2.15	0.47
1:I:136:ARG:HH21	1:I:220:ASP:CG	2.21	0.47
1:D:255:VAL:O	1:D:258:LYS:NZ	2.45	0.47
1:G:97:GLN:OE1	1:G:97:GLN:N	2.29	0.47
1:K:298:GLY:O	1:K:302:LYS:NZ	2.41	0.47
1:K:379:LEU:HB3	1:K:401:ILE:HD13	1.97	0.47
1:L:429:TYR:OH	1:L:518:ALA:HB2	2.15	0.47
1:A:108:ILE:HG12	1:C:121:PRO:HB3	1.96	0.47
1:A:404:GLY:O	1:A:431:ASN:ND2	2.46	0.47
1:B:136:ARG:NE	1:B:220:ASP:OD2	2.44	0.47
1:D:129:TRP:CH2	1:F:555:VAL:HB	2.50	0.47
1:D:190:PRO:HG3	1:D:227:SER:HB3	1.96	0.47
1:D:269:ILE:HD12	1:D:269:ILE:H	1.79	0.47
1:D:305:VAL:HG13	1:D:329:THR:HB	1.96	0.47
1:I:287:ALA:O	1:I:290:MET:HG2	2.15	0.47
1:K:290:MET:HA	1:K:290:MET:HE3	1.97	0.47
3:K:601:NAI:H71N	3:K:601:NAI:H4N	1.58	0.47
1:B:471:GLN:NE2	1:B:485:ILE:O	2.33	0.47
1:D:156:VAL:HG11	1:D:185:GLY:HA3	1.97	0.47
1:H:384:SER:N	1:H:387:GLN:HE22	2.12	0.47
1:J:136:ARG:HD2	1:J:184:ALA:HB2	1.96	0.47
1:K:130:GLU:OE2	1:K:193:TYR:OH	2.29	0.47
1:K:407:GLY:N	1:K:427:ASP:OD2	2.48	0.47
1:L:518:ALA:O	1:L:522:MET:HG2	2.15	0.47
1:A:444:ASN:O	3:A:604:NAI:O3D	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:309:PHE:HD2	1:D:352:LYS:HD3	1.79	0.46
1:D:312:VAL:HG13	1:D:382:ALA:HB1	1.96	0.46
1:F:268:ARG:NE	1:F:438:SER:OG	2.49	0.46
1:I:530:LEU:HD12	1:I:533:ASP:HB3	1.97	0.46
1:C:175:VAL:HG23	1:C:177:VAL:HG23	1.96	0.46
1:F:115:VAL:HG21	1:F:162:LYS:HD3	1.96	0.46
1:A:174:VAL:HG23	1:A:542:ALA:HB2	1.97	0.46
1:C:552:GLU:HG3	1:E:261:SER:OG	2.15	0.46
1:H:140:SER:OG	1:H:142:HIS:ND1	2.38	0.46
1:C:489:PRO:HB3	1:C:493:PHE:HD2	1.81	0.46
1:H:168:MET:HE1	1:H:435:VAL:HG21	1.97	0.46
1:H:372:LEU:HD13	1:H:388:LEU:HD23	1.97	0.46
1:C:115:VAL:HG21	1:C:162:LYS:HD3	1.97	0.46
1:D:280:ILE:O	1:D:284:ILE:N	2.48	0.46
1:D:113:ASN:ND2	1:D:141:GLN:OE1	2.40	0.46
1:F:328:ILE:HG13	1:F:339:ASN:O	2.15	0.46
1:H:276:VAL:HG23	1:H:430:LEU:HD21	1.97	0.46
1:I:332:GLU:OE2	3:I:602:NAI:O2B	2.28	0.46
1:B:298:GLY:O	1:B:302:LYS:NZ	2.40	0.46
1:C:473:SER:HB2	1:D:487:ILE:HD13	1.97	0.46
1:G:528:TYR:HB2	1:G:530:LEU:HD11	1.97	0.46
1:I:268:ARG:O	1:I:268:ARG:NH1	2.44	0.46
1:K:371:ILE:HG23	1:K:372:LEU:HD12	1.96	0.46
1:L:379:LEU:HB3	1:L:401:ILE:HD13	1.98	0.46
1:B:489:PRO:HB3	1:B:493:PHE:CD2	2.50	0.46
1:E:361:PHE:CE2	1:E:363:LYS:HB3	2.51	0.46
1:J:129:TRP:N	1:J:129:TRP:CD1	2.84	0.46
1:A:354:GLN:HG3	1:A:355:HIS:ND1	2.31	0.46
1:E:93:GLU:HB2	1:E:97:GLN:HB2	1.98	0.46
1:G:327:CYS:O	1:G:342:GLY:HA2	2.16	0.46
1:J:339:ASN:HD22	1:J:364:ALA:HA	1.80	0.46
1:L:502:GLU:OE1	1:L:502:GLU:N	2.36	0.46
1:C:423:MET:HB2	1:C:532:LEU:HD13	1.97	0.46
1:E:130:GLU:OE2	1:E:193:TYR:OH	2.34	0.46
1:H:223:ALA:C	1:H:233:MET:HE3	2.40	0.46
1:I:77:GLY:O	1:I:81:VAL:HG12	2.15	0.46
1:J:403:GLU:HB3	1:J:427:ASP:HB3	1.98	0.46
1:K:328:ILE:HG13	1:K:329:THR:N	2.31	0.46
1:L:426:PRO:HG2	1:L:429:TYR:HB3	1.97	0.46
1:B:117:SER:HB2	1:E:115:VAL:HB	1.99	0.45
1:E:428:LEU:HD23	1:E:428:LEU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:171:LYS:NZ	1:H:406:ASN:HD21	2.14	0.45
1:A:337:ILE:HG12	1:A:358:ILE:HD12	1.98	0.45
1:E:468:MET:HA	1:E:468:MET:HE2	1.98	0.45
1:F:444:ASN:O	3:F:601:NAI:O3D	2.34	0.45
1:H:289:TYR:HB3	1:H:423:MET:HE1	1.97	0.45
1:I:396:VAL:HG22	1:I:398:ALA:H	1.81	0.45
1:L:164:LEU:HD13	1:L:183:LYS:HE3	1.99	0.45
1:L:274:ARG:NH2	1:L:319:TYR:OH	2.49	0.45
1:B:456:PHE:CZ	1:B:501:SER:HA	2.48	0.45
1:H:469:SER:HA	1:L:490:THR:HG23	1.98	0.45
1:C:304:PHE:CZ	1:C:327:CYS:HB2	2.52	0.45
1:D:136:ARG:NE	1:D:220:ASP:OD2	2.48	0.45
1:F:283:PHE:CE2	1:F:425:ILE:HG23	2.51	0.45
1:C:94:THR:HG23	1:C:97:GLN:H	1.82	0.45
1:F:82:GLU:OE2	1:F:99:ARG:NH1	2.49	0.45
1:G:411:PRO:HA	1:G:414:ASP:HB2	1.98	0.45
1:L:268:ARG:O	1:L:268:ARG:NH1	2.45	0.45
1:L:304:PHE:CE2	1:L:327:CYS:HB2	2.52	0.45
1:A:298:GLY:O	1:A:302:LYS:NZ	2.28	0.45
1:A:489:PRO:HB3	1:A:493:PHE:HD2	1.81	0.45
1:B:367:TYR:CZ	1:B:374:VAL:HG12	2.52	0.45
1:J:530:LEU:HD12	1:J:537:ALA:HB2	1.99	0.45
1:K:65:ASN:ND2	1:K:159:ASP:OD2	2.46	0.45
1:B:215:ILE:HG13	1:B:222:PRO:HD3	1.99	0.45
1:H:384:SER:H	1:H:387:GLN:HE22	1.65	0.45
1:C:66:PHE:CD1	1:C:69:MET:HE2	2.51	0.45
1:D:392:ASN:HA	1:D:395:ARG:HE	1.81	0.45
1:D:396:VAL:HG22	1:D:398:ALA:H	1.82	0.45
1:D:457:LYS:HB2	1:E:512:TYR:HB2	1.98	0.45
1:D:489:PRO:HB3	1:D:493:PHE:CD2	2.51	0.45
1:E:115:VAL:HG21	1:E:162:LYS:HD3	1.98	0.45
1:G:318:ARG:HG2	1:G:345:PRO:HB2	1.99	0.45
1:I:293:LEU:HD11	1:I:399:LYS:HB3	1.99	0.45
1:L:231:ARG:O	1:L:234:SER:OG	2.33	0.45
1:L:456:PHE:CZ	1:L:501:SER:HA	2.52	0.45
1:F:223:ALA:C	1:F:233:MET:HE3	2.42	0.45
1:F:471:GLN:HG3	1:F:485:ILE:O	2.17	0.45
1:H:371:ILE:O	1:H:374:VAL:HG12	2.16	0.45
1:I:257:GLY:HA2	1:I:268:ARG:HG2	1.97	0.45
1:B:456:PHE:HD2	1:F:512:TYR:CE2	2.34	0.45
1:C:190:PRO:HG3	1:C:227:SER:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:261:SER:OG	1:E:552:GLU:HG3	2.15	0.45
1:D:428:LEU:H	1:D:428:LEU:HD23	1.82	0.45
1:D:518:ALA:O	1:D:522:MET:HG3	2.17	0.45
1:F:318:ARG:HG2	1:F:345:PRO:HB3	1.98	0.45
1:G:277:PHE:CE1	1:G:319:TYR:HB3	2.52	0.45
1:H:322:ARG:HH22	2:H:601:GTP:PG	2.40	0.45
1:B:138:GLN:OE1	1:B:141:GLN:NE2	2.50	0.44
1:B:301:ASP:OD1	1:B:301:ASP:N	2.34	0.44
1:C:279:GLY:HA3	1:C:430:LEU:HD12	1.98	0.44
1:E:328:ILE:HG22	1:E:338:TRP:CD1	2.51	0.44
1:G:378:ILE:HG12	1:G:400:ILE:HB	1.99	0.44
1:J:115:VAL:HB	1:L:117:SER:HB2	1.99	0.44
1:J:382:ALA:HA	1:J:405:ALA:HB2	1.99	0.44
1:L:304:PHE:HE1	1:L:306:VAL:HG23	1.82	0.44
1:A:124:ARG:HE	1:A:197:GLU:CD	2.26	0.44
1:A:261:SER:OG	1:B:552:GLU:HG3	2.16	0.44
1:A:472:GLU:OE2	1:A:476:ARG:NE	2.48	0.44
1:B:237:ALA:HA	1:B:254:CYS:SG	2.58	0.44
1:D:150:ILE:HD12	1:D:236:ILE:HD11	1.99	0.44
1:E:276:VAL:HG23	1:E:430:LEU:HG	1.98	0.44
1:F:329:THR:HG1	1:F:338:TRP:CD1	2.34	0.44
1:I:490:THR:HG23	1:I:493:PHE:H	1.83	0.44
1:J:322:ARG:HH22	2:J:601:GTP:PG	2.40	0.44
1:J:425:ILE:HG21	1:J:430:LEU:HD13	1.99	0.44
1:B:296:THR:OG1	1:B:301:ASP:OD2	2.36	0.44
1:C:260:ILE:HD12	1:C:260:ILE:H	1.82	0.44
1:C:423:MET:HB2	1:C:532:LEU:HD22	2.00	0.44
1:C:466:LEU:HD23	1:E:466:LEU:HD11	1.99	0.44
1:F:295:MET:HE1	1:F:377:ASP:HB3	2.00	0.44
1:G:64:PRO:HB2	1:G:69:MET:HE2	1.99	0.44
1:G:289:TYR:CG	1:G:423:MET:HE1	2.52	0.44
1:H:295:MET:HE2	1:H:295:MET:HA	1.99	0.44
1:K:521:ILE:HG23	1:K:522:MET:SD	2.57	0.44
1:L:122:ILE:HG21	1:L:201:ILE:HG12	1.99	0.44
1:A:147:LYS:HD2	1:A:221:VAL:O	2.17	0.44
1:G:426:PRO:HG2	1:G:429:TYR:HB3	1.99	0.44
1:I:86:VAL:HG21	1:I:99:ARG:HH11	1.82	0.44
1:A:339:ASN:HD22	1:A:364:ALA:HA	1.83	0.44
1:C:195:ASP:OD2	1:C:231:ARG:NH1	2.50	0.44
1:D:344:ASP:HB3	1:D:347:GLU:HG2	2.00	0.44
1:F:226:MET:HE2	1:F:226:MET:HB3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:190:PRO:HG3	1:I:227:SER:HB2	1.98	0.44
1:D:307:GLN:HG3	1:D:371:ILE:HG21	2.00	0.44
1:H:378:ILE:HG12	1:H:400:ILE:HB	1.99	0.44
1:K:154:THR:HG23	1:K:189:ASN:HB2	2.00	0.44
1:K:332:GLU:HB2	1:K:358:ILE:HD11	1.98	0.44
1:B:426:PRO:HG2	1:B:429:TYR:HB3	2.00	0.44
1:F:505:ILE:HD13	1:F:505:ILE:HA	1.89	0.44
1:I:265:ILE:N	1:I:441:GLU:OE1	2.39	0.44
1:K:85:LEU:HD12	1:K:85:LEU:HA	1.83	0.44
1:K:309:PHE:HD2	1:K:352:LYS:HD2	1.83	0.44
1:L:349:GLU:OE2	2:L:602:GTP:N2	2.36	0.44
1:L:361:PHE:CD1	1:L:362:PRO:HD2	2.53	0.44
1:D:304:PHE:CZ	1:D:327:CYS:HB2	2.51	0.44
1:E:414:ASP:OD2	1:E:535:ARG:NE	2.48	0.44
1:G:332:GLU:HB2	1:G:358:ILE:HD11	1.99	0.44
1:H:380:ILE:HA	1:H:402:ALA:O	2.18	0.44
1:J:266:HIS:N	1:J:502:GLU:OE2	2.46	0.44
1:E:279:GLY:HA3	1:E:430:LEU:HD12	2.00	0.44
1:E:329:THR:HG1	1:E:338:TRP:HD1	1.65	0.44
1:E:371:ILE:HG23	1:E:372:LEU:HG	2.00	0.44
1:G:129:TRP:CH2	1:I:555:VAL:HB	2.53	0.44
1:K:169:THR:OG1	1:K:181:GLY:HA3	2.18	0.44
1:K:518:ALA:HA	1:K:521:ILE:HG22	2.00	0.44
1:B:497:ILE:HD12	1:B:497:ILE:HA	1.80	0.43
1:C:230:GLU:HB3	1:C:269:ILE:HD11	1.99	0.43
1:C:387:GLN:OE1	1:C:387:GLN:HA	2.18	0.43
1:D:378:ILE:HG12	1:D:400:ILE:HB	2.00	0.43
1:F:239:THR:O	1:F:243:THR:OG1	2.31	0.43
1:L:130:GLU:OE2	1:L:193:TYR:OH	2.31	0.43
1:B:262:GLN:NE2	1:F:553:ALA:HB2	2.33	0.43
1:H:393:ALA:O	1:H:420:ARG:NH1	2.50	0.43
1:H:505:ILE:HD13	1:H:505:ILE:HA	1.87	0.43
1:I:142:HIS:CD2	1:I:143:ARG:HG2	2.54	0.43
1:J:332:GLU:OE2	3:J:602:NAI:O3B	2.25	0.43
1:E:341:ASP:N	1:E:341:ASP:OD1	2.49	0.43
1:E:464:TYR:HE1	1:E:497:ILE:HG12	1.83	0.43
1:F:257:GLY:HA2	1:F:268:ARG:HG2	1.99	0.43
1:I:426:PRO:HG2	1:I:429:TYR:HB3	2.01	0.43
1:A:289:TYR:CE2	1:A:522:MET:HG2	2.46	0.43
1:D:283:PHE:CD1	1:D:522:MET:HE2	2.53	0.43
1:D:448:HIS:O	1:E:439:TYR:OH	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:403:GLU:HB3	1:E:427:ASP:HB3	2.01	0.43
1:H:136:ARG:NE	1:H:220:ASP:OD2	2.47	0.43
1:J:153:SER:HB3	1:J:156:VAL:HG23	1.99	0.43
1:L:464:TYR:CE1	1:L:497:ILE:HG12	2.53	0.43
1:A:489:PRO:HB3	1:A:493:PHE:CD2	2.53	0.43
1:D:74:PHE:CE2	1:D:543:ILE:HG12	2.53	0.43
1:D:174:VAL:HG23	1:D:542:ALA:HB2	2.01	0.43
1:D:410:THR:HG22	1:D:412:GLU:H	1.83	0.43
1:C:393:ALA:O	1:C:396:VAL:HG12	2.19	0.43
1:J:466:LEU:HD23	1:J:466:LEU:HA	1.83	0.43
1:K:116:LEU:HG	1:K:118:LEU:HD12	2.00	0.43
1:A:477:LYS:HZ3	1:B:485:ILE:HG23	1.84	0.43
1:B:81:VAL:O	1:B:85:LEU:HG	2.18	0.43
1:D:286:GLU:HG3	1:D:522:MET:HE1	2.01	0.43
1:E:206:THR:HG23	1:E:215:ILE:HD13	2.01	0.43
1:J:407:GLY:N	1:J:427:ASP:OD2	2.51	0.43
1:K:152:TYR:O	1:K:227:SER:OG	2.29	0.43
1:A:361:PHE:CD1	1:A:362:PRO:HD2	2.54	0.43
1:B:379:LEU:HB3	1:B:401:ILE:HD13	2.01	0.43
1:F:351:PHE:CD2	1:F:361:PHE:HD1	2.36	0.43
1:H:338:TRP:CD1	1:H:338:TRP:C	2.97	0.43
1:L:309:PHE:CZ	1:L:314:LEU:HD13	2.54	0.43
1:G:299:PHE:HB3	1:G:325:ALA:HB2	2.00	0.43
1:H:283:PHE:HE1	1:H:522:MET:HG3	1.84	0.43
1:I:246:HIS:CG	1:L:211:LYS:HD2	2.54	0.43
1:I:518:ALA:O	1:I:522:MET:HG3	2.19	0.43
1:J:380:ILE:HG13	1:J:402:ALA:HB3	2.01	0.43
1:K:156:VAL:HA	1:K:160:GLU:CD	2.43	0.43
1:L:286:GLU:HG3	1:L:522:MET:HE3	2.00	0.43
1:C:380:ILE:HG12	1:C:402:ALA:HB3	2.01	0.43
1:F:153:SER:HB3	1:F:156:VAL:HG23	2.01	0.43
1:I:118:LEU:HD21	1:I:208:GLU:HB2	2.00	0.43
1:J:275:GLY:O	1:J:514:MET:HE1	2.19	0.43
1:L:429:TYR:CD1	1:L:429:TYR:C	2.97	0.43
1:A:71:GLU:HG2	1:A:110:LYS:NZ	2.34	0.42
1:B:326:LYS:HD2	1:B:341:ASP:O	2.19	0.42
1:C:331:GLY:HA3	1:C:371:ILE:HG12	2.01	0.42
1:F:460:ARG:HE	1:F:498:SER:HA	1.84	0.42
1:I:439:TYR:CZ	1:I:443:LEU:HD11	2.54	0.42
1:J:304:PHE:CZ	1:J:327:CYS:HB2	2.54	0.42
1:D:393:ALA:O	1:D:396:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:505:ILE:HD13	1:D:505:ILE:HA	1.89	0.42
1:E:168:MET:HE3	1:E:168:MET:HB3	1.65	0.42
1:H:114:HIS:NE2	1:K:208:GLU:OE1	2.52	0.42
1:D:121:PRO:HB3	1:F:108:ILE:HG12	2.00	0.42
1:F:264:GLY:HA2	1:F:441:GLU:OE2	2.18	0.42
1:F:283:PHE:CD2	1:F:425:ILE:HG23	2.54	0.42
1:J:400:ILE:HG12	1:J:423:MET:SD	2.59	0.42
1:D:450:SER:HB3	3:D:604:NAI:O1N	2.19	0.42
1:E:260:ILE:HD12	1:E:260:ILE:H	1.83	0.42
1:F:418:LEU:HD12	1:F:418:LEU:HA	1.80	0.42
1:J:136:ARG:HH21	1:J:220:ASP:CG	2.24	0.42
1:J:175:VAL:HG23	1:J:177:VAL:HG23	2.01	0.42
3:J:603:NAI:H71N	3:J:603:NAI:H4N	1.66	0.42
1:D:321:HIS:NE2	1:D:344:ASP:OD1	2.53	0.42
1:E:177:VAL:O	1:E:179:PHE:N	2.52	0.42
1:E:339:ASN:ND2	1:E:364:ALA:HA	2.34	0.42
1:H:130:GLU:OE2	1:H:193:TYR:OH	2.35	0.42
1:I:207:MET:HE3	1:I:207:MET:HA	2.01	0.42
1:I:268:ARG:NE	1:I:438:SER:OG	2.52	0.42
1:K:329:THR:HG22	1:K:338:TRP:HB2	2.01	0.42
1:L:341:ASP:OD2	1:L:363:LYS:NZ	2.53	0.42
1:A:211:LYS:HD2	1:E:246:HIS:CE1	2.55	0.42
1:E:78:ALA:HB1	1:E:106:LEU:HD13	2.02	0.42
1:J:293:LEU:HD11	1:J:399:LYS:HB3	2.01	0.42
1:A:167:LEU:HD23	1:A:167:LEU:HA	1.83	0.42
1:B:346:LYS:HD2	1:B:346:LYS:HA	1.77	0.42
1:G:393:ALA:O	1:G:396:VAL:HG22	2.20	0.42
1:H:393:ALA:O	1:H:396:VAL:HG12	2.19	0.42
1:I:425:ILE:HG21	1:I:430:LEU:HD13	2.01	0.42
1:I:430:LEU:HD12	1:I:430:LEU:HA	1.78	0.42
1:J:338:TRP:HB3	1:J:367:TYR:HB2	2.02	0.42
1:K:378:ILE:HG12	1:K:400:ILE:HD12	2.02	0.42
1:K:520:GLN:HG2	1:K:523:ARG:HH22	1.84	0.42
1:A:289:TYR:HB3	1:A:423:MET:HE1	2.02	0.42
3:F:601:NAI:H71N	3:F:601:NAI:H4N	1.70	0.42
1:G:150:ILE:HG12	1:G:184:ALA:HB3	2.00	0.42
1:G:339:ASN:ND2	1:G:364:ALA:HA	2.34	0.42
1:H:415:LYS:HE2	1:H:415:LYS:HB2	1.83	0.42
1:L:149:GLY:H	1:L:183:LYS:HD2	1.85	0.42
1:L:304:PHE:CE1	1:L:306:VAL:HG23	2.54	0.42
1:A:288:SER:O	1:A:292:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:372:LEU:H	1:J:372:LEU:HD12	1.84	0.42
1:D:263:GLY:HA2	3:D:604:NAI:H2D	2.02	0.42
1:D:320:LEU:HD13	1:D:320:LEU:HA	1.87	0.42
1:E:290:MET:HE2	1:E:290:MET:HA	2.02	0.42
1:G:278:HIS:O	1:G:282:ASN:ND2	2.53	0.42
1:H:215:ILE:HA	1:H:220:ASP:HB3	2.02	0.42
1:I:516:ARG:O	1:I:520:GLN:NE2	2.46	0.42
1:L:401:ILE:HD13	1:L:401:ILE:HA	1.96	0.42
1:A:203:ARG:HG2	1:A:239:THR:OG1	2.19	0.41
1:B:505:ILE:HD13	1:B:505:ILE:HA	1.92	0.41
1:D:335:GLY:HA3	1:D:359:LEU:HD21	2.01	0.41
1:E:327:CYS:O	1:E:342:GLY:HA2	2.20	0.41
1:F:260:ILE:H	1:F:260:ILE:HD12	1.85	0.41
1:G:384:SER:HB2	1:G:387:GLN:HE21	1.85	0.41
1:H:169:THR:OG1	1:H:181:GLY:HA3	2.20	0.41
1:I:347:GLU:CD	1:I:347:GLU:N	2.77	0.41
3:J:603:NAI:O1A	3:J:603:NAI:H8A	2.19	0.41
1:A:82:GLU:O	1:A:86:VAL:HG12	2.19	0.41
1:D:164:LEU:HB2	1:D:183:LYS:HG2	2.02	0.41
1:E:329:THR:HG1	1:E:338:TRP:CD1	2.37	0.41
1:F:456:PHE:CZ	1:F:501:SER:HA	2.54	0.41
1:I:427:ASP:OD1	1:I:427:ASP:N	2.52	0.41
1:L:224:PRO:HA	1:L:233:MET:HE3	2.00	0.41
1:L:494:GLN:OE1	1:L:494:GLN:HA	2.19	0.41
1:D:168:MET:HB3	1:D:181:GLY:HA2	2.02	0.41
1:G:530:LEU:HB3	1:G:533:ASP:HB3	2.02	0.41
1:I:78:ALA:HB1	1:I:106:LEU:HD13	2.02	0.41
1:I:468:MET:HA	1:I:471:GLN:HB3	2.02	0.41
1:L:76:ARG:O	1:L:80:ILE:HG12	2.19	0.41
1:L:352:LYS:HD3	1:L:358:ILE:HG23	2.02	0.41
1:A:393:ALA:O	1:A:396:VAL:HG12	2.21	0.41
1:B:378:ILE:HG12	1:B:400:ILE:HB	2.02	0.41
1:B:386:LYS:H	1:B:408:PRO:HA	1.85	0.41
1:F:81:VAL:HG21	1:F:544:GLU:HG3	2.01	0.41
1:G:499:GLY:O	1:L:458:TYR:OH	2.31	0.41
1:H:407:GLY:N	1:H:427:ASP:OD2	2.53	0.41
1:L:257:GLY:HA2	1:L:268:ARG:HG2	2.02	0.41
1:B:361:PHE:CE2	1:B:363:LYS:HB2	2.55	0.41
1:H:94:THR:O	1:H:98:LYS:HG3	2.19	0.41
1:I:94:THR:HG22	1:I:97:GLN:OE1	2.20	0.41
1:J:456:PHE:HD2	1:K:512:TYR:CZ	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:87:GLU:O	1:K:90:LYS:NZ	2.41	0.41
1:K:290:MET:HE1	1:K:293:LEU:HD23	2.02	0.41
1:A:269:ILE:HD13	1:A:269:ILE:HA	1.91	0.41
1:C:384:SER:HB2	1:C:387:GLN:NE2	2.35	0.41
1:D:136:ARG:HG2	1:D:214:PHE:HD2	1.85	0.41
1:F:326:LYS:HD2	1:F:341:ASP:O	2.20	0.41
1:A:512:TYR:HB2	1:F:457:LYS:HB2	2.02	0.41
1:B:279:GLY:HA3	1:B:430:LEU:HD12	2.01	0.41
1:B:290:MET:HE1	1:B:295:MET:HE3	2.02	0.41
1:F:226:MET:HE3	3:F:603:NAI:H51A	2.03	0.41
1:G:426:PRO:HB3	1:G:535:ARG:HA	2.03	0.41
1:H:396:VAL:HG22	1:H:398:ALA:H	1.85	0.41
1:I:446:LEU:HD23	1:I:446:LEU:HA	1.90	0.41
1:K:97:GLN:OE1	1:K:97:GLN:N	2.33	0.41
1:K:233:MET:SD	1:K:236:ILE:HD12	2.61	0.41
1:L:444:ASN:O	3:L:601:NAI:O3D	2.38	0.41
1:A:130:GLU:OE2	1:A:193:TYR:OH	2.35	0.41
1:A:465:HIS:CE1	1:B:496:ARG:HH21	2.39	0.41
1:D:146:CYS:HB3	1:D:182:ALA:HB2	2.03	0.41
1:D:304:PHE:HA	1:D:378:ILE:O	2.21	0.41
1:E:207:MET:HE1	1:E:244:ILE:HG12	2.03	0.41
1:E:489:PRO:HB3	1:E:493:PHE:CD2	2.53	0.41
1:F:168:MET:HE2	1:F:168:MET:HB2	1.73	0.41
1:L:439:TYR:CZ	1:L:443:LEU:HD11	2.56	0.41
1:A:338:TRP:HB3	1:A:367:TYR:HB2	2.02	0.41
1:B:137:ALA:O	1:B:182:ALA:HA	2.21	0.41
1:B:353:LEU:HD23	1:B:353:LEU:HA	1.86	0.41
1:B:528:TYR:HB2	1:B:530:LEU:CD1	2.51	0.41
1:C:389:THR:HG22	1:C:390:LYS:N	2.35	0.41
1:F:278:HIS:HA	1:F:281:GLU:OE2	2.21	0.41
1:G:124:ARG:HE	1:G:197:GLU:CD	2.29	0.41
1:G:392:ASN:HA	1:G:395:ARG:HE	1.85	0.41
1:G:464:TYR:O	1:G:468:MET:HG2	2.21	0.41
1:H:329:THR:HG23	1:H:338:TRP:HB2	2.03	0.41
1:H:361:PHE:CD1	1:H:362:PRO:HD2	2.55	0.41
1:J:261:SER:OG	1:K:552:GLU:HG3	2.21	0.41
1:L:174:VAL:HG23	1:L:542:ALA:HB2	2.02	0.41
1:C:371:ILE:O	1:C:374:VAL:HG12	2.21	0.41
1:C:385:GLU:CD	1:C:385:GLU:H	2.29	0.41
1:E:444:ASN:O	3:E:601:NAI:O3D	2.33	0.41
1:G:402:ALA:HA	1:G:425:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:338:TRP:CZ2	1:I:340:PRO:HD3	2.56	0.41
1:J:66:PHE:O	1:J:70:VAL:HG23	2.21	0.41
1:J:333:SER:HB3	3:J:602:NAI:C5A	2.51	0.41
1:J:406:ASN:ND2	3:J:602:NAI:O2D	2.53	0.41
1:B:304:PHE:O	1:B:327:CYS:HA	2.21	0.40
1:C:301:ASP:OD1	1:C:302:LYS:NZ	2.53	0.40
1:E:124:ARG:HD3	1:E:130:GLU:OE1	2.20	0.40
1:E:334:ASP:HB2	1:E:359:LEU:HD11	2.02	0.40
1:G:72:GLY:O	1:G:76:ARG:HG3	2.21	0.40
1:G:380:ILE:HA	1:G:402:ALA:O	2.21	0.40
1:G:489:PRO:HB3	1:G:493:PHE:CD2	2.54	0.40
1:H:301:ASP:OD1	1:H:301:ASP:N	2.50	0.40
1:K:401:ILE:HB	1:K:424:VAL:HG22	2.03	0.40
1:A:92:ARG:HA	1:A:92:ARG:CZ	2.51	0.40
1:F:279:GLY:HA3	1:F:430:LEU:HD12	2.03	0.40
1:H:78:ALA:HB1	1:H:106:LEU:HD13	2.03	0.40
1:J:311:ASN:ND2	3:J:602:NAI:O1N	2.55	0.40
1:K:339:ASN:HD22	1:K:364:ALA:HA	1.86	0.40
1:A:478:PHE:HE2	1:H:297:PRO:CD	2.33	0.40
1:C:233:MET:HE2	1:C:233:MET:N	2.37	0.40
1:C:304:PHE:CZ	1:C:317:MET:HG3	2.57	0.40
1:D:215:ILE:HG13	1:D:222:PRO:HD3	2.03	0.40
1:D:492:GLU:OE1	1:D:492:GLU:N	2.52	0.40
1:E:338:TRP:CZ3	1:E:365:LYS:HE3	2.57	0.40
1:G:404:GLY:O	1:G:431:ASN:ND2	2.51	0.40
1:J:124:ARG:HE	1:J:197:GLU:CD	2.29	0.40
1:J:295:MET:HE2	1:J:399:LYS:HG3	2.04	0.40
1:L:389:THR:HG22	1:L:390:LYS:H	1.86	0.40
1:A:168:MET:HE1	4:A:603:GGL:C	2.51	0.40
1:A:285:ASN:OD1	1:A:285:ASN:C	2.65	0.40
1:B:530:LEU:HD22	1:B:537:ALA:HB2	2.02	0.40
1:D:226:MET:HB2	1:D:226:MET:HE3	1.81	0.40
1:D:233:MET:HE3	1:D:255:VAL:CG2	2.51	0.40
1:F:351:PHE:HE1	1:F:355:HIS:CG	2.40	0.40
1:G:122:ILE:HG21	1:G:201:ILE:HG12	2.03	0.40
1:G:257:GLY:H	1:G:441:GLU:CD	2.28	0.40
1:G:307:GLN:HG3	1:G:371:ILE:HG21	2.02	0.40
1:G:467:LEU:HD21	1:L:466:LEU:HD11	2.04	0.40
1:L:363:LYS:HD2	1:L:363:LYS:HA	1.92	0.40
1:L:426:PRO:HB3	1:L:535:ARG:HA	2.04	0.40
1:A:164:LEU:HD13	1:A:183:LYS:HE3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:LYS:HD2	1:A:363:LYS:HA	1.90	0.40
1:D:108:ILE:HG12	1:F:121:PRO:HB3	2.04	0.40
1:E:147:LYS:HD2	1:E:221:VAL:O	2.22	0.40
1:E:272:THR:OG1	3:E:603:NAI:H42N	2.22	0.40
1:F:394:PRO:O	1:F:420:ARG:NH1	2.54	0.40
1:G:109:ILE:O	1:G:139:HIS:NE2	2.54	0.40
1:H:456:PHE:HZ	1:H:501:SER:HA	1.87	0.40
1:I:186:VAL:HG12	1:I:188:ILE:HG23	2.04	0.40
1:I:456:PHE:HZ	1:I:501:SER:HA	1.86	0.40
1:J:215:ILE:HG13	1:J:222:PRO:HD3	2.02	0.40
1:K:215:ILE:HA	1:K:220:ASP:HB3	2.02	0.40
1:K:233:MET:SD	1:K:233:MET:N	2.93	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	491/558 (88%)	484 (99%)	7 (1%)	0	100	100
1	B	491/558 (88%)	483 (98%)	8 (2%)	0	100	100
1	C	491/558 (88%)	480 (98%)	11 (2%)	0	100	100
1	D	491/558 (88%)	481 (98%)	10 (2%)	0	100	100
1	E	491/558 (88%)	483 (98%)	8 (2%)	0	100	100
1	F	491/558 (88%)	476 (97%)	15 (3%)	0	100	100
1	G	491/558 (88%)	479 (98%)	12 (2%)	0	100	100
1	H	491/558 (88%)	482 (98%)	9 (2%)	0	100	100
1	I	491/558 (88%)	485 (99%)	6 (1%)	0	100	100
1	J	491/558 (88%)	482 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	491/558 (88%)	481 (98%)	10 (2%)	0	100	100
1	L	491/558 (88%)	483 (98%)	8 (2%)	0	100	100
All	All	5892/6696 (88%)	5779 (98%)	113 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	413/456 (91%)	411 (100%)	2 (0%)	81	80
1	B	413/456 (91%)	410 (99%)	3 (1%)	76	78
1	C	413/456 (91%)	413 (100%)	0	100	100
1	D	413/456 (91%)	411 (100%)	2 (0%)	81	80
1	E	413/456 (91%)	410 (99%)	3 (1%)	76	78
1	F	413/456 (91%)	409 (99%)	4 (1%)	68	75
1	G	413/456 (91%)	413 (100%)	0	100	100
1	H	413/456 (91%)	411 (100%)	2 (0%)	81	80
1	I	413/456 (91%)	413 (100%)	0	100	100
1	J	413/456 (91%)	413 (100%)	0	100	100
1	K	413/456 (91%)	412 (100%)	1 (0%)	87	85
1	L	413/456 (91%)	409 (99%)	4 (1%)	68	75
All	All	4956/5472 (91%)	4935 (100%)	21 (0%)	81	81

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	262	GLN
1	A	282	ASN
1	B	341	ASP
1	B	343	ILE

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Mol	Chain	Res	Type
1	B	346	LYS
1	D	159	ASP
1	D	529	ASN
1	E	262	GLN
1	E	456	PHE
1	E	481	HIS
1	F	343	ILE
1	F	346	LYS
1	F	484	THR
1	F	488	VAL
1	H	66	PHE
1	H	68	LYS
1	K	262	GLN
1	L	295	MET
1	L	296	THR
1	L	299	PHE
1	L	532	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	246	HIS
1	A	354	GLN
1	B	266	HIS
1	C	285	ASN
1	C	481	HIS
1	D	285	ASN
1	D	354	GLN
1	D	421	ASN
1	E	192	ASN
1	E	266	HIS
1	E	285	ASN
1	E	339	ASN
1	E	444	ASN
1	F	192	ASN
1	F	246	HIS
1	F	252	HIS
1	F	262	GLN
1	F	282	ASN
1	F	465	HIS
1	G	65	ASN
1	G	262	GLN

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Mol	Chain	Res	Type
1	H	406	ASN
1	H	421	ASN
1	H	444	ASN
1	I	285	ASN
1	I	444	ASN
1	I	463	ASN
1	J	262	GLN
1	J	285	ASN
1	J	311	ASN
1	J	406	ASN
1	J	444	ASN
1	J	551	ASN
1	K	285	ASN
1	K	406	ASN
1	K	520	GLN
1	K	529	ASN
1	L	141	GLN
1	L	262	GLN
1	L	266	HIS
1	L	444	ASN
1	L	471	GLN
1	L	541	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

42 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GGL	F	604	-	8,9,9	1.12	0	8,11,11	0.67	0
2	GTP	E	602	-	33,34,34	2.34	8 (24%)	50,54,54	1.78	11 (22%)
3	NAI	G	603	-	47,48,48	1.28	2 (4%)	64,73,73	1.02	3 (4%)
4	GGL	C	603	-	8,9,9	1.13	0	8,11,11	0.64	0
2	GTP	H	601	-	33,34,34	2.37	9 (27%)	50,54,54	1.77	10 (20%)
3	NAI	C	602	-	47,48,48	1.27	4 (8%)	64,73,73	1.04	3 (4%)
3	NAI	E	601	-	47,48,48	1.25	2 (4%)	64,73,73	1.01	3 (4%)
2	GTP	K	602	-	33,34,34	2.35	9 (27%)	50,54,54	1.79	11 (22%)
3	NAI	B	602	-	47,48,48	1.31	5 (10%)	64,73,73	1.04	3 (4%)
2	GTP	A	601	-	33,34,34	2.31	9 (27%)	50,54,54	1.77	11 (22%)
2	GTP	J	601	-	33,34,34	2.36	9 (27%)	50,54,54	1.76	11 (22%)
3	NAI	K	601	-	47,48,48	1.29	4 (8%)	64,73,73	1.03	3 (4%)
2	GTP	L	602	-	33,34,34	2.35	9 (27%)	50,54,54	1.77	11 (22%)
3	NAI	H	603	-	47,48,48	1.27	3 (6%)	64,73,73	1.02	4 (6%)
3	NAI	C	604	-	47,48,48	1.24	4 (8%)	64,73,73	1.02	3 (4%)
3	NAI	F	601	-	47,48,48	1.22	3 (6%)	64,73,73	1.03	3 (4%)
3	NAI	L	601	-	47,48,48	1.27	3 (6%)	64,73,73	1.03	2 (3%)
2	GTP	C	601	-	33,34,34	2.33	7 (21%)	50,54,54	1.80	11 (22%)
3	NAI	A	604	-	47,48,48	1.28	3 (6%)	64,73,73	1.00	2 (3%)
2	GTP	B	601	-	33,34,34	2.31	9 (27%)	50,54,54	1.80	11 (22%)
2	GTP	D	601	-	33,34,34	2.32	9 (27%)	50,54,54	1.77	11 (22%)
3	NAI	D	602	-	47,48,48	1.31	5 (10%)	64,73,73	1.05	3 (4%)
3	NAI	J	603	-	47,48,48	1.29	4 (8%)	64,73,73	1.03	3 (4%)
2	GTP	G	601	-	33,34,34	2.34	9 (27%)	50,54,54	1.77	10 (20%)
4	GGL	B	603	-	8,9,9	1.15	0	8,11,11	0.75	0
3	NAI	F	603	-	47,48,48	1.34	5 (10%)	64,73,73	1.04	2 (3%)
4	GGL	E	604	-	8,9,9	1.15	0	8,11,11	0.61	0
4	GGL	A	603	-	8,9,9	1.10	0	8,11,11	0.75	0
2	GTP	I	601	-	33,34,34	2.35	9 (27%)	50,54,54	1.77	11 (22%)
3	NAI	I	603	-	47,48,48	1.30	4 (8%)	64,73,73	1.01	4 (6%)
3	NAI	G	602	-	47,48,48	1.30	4 (8%)	64,73,73	1.03	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAI	A	602	-	47,48,48	1.28	5 (10%)	64,73,73	1.01	3 (4%)
3	NAI	H	602	-	47,48,48	1.30	6 (12%)	64,73,73	1.05	2 (3%)
3	NAI	J	602	-	47,48,48	1.32	6 (12%)	64,73,73	1.03	2 (3%)
3	NAI	L	603	-	47,48,48	1.28	4 (8%)	64,73,73	1.07	3 (4%)
3	NAI	D	604	-	47,48,48	1.24	2 (4%)	64,73,73	1.01	3 (4%)
3	NAI	E	603	-	47,48,48	1.27	5 (10%)	64,73,73	1.11	4 (6%)
3	NAI	B	604	-	47,48,48	1.23	4 (8%)	64,73,73	1.02	3 (4%)
2	GTP	F	602	-	33,34,34	2.33	9 (27%)	50,54,54	1.81	11 (22%)
3	NAI	I	602	-	47,48,48	1.30	6 (12%)	64,73,73	1.05	2 (3%)
3	NAI	K	603	-	47,48,48	1.30	5 (10%)	64,73,73	1.01	2 (3%)
4	GGL	D	603	-	8,9,9	1.13	0	8,11,11	0.65	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GGL	F	604	-	-	5/9/9/9	-
2	GTP	E	602	-	-	6/22/38/38	0/3/3/3
3	NAI	G	603	-	-	13/29/72/72	0/5/5/5
4	GGL	C	603	-	-	3/9/9/9	-
2	GTP	H	601	-	-	3/22/38/38	0/3/3/3
3	NAI	C	602	-	-	10/29/72/72	0/5/5/5
3	NAI	E	601	-	-	16/29/72/72	0/5/5/5
2	GTP	K	602	-	-	5/22/38/38	0/3/3/3
3	NAI	B	602	-	-	8/29/72/72	0/5/5/5
2	GTP	A	601	-	-	7/22/38/38	0/3/3/3
2	GTP	J	601	-	-	5/22/38/38	0/3/3/3
3	NAI	K	601	-	-	11/29/72/72	0/5/5/5
2	GTP	L	602	-	-	2/22/38/38	0/3/3/3
3	NAI	H	603	-	-	9/29/72/72	0/5/5/5
3	NAI	C	604	-	-	15/29/72/72	0/5/5/5
3	NAI	F	601	-	-	9/29/72/72	0/5/5/5
3	NAI	L	601	-	-	10/29/72/72	0/5/5/5
2	GTP	C	601	-	-	4/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAI	A	604	-	-	16/29/72/72	0/5/5/5
2	GTP	B	601	-	-	1/22/38/38	0/3/3/3
2	GTP	D	601	-	-	6/22/38/38	0/3/3/3
3	NAI	D	602	-	-	7/29/72/72	0/5/5/5
3	NAI	J	603	-	-	9/29/72/72	0/5/5/5
2	GTP	G	601	-	-	4/22/38/38	0/3/3/3
4	GGL	B	603	-	-	5/9/9/9	-
3	NAI	F	603	-	-	2/29/72/72	0/5/5/5
4	GGL	E	604	-	-	3/9/9/9	-
4	GGL	A	603	-	-	5/9/9/9	-
2	GTP	I	601	-	-	4/22/38/38	0/3/3/3
3	NAI	I	603	-	-	17/29/72/72	0/5/5/5
3	NAI	G	602	-	-	11/29/72/72	0/5/5/5
3	NAI	A	602	-	-	5/29/72/72	0/5/5/5
3	NAI	H	602	-	-	9/29/72/72	0/5/5/5
3	NAI	J	602	-	-	11/29/72/72	0/5/5/5
3	NAI	L	603	-	-	10/29/72/72	0/5/5/5
3	NAI	D	604	-	-	13/29/72/72	0/5/5/5
3	NAI	E	603	-	-	7/29/72/72	0/5/5/5
3	NAI	B	604	-	-	15/29/72/72	0/5/5/5
2	GTP	F	602	-	-	1/22/38/38	0/3/3/3
3	NAI	I	602	-	-	7/29/72/72	0/5/5/5
3	NAI	K	603	-	-	14/29/72/72	0/5/5/5
4	GGL	D	603	-	-	3/9/9/9	-

All (203) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	601	GTP	PB-O3A	8.02	1.68	1.59
2	K	602	GTP	PB-O3A	7.90	1.68	1.59
2	L	602	GTP	PB-O3A	7.78	1.67	1.59
2	H	601	GTP	PB-O3A	7.77	1.67	1.59
2	G	601	GTP	PB-O3A	7.70	1.67	1.59
2	F	602	GTP	PB-O3A	7.66	1.67	1.59
2	I	601	GTP	PB-O3A	7.64	1.67	1.59
2	C	601	GTP	PB-O3A	7.60	1.67	1.59
2	E	602	GTP	PB-O3A	7.44	1.67	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	GTP	PB-O3A	7.39	1.67	1.59
2	B	601	GTP	PB-O3A	7.16	1.67	1.59
2	A	601	GTP	PB-O3A	7.15	1.67	1.59
2	I	601	GTP	PA-O5'	6.22	1.83	1.59
2	J	601	GTP	PA-O5'	6.11	1.83	1.59
2	G	601	GTP	PA-O5'	6.08	1.83	1.59
2	H	601	GTP	PA-O5'	6.07	1.83	1.59
2	K	602	GTP	PA-O5'	6.05	1.83	1.59
2	E	602	GTP	PA-O5'	6.00	1.82	1.59
2	L	602	GTP	PA-O5'	5.99	1.82	1.59
2	A	601	GTP	PA-O5'	5.85	1.82	1.59
2	D	601	GTP	PA-O5'	5.83	1.82	1.59
2	F	602	GTP	PA-O5'	5.77	1.82	1.59
2	B	601	GTP	PA-O5'	5.72	1.81	1.59
2	C	601	GTP	PA-O5'	5.65	1.81	1.59
2	B	601	GTP	PA-O3A	-4.77	1.54	1.59
2	A	601	GTP	PA-O3A	-4.75	1.54	1.59
2	E	602	GTP	PA-O3A	-4.70	1.54	1.59
2	B	601	GTP	PB-O3B	-4.64	1.54	1.59
2	C	601	GTP	PA-O3A	-4.64	1.54	1.59
2	E	602	GTP	PB-O3B	-4.60	1.54	1.59
2	H	601	GTP	PB-O3B	-4.57	1.54	1.59
2	D	601	GTP	PA-O3A	-4.55	1.54	1.59
2	D	601	GTP	PB-O3B	-4.53	1.54	1.59
2	C	601	GTP	PB-O3B	-4.53	1.54	1.59
2	A	601	GTP	PB-O3B	-4.52	1.54	1.59
2	L	602	GTP	PB-O3B	-4.43	1.54	1.59
2	F	602	GTP	PB-O3B	-4.34	1.54	1.59
2	F	602	GTP	PA-O3A	-4.33	1.54	1.59
2	H	601	GTP	PA-O3A	-4.32	1.54	1.59
2	I	601	GTP	PA-O3A	-4.27	1.54	1.59
2	G	601	GTP	PA-O3A	-4.26	1.54	1.59
2	K	602	GTP	PA-O3A	-4.24	1.54	1.59
2	I	601	GTP	PB-O3B	-4.21	1.54	1.59
2	L	602	GTP	PA-O3A	-4.15	1.55	1.59
2	G	601	GTP	PB-O3B	-4.15	1.55	1.59
2	K	602	GTP	PB-O3B	-4.13	1.55	1.59
2	J	601	GTP	PA-O3A	-4.11	1.55	1.59
2	J	601	GTP	PB-O3B	-4.10	1.55	1.59
3	A	604	NAI	PN-O5D	3.29	1.72	1.59
3	E	601	NAI	PN-O5D	3.25	1.72	1.59
3	I	603	NAI	PN-O5D	3.24	1.72	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	601	NAI	PN-O5D	3.20	1.71	1.59
3	F	601	NAI	PN-O5D	3.17	1.71	1.59
3	C	604	NAI	PN-O5D	3.15	1.71	1.59
3	G	603	NAI	PN-O5D	3.13	1.71	1.59
3	F	603	NAI	PN-O5D	3.13	1.71	1.59
3	H	603	NAI	PN-O5D	3.10	1.71	1.59
3	J	602	NAI	PN-O5D	3.10	1.71	1.59
3	D	604	NAI	PN-O5D	3.10	1.71	1.59
3	I	602	NAI	PN-O5D	3.09	1.71	1.59
3	K	603	NAI	PN-O5D	3.08	1.71	1.59
3	J	603	NAI	PN-O5D	3.08	1.71	1.59
3	L	601	NAI	PN-O5D	3.07	1.71	1.59
3	L	603	NAI	PN-O5D	3.03	1.71	1.59
3	A	602	NAI	PN-O5D	3.03	1.71	1.59
3	H	602	NAI	PN-O5D	2.99	1.71	1.59
3	H	603	NAI	PA-O5B	2.97	1.71	1.59
3	B	604	NAI	PN-O5D	2.96	1.71	1.59
3	A	604	NAI	PA-O5B	2.95	1.71	1.59
3	E	601	NAI	PA-O5B	2.94	1.70	1.59
3	D	602	NAI	PN-O5D	2.93	1.70	1.59
3	G	602	NAI	PN-O5D	2.92	1.70	1.59
3	C	602	NAI	PN-O5D	2.89	1.70	1.59
3	I	603	NAI	PA-O5B	2.88	1.70	1.59
3	G	603	NAI	PA-O5B	2.86	1.70	1.59
3	D	604	NAI	PA-O5B	2.85	1.70	1.59
3	B	602	NAI	PN-O5D	2.83	1.70	1.59
3	B	604	NAI	PA-O5B	2.83	1.70	1.59
3	F	601	NAI	PA-O5B	2.82	1.70	1.59
3	I	602	NAI	PA-O5B	2.82	1.70	1.59
3	K	603	NAI	PA-O5B	2.79	1.70	1.59
3	G	602	NAI	PA-O5B	2.78	1.70	1.59
3	E	603	NAI	PN-O5D	2.77	1.70	1.59
3	A	602	NAI	PA-O5B	2.76	1.70	1.59
3	J	602	NAI	PA-O5B	2.76	1.70	1.59
3	C	604	NAI	PA-O5B	2.74	1.70	1.59
3	K	601	NAI	PA-O5B	2.74	1.70	1.59
3	H	602	NAI	PA-O5B	2.70	1.70	1.59
3	J	603	NAI	PA-O5B	2.68	1.69	1.59
3	L	601	NAI	PA-O5B	2.65	1.69	1.59
3	L	603	NAI	PA-O5B	2.65	1.69	1.59
3	E	603	NAI	PA-O5B	2.61	1.69	1.59
3	B	602	NAI	PA-O5B	2.60	1.69	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	602	NAI	PA-O5B	2.59	1.69	1.59
2	C	601	GTP	O5'-C5'	-2.59	1.34	1.44
2	B	601	GTP	O5'-C5'	-2.54	1.35	1.44
2	J	601	GTP	C4-N3	2.53	1.40	1.34
2	G	601	GTP	C4-N3	2.53	1.40	1.34
2	L	602	GTP	O5'-C5'	-2.52	1.35	1.44
2	F	602	GTP	O5'-C5'	-2.52	1.35	1.44
2	E	602	GTP	O5'-C5'	-2.51	1.35	1.44
2	D	601	GTP	O5'-C5'	-2.49	1.35	1.44
2	K	602	GTP	O5'-C5'	-2.49	1.35	1.44
2	H	601	GTP	O5'-C5'	-2.49	1.35	1.44
2	G	601	GTP	O5'-C5'	-2.49	1.35	1.44
2	I	601	GTP	C4-N3	2.48	1.39	1.34
2	K	602	GTP	C4-N3	2.48	1.39	1.34
3	F	603	NAI	PA-O5B	2.48	1.69	1.59
2	J	601	GTP	O5'-C5'	-2.47	1.35	1.44
2	A	601	GTP	O5'-C5'	-2.44	1.35	1.44
3	D	602	NAI	PA-O5B	2.44	1.68	1.59
2	I	601	GTP	O5'-C5'	-2.43	1.35	1.44
2	L	602	GTP	C4-N3	2.42	1.39	1.34
3	K	603	NAI	C8A-N9A	2.41	1.41	1.37
2	F	602	GTP	C4-N3	2.41	1.39	1.34
2	I	601	GTP	C2-N2	2.40	1.39	1.34
2	K	602	GTP	C2-N2	2.37	1.39	1.34
2	B	601	GTP	C2-N2	2.37	1.39	1.34
2	G	601	GTP	C2-N2	2.37	1.39	1.34
2	J	601	GTP	C2-N2	2.36	1.39	1.34
2	L	602	GTP	C2-N2	2.35	1.39	1.34
3	J	602	NAI	C8A-N9A	2.34	1.41	1.37
2	F	602	GTP	C2-N2	2.33	1.39	1.34
2	H	601	GTP	C4-N3	2.33	1.39	1.34
2	A	601	GTP	C4-N3	2.33	1.39	1.34
3	F	603	NAI	O5B-C5B	-2.33	1.35	1.44
3	G	602	NAI	C8A-N9A	2.32	1.41	1.37
2	D	601	GTP	C4-N3	2.32	1.39	1.34
3	I	602	NAI	C8A-N9A	2.32	1.41	1.37
2	B	601	GTP	C4-N3	2.29	1.39	1.34
3	H	602	NAI	C8A-N9A	2.29	1.41	1.37
2	E	602	GTP	C4-N3	2.28	1.39	1.34
2	A	601	GTP	C2-N2	2.27	1.39	1.34
2	H	601	GTP	C2-N2	2.27	1.39	1.34
2	H	601	GTP	C6-N1	2.27	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	603	NAI	PN-O3	-2.27	1.57	1.59
3	A	604	NAI	O4D-C4D	-2.26	1.40	1.45
2	I	601	GTP	C6-N1	2.26	1.43	1.38
2	E	602	GTP	C2-N2	2.26	1.39	1.34
2	K	602	GTP	C6-N1	2.25	1.43	1.38
2	C	601	GTP	C4-N3	2.25	1.39	1.34
3	D	602	NAI	O5B-C5B	-2.24	1.36	1.44
2	D	601	GTP	C2-N2	2.24	1.39	1.34
2	G	601	GTP	C6-N1	2.23	1.43	1.38
2	F	602	GTP	C6-N1	2.23	1.43	1.38
2	H	601	GTP	C8-N9	2.23	1.42	1.37
3	L	603	NAI	O5B-C5B	-2.22	1.36	1.44
2	J	601	GTP	C6-N1	2.22	1.43	1.38
2	K	602	GTP	C8-N9	2.20	1.42	1.37
3	E	603	NAI	O5B-C5B	-2.20	1.36	1.44
3	A	602	NAI	C8A-N9A	2.20	1.41	1.37
3	B	602	NAI	PN-O3	-2.20	1.57	1.59
3	B	602	NAI	O5B-C5B	-2.18	1.36	1.44
2	I	601	GTP	C8-N9	2.18	1.42	1.37
2	G	601	GTP	C8-N9	2.17	1.42	1.37
2	C	601	GTP	C2-N2	2.17	1.39	1.34
3	L	603	NAI	C8A-N9A	2.17	1.41	1.37
3	J	603	NAI	C8A-N9A	2.16	1.41	1.37
2	A	601	GTP	C8-N9	2.16	1.42	1.37
2	L	602	GTP	C6-N1	2.16	1.42	1.38
3	F	603	NAI	PN-O3	-2.15	1.57	1.59
3	D	602	NAI	O4B-C4B	-2.15	1.40	1.45
3	H	603	NAI	C8A-N9A	2.15	1.41	1.37
3	J	602	NAI	C5A-C4A	2.15	1.42	1.39
3	F	603	NAI	C8A-N9A	2.14	1.41	1.37
3	B	604	NAI	O4D-C4D	-2.13	1.40	1.45
3	J	602	NAI	O5B-C5B	-2.13	1.36	1.44
2	J	601	GTP	C8-N9	2.13	1.42	1.37
2	L	602	GTP	C8-N9	2.13	1.42	1.37
3	J	602	NAI	C2A-N1A	2.12	1.37	1.33
3	A	602	NAI	O5B-C5B	-2.12	1.36	1.44
3	C	602	NAI	O5B-C5B	-2.11	1.36	1.44
3	J	603	NAI	O5B-C5B	-2.11	1.36	1.44
3	I	602	NAI	O5B-C5B	-2.11	1.36	1.44
3	B	602	NAI	C8A-N9A	2.11	1.41	1.37
3	K	603	NAI	O5B-C5B	-2.10	1.36	1.44
2	B	601	GTP	C6-N1	2.10	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	GTP	C6-N1	2.10	1.42	1.38
3	H	602	NAI	O5B-C5B	-2.10	1.36	1.44
3	H	602	NAI	C2A-N1A	2.10	1.37	1.33
3	G	602	NAI	O5B-C5B	-2.09	1.36	1.44
3	B	604	NAI	O5D-C5D	-2.09	1.36	1.44
3	K	603	NAI	C5A-C4A	2.09	1.42	1.39
3	K	601	NAI	C8A-N9A	2.08	1.41	1.37
3	C	604	NAI	O5B-C5B	-2.08	1.36	1.44
3	L	601	NAI	O5B-C5B	-2.08	1.36	1.44
3	F	601	NAI	O5B-C5B	-2.08	1.36	1.44
2	E	602	GTP	C6-N1	2.08	1.42	1.38
3	I	603	NAI	C8A-N9A	2.06	1.41	1.37
3	H	602	NAI	C5A-C4A	2.06	1.42	1.39
3	I	602	NAI	C2A-N1A	2.06	1.37	1.33
3	D	602	NAI	PN-O3	-2.06	1.57	1.59
3	E	603	NAI	O5D-C5D	-2.05	1.36	1.44
2	F	602	GTP	C8-N9	2.05	1.42	1.37
3	I	603	NAI	O5B-C5B	-2.05	1.36	1.44
3	A	602	NAI	PN-O3	-2.05	1.57	1.59
2	D	601	GTP	C5'-C4'	2.04	1.57	1.51
3	K	601	NAI	O5B-C5B	-2.03	1.36	1.44
3	I	602	NAI	C5A-C4A	2.03	1.42	1.39
3	C	604	NAI	O5D-C5D	-2.02	1.36	1.44
2	D	601	GTP	C6-N1	2.01	1.42	1.38
2	B	601	GTP	C8-N9	2.01	1.42	1.37
3	C	602	NAI	O4D-C4D	-2.00	1.40	1.45

All (197) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	602	GTP	O2B-PB-O3A	-5.32	92.89	107.27
2	C	601	GTP	O2B-PB-O3A	-5.32	92.89	107.27
2	B	601	GTP	O2B-PB-O3A	-5.28	93.01	107.27
2	I	601	GTP	O2B-PB-O3A	-5.26	93.05	107.27
2	A	601	GTP	O2B-PB-O3A	-5.24	93.10	107.27
2	K	602	GTP	O2B-PB-O3A	-5.24	93.10	107.27
2	E	602	GTP	O2B-PB-O3A	-5.20	93.21	107.27
2	L	602	GTP	O2B-PB-O3A	-5.20	93.22	107.27
2	H	601	GTP	O2B-PB-O3A	-5.20	93.22	107.27
2	G	601	GTP	O2B-PB-O3A	-5.19	93.25	107.27
2	D	601	GTP	O2B-PB-O3A	-5.13	93.40	107.27
2	J	601	GTP	O2B-PB-O3A	-5.07	93.58	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	GTP	O5'-PA-O1A	-4.34	91.73	108.94
2	F	602	GTP	O5'-PA-O1A	-4.27	92.00	108.94
2	C	601	GTP	O5'-PA-O1A	-4.25	92.08	108.94
2	E	602	GTP	O5'-PA-O1A	-4.23	92.17	108.94
2	K	602	GTP	O5'-PA-O1A	-4.21	92.25	108.94
2	H	601	GTP	O5'-PA-O1A	-4.20	92.30	108.94
2	I	601	GTP	O5'-PA-O1A	-4.10	92.70	108.94
2	D	601	GTP	O5'-PA-O1A	-4.08	92.77	108.94
2	A	601	GTP	O5'-PA-O1A	-4.07	92.81	108.94
2	L	602	GTP	O5'-PA-O1A	-4.07	92.81	108.94
2	J	601	GTP	O5'-PA-O1A	-3.98	93.15	108.94
2	G	601	GTP	O5'-PA-O1A	-3.89	93.51	108.94
2	B	601	GTP	O3A-PA-O1A	3.73	121.93	110.70
2	A	601	GTP	O3A-PA-O1A	3.69	121.79	110.70
2	L	602	GTP	O3A-PA-O1A	3.65	121.69	110.70
2	C	601	GTP	O3A-PA-O1A	3.64	121.66	110.70
2	H	601	GTP	O3A-PA-O1A	3.63	121.64	110.70
2	I	601	GTP	O3A-PA-O1A	3.63	121.62	110.70
2	E	602	GTP	O3A-PA-O1A	3.62	121.61	110.70
2	G	601	GTP	O3A-PA-O1A	3.60	121.52	110.70
2	D	601	GTP	O3A-PA-O1A	3.59	121.49	110.70
2	K	602	GTP	O3A-PA-O1A	3.58	121.48	110.70
2	F	602	GTP	O3A-PA-O1A	3.57	121.44	110.70
2	J	601	GTP	O2A-PA-O3A	3.55	116.87	107.27
2	J	601	GTP	O3A-PA-O1A	3.48	121.16	110.70
2	F	602	GTP	O2A-PA-O3A	3.47	116.65	107.27
2	K	602	GTP	O2A-PA-O3A	3.46	116.63	107.27
2	C	601	GTP	O2A-PA-O3A	3.38	116.42	107.27
2	D	601	GTP	O2A-PA-O3A	3.37	116.39	107.27
2	G	601	GTP	O2A-PA-O3A	3.33	116.29	107.27
2	H	601	GTP	O2A-PA-O3A	3.33	116.28	107.27
2	L	602	GTP	O2A-PA-O3A	3.32	116.26	107.27
2	F	602	GTP	O2B-PB-O3B	3.32	116.25	107.27
2	I	601	GTP	O2A-PA-O3A	3.29	116.18	107.27
2	C	601	GTP	O2B-PB-O3B	3.29	116.17	107.27
2	E	602	GTP	O2A-PA-O3A	3.29	116.16	107.27
2	J	601	GTP	O2B-PB-O3B	3.27	116.11	107.27
2	G	601	GTP	O2B-PB-O3B	3.24	116.04	107.27
2	D	601	GTP	O2B-PB-O3B	3.23	116.01	107.27
2	I	601	GTP	O2B-PB-O3B	3.23	115.99	107.27
2	K	602	GTP	O2B-PB-O3B	3.21	115.95	107.27
2	A	601	GTP	O2B-PB-O3B	3.20	115.91	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	602	GTP	O2B-PB-O3B	3.19	115.88	107.27
2	B	601	GTP	O2A-PA-O3A	3.18	115.87	107.27
2	E	602	GTP	O2B-PB-O3B	3.17	115.83	107.27
2	A	601	GTP	O2A-PA-O3A	3.15	115.80	107.27
2	B	601	GTP	O2B-PB-O3B	3.15	115.79	107.27
2	H	601	GTP	O2B-PB-O3B	3.14	115.76	107.27
3	F	603	NAI	O1N-PN-O2N	3.04	126.61	112.44
3	D	602	NAI	O1N-PN-O2N	3.04	126.57	112.44
3	A	602	NAI	O1N-PN-O2N	3.02	126.50	112.44
3	E	603	NAI	O1N-PN-O2N	2.98	126.33	112.44
3	B	602	NAI	O1N-PN-O2N	2.96	126.23	112.44
3	C	602	NAI	O1N-PN-O2N	2.95	126.16	112.44
3	H	602	NAI	O1N-PN-O2N	2.94	126.11	112.44
3	L	603	NAI	O1N-PN-O2N	2.93	126.06	112.44
3	I	602	NAI	O1N-PN-O2N	2.92	126.03	112.44
3	J	602	NAI	O1N-PN-O2N	2.92	126.02	112.44
3	I	603	NAI	O1N-PN-O2N	2.89	125.87	112.44
3	K	603	NAI	O1N-PN-O2N	2.88	125.83	112.44
3	J	603	NAI	O1N-PN-O2N	2.87	125.79	112.44
3	K	601	NAI	O1N-PN-O2N	2.87	125.78	112.44
3	A	604	NAI	O1N-PN-O2N	2.85	125.69	112.44
3	G	602	NAI	O1N-PN-O2N	2.84	125.66	112.44
3	E	601	NAI	O1N-PN-O2N	2.84	125.64	112.44
3	G	603	NAI	O1N-PN-O2N	2.83	125.61	112.44
3	L	601	NAI	O1N-PN-O2N	2.81	125.52	112.44
3	F	601	NAI	O1N-PN-O2N	2.80	125.48	112.44
3	D	604	NAI	O1N-PN-O2N	2.80	125.48	112.44
3	H	603	NAI	O1N-PN-O2N	2.80	125.47	112.44
3	C	604	NAI	O1N-PN-O2N	2.80	125.45	112.44
3	B	604	NAI	O1N-PN-O2N	2.77	125.32	112.44
2	F	602	GTP	C3'-C2'-C1'	-2.57	96.59	101.46
2	K	602	GTP	C3'-C2'-C1'	-2.53	96.67	101.46
2	E	602	GTP	C2-N1-C6	-2.50	120.57	125.11
2	A	601	GTP	C2-N1-C6	-2.44	120.68	125.11
2	G	601	GTP	C2-N1-C6	-2.44	120.68	125.11
2	L	602	GTP	C2-N1-C6	-2.44	120.68	125.11
2	H	601	GTP	C2-N1-C6	-2.44	120.69	125.11
2	I	601	GTP	C2-N1-C6	-2.44	120.69	125.11
2	D	601	GTP	C2-N1-C6	-2.44	120.69	125.11
2	G	601	GTP	O6-C6-N1	-2.43	115.55	120.11
2	B	601	GTP	C2-N1-C6	-2.43	120.71	125.11
3	E	603	NAI	O2A-PA-O1A	2.43	123.73	112.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	602	GTP	C2-N1-C6	-2.42	120.72	125.11
2	F	602	GTP	C2-N1-C6	-2.42	120.72	125.11
3	B	602	NAI	O2A-PA-O1A	2.42	123.69	112.44
3	L	601	NAI	O2A-PA-O1A	2.41	123.65	112.44
2	J	601	GTP	C2-N1-C6	-2.41	120.74	125.11
2	L	602	GTP	O6-C6-N1	-2.41	115.59	120.11
2	C	601	GTP	C2-N1-C6	-2.41	120.75	125.11
2	B	601	GTP	O6-C6-N1	-2.41	115.59	120.11
2	J	601	GTP	O6-C6-N1	-2.40	115.59	120.11
2	K	602	GTP	O6-C6-N1	-2.40	115.61	120.11
2	E	602	GTP	C3'-C2'-C1'	-2.40	96.93	101.46
3	F	603	NAI	O2A-PA-O1A	2.40	123.59	112.44
3	J	603	NAI	O2A-PA-O1A	2.40	123.59	112.44
3	H	603	NAI	O2A-PA-O1A	2.39	123.57	112.44
3	K	601	NAI	O2A-PA-O1A	2.39	123.56	112.44
3	I	603	NAI	O2A-PA-O1A	2.39	123.55	112.44
3	G	603	NAI	C3N-C2N-N1N	-2.39	119.70	123.20
2	J	601	GTP	O2A-PA-O5'	-2.38	96.76	107.57
3	C	604	NAI	O2A-PA-O1A	2.38	123.53	112.44
3	L	603	NAI	O2A-PA-O1A	2.38	123.53	112.44
3	A	604	NAI	O2A-PA-O1A	2.38	123.51	112.44
3	J	602	NAI	O2A-PA-O1A	2.38	123.51	112.44
3	D	604	NAI	O2A-PA-O1A	2.38	123.51	112.44
3	I	602	NAI	O2A-PA-O1A	2.38	123.50	112.44
3	B	604	NAI	O2A-PA-O1A	2.37	123.49	112.44
3	A	602	NAI	O2A-PA-O1A	2.37	123.48	112.44
3	E	601	NAI	O2A-PA-O1A	2.37	123.48	112.44
2	H	601	GTP	O6-C6-N1	-2.37	115.66	120.11
3	H	602	NAI	O2A-PA-O1A	2.37	123.48	112.44
3	F	601	NAI	O2A-PA-O1A	2.37	123.46	112.44
2	I	601	GTP	O6-C6-N1	-2.37	115.67	120.11
3	D	602	NAI	O2A-PA-O1A	2.36	123.44	112.44
2	A	601	GTP	O2A-PA-O5'	-2.36	96.86	107.57
3	C	602	NAI	O2A-PA-O1A	2.36	123.42	112.44
3	G	603	NAI	O2A-PA-O1A	2.36	123.42	112.44
2	L	602	GTP	O2A-PA-O5'	-2.36	96.88	107.57
3	G	602	NAI	O2A-PA-O1A	2.36	123.41	112.44
2	F	602	GTP	O2A-PA-O5'	-2.35	96.91	107.57
2	B	601	GTP	O2A-PA-O5'	-2.35	96.92	107.57
2	C	601	GTP	N1-C2-N3	2.35	127.62	123.32
2	G	601	GTP	O2A-PA-O5'	-2.35	96.94	107.57
2	A	601	GTP	O6-C6-N1	-2.34	115.70	120.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	GTP	N1-C2-N3	2.34	127.61	123.32
2	E	602	GTP	N1-C2-N3	2.33	127.59	123.32
2	A	601	GTP	N1-C2-N3	2.33	127.58	123.32
3	K	603	NAI	O2A-PA-O1A	2.33	123.28	112.44
2	D	601	GTP	O2A-PA-O5'	-2.33	97.01	107.57
2	C	601	GTP	O2A-PA-O5'	-2.32	97.04	107.57
2	B	601	GTP	N1-C2-N3	2.32	127.56	123.32
2	H	601	GTP	N1-C2-N3	2.31	127.55	123.32
2	D	601	GTP	O6-C6-N1	-2.31	115.77	120.11
2	I	601	GTP	N1-C2-N3	2.31	127.55	123.32
2	C	601	GTP	O6-C6-N1	-2.31	115.78	120.11
2	L	602	GTP	N1-C2-N3	2.31	127.54	123.32
2	K	602	GTP	O2A-PA-O5'	-2.30	97.12	107.57
2	I	601	GTP	O2A-PA-O5'	-2.30	97.14	107.57
2	F	602	GTP	O6-C6-N1	-2.30	115.79	120.11
2	G	601	GTP	N1-C2-N3	2.30	127.52	123.32
2	H	601	GTP	O2A-PA-O5'	-2.28	97.21	107.57
2	J	601	GTP	N1-C2-N3	2.28	127.49	123.32
2	F	602	GTP	O3'-C3'-C4'	-2.28	104.54	111.08
2	E	602	GTP	O2A-PA-O5'	-2.27	97.26	107.57
2	E	602	GTP	O6-C6-N1	-2.27	115.85	120.11
2	C	601	GTP	O3'-C3'-C4'	-2.27	104.57	111.08
2	F	602	GTP	N1-C2-N3	2.27	127.47	123.32
3	B	604	NAI	O3D-C3D-C4D	-2.26	104.58	111.08
2	D	601	GTP	O3'-C3'-C4'	-2.23	104.67	111.08
3	E	603	NAI	O3D-C3D-C4D	-2.23	104.68	111.08
2	K	602	GTP	N1-C2-N3	2.23	127.39	123.32
2	B	601	GTP	O3'-C3'-C4'	-2.19	104.79	111.08
2	K	602	GTP	O3'-C3'-C4'	-2.17	104.85	111.08
2	C	601	GTP	C2'-C1'-N9	-2.16	107.23	113.25
3	K	601	NAI	C3N-C2N-N1N	-2.15	120.05	123.20
2	A	601	GTP	C2'-C1'-N9	-2.15	107.27	113.25
3	D	604	NAI	O3D-C3D-C4D	-2.14	104.92	111.08
2	B	601	GTP	C3'-C2'-C1'	-2.14	97.41	101.46
2	H	601	GTP	O3'-C3'-C4'	-2.13	104.96	111.08
2	J	601	GTP	O3'-C3'-C4'	-2.13	104.98	111.08
3	F	601	NAI	C3N-C2N-N1N	-2.12	120.09	123.20
2	A	601	GTP	O3'-C3'-C4'	-2.12	105.00	111.08
3	E	603	NAI	C3N-C2N-N1N	-2.11	120.11	123.20
3	D	602	NAI	O3D-C3D-C4D	-2.11	105.03	111.08
2	I	601	GTP	O3'-C3'-C4'	-2.10	105.04	111.08
2	L	602	GTP	O3'-C3'-C4'	-2.10	105.05	111.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	602	GTP	O3'-C3'-C4'	-2.10	105.05	111.08
2	I	601	GTP	C2'-C1'-N9	-2.10	107.41	113.25
2	G	601	GTP	O3'-C3'-C4'	-2.09	105.07	111.08
3	H	603	NAI	C3N-C2N-N1N	-2.08	120.15	123.20
3	C	602	NAI	O3D-C3D-C4D	-2.08	105.11	111.08
3	E	601	NAI	O3D-C3D-C4D	-2.07	105.13	111.08
3	L	603	NAI	C3N-C2N-N1N	-2.07	120.17	123.20
2	L	602	GTP	C2'-C1'-N9	-2.07	107.50	113.25
2	D	601	GTP	C2'-C1'-N9	-2.06	107.53	113.25
2	J	601	GTP	C3'-C2'-C1'	-2.05	97.58	101.46
3	H	603	NAI	O3D-C3D-C4D	-2.03	105.25	111.08
3	C	604	NAI	O3D-C3D-C4D	-2.03	105.25	111.08
3	I	603	NAI	C3N-C2N-N1N	-2.02	120.24	123.20
3	A	602	NAI	O3D-C3D-C4D	-2.02	105.28	111.08
3	B	602	NAI	O3D-C3D-C4D	-2.01	105.30	111.08
3	I	603	NAI	O3D-C3D-C4D	-2.01	105.32	111.08
3	J	603	NAI	C3N-C2N-N1N	-2.00	120.27	123.20

There are no chirality outliers.

All (326) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GTP	PB-O3B-PG-O3G
2	A	601	GTP	C5'-O5'-PA-O3A
2	A	601	GTP	C5'-O5'-PA-O2A
2	A	601	GTP	O4'-C4'-C5'-O5'
2	C	601	GTP	PB-O3B-PG-O3G
2	D	601	GTP	PB-O3B-PG-O2G
2	D	601	GTP	C5'-O5'-PA-O3A
2	D	601	GTP	C5'-O5'-PA-O1A
2	E	602	GTP	PB-O3B-PG-O3G
2	G	601	GTP	PB-O3B-PG-O3G
2	H	601	GTP	PB-O3B-PG-O2G
2	H	601	GTP	PB-O3B-PG-O3G
2	I	601	GTP	PB-O3B-PG-O3G
2	J	601	GTP	C5'-O5'-PA-O1A
2	K	602	GTP	C5'-O5'-PA-O1A
2	L	602	GTP	PB-O3B-PG-O3G
3	A	602	NAI	O4D-C1D-N1N-C6N
3	A	604	NAI	O4B-C4B-C5B-O5B
3	A	604	NAI	C5D-O5D-PN-O3
3	A	604	NAI	C5D-O5D-PN-O1N

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Mol	Chain	Res	Type	Atoms
3	A	604	NAI	C5D-O5D-PN-O2N
3	B	602	NAI	PN-O3-PA-O5B
3	B	602	NAI	C5D-O5D-PN-O2N
3	B	604	NAI	O4B-C4B-C5B-O5B
3	B	604	NAI	C5D-O5D-PN-O3
3	B	604	NAI	C5D-O5D-PN-O1N
3	B	604	NAI	C5D-O5D-PN-O2N
3	C	602	NAI	C5B-O5B-PA-O1A
3	C	602	NAI	C5D-O5D-PN-O2N
3	C	604	NAI	C5D-O5D-PN-O1N
3	D	602	NAI	PN-O3-PA-O5B
3	D	602	NAI	C5D-O5D-PN-O3
3	D	602	NAI	C5D-O5D-PN-O2N
3	D	604	NAI	O4B-C4B-C5B-O5B
3	D	604	NAI	C5D-O5D-PN-O1N
3	E	601	NAI	C5B-O5B-PA-O2A
3	E	601	NAI	C5D-O5D-PN-O1N
3	E	603	NAI	PN-O3-PA-O5B
3	E	603	NAI	C5D-O5D-PN-O3
3	E	603	NAI	C5D-O5D-PN-O2N
3	F	601	NAI	C5D-O5D-PN-O1N
3	G	602	NAI	C5B-O5B-PA-O1A
3	G	602	NAI	C5B-O5B-PA-O3
3	G	602	NAI	PN-O3-PA-O5B
3	G	602	NAI	O4D-C1D-N1N-C6N
3	G	603	NAI	O4B-C4B-C5B-O5B
3	G	603	NAI	C5D-O5D-PN-O3
3	G	603	NAI	C5D-O5D-PN-O1N
3	G	603	NAI	C5D-O5D-PN-O2N
3	H	602	NAI	C5B-O5B-PA-O1A
3	H	602	NAI	C5D-O5D-PN-O2N
3	H	603	NAI	C5B-O5B-PA-O1A
3	I	602	NAI	C5B-O5B-PA-O1A
3	I	602	NAI	C5B-O5B-PA-O3
3	I	603	NAI	C5D-O5D-PN-O3
3	I	603	NAI	C5D-O5D-PN-O1N
3	J	602	NAI	C5B-O5B-PA-O1A
3	J	602	NAI	C5D-O5D-PN-O3
3	J	602	NAI	C5D-O5D-PN-O2N
3	K	603	NAI	C5B-O5B-PA-O1A
3	K	603	NAI	C5D-O5D-PN-O3
3	K	603	NAI	C5D-O5D-PN-O2N

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Mol	Chain	Res	Type	Atoms
3	L	603	NAI	C5B-O5B-PA-O1A
3	L	603	NAI	O4D-C1D-N1N-C6N
4	A	603	GGL	N-CA-CB-CG
4	A	603	GGL	C-CA-CB-CG
2	K	602	GTP	O4'-C4'-C5'-O5'
3	C	604	NAI	O4B-C4B-C5B-O5B
3	E	601	NAI	O4B-C4B-C5B-O5B
3	G	602	NAI	O4D-C4D-C5D-O5D
3	L	603	NAI	O4D-C4D-C5D-O5D
3	B	602	NAI	O4D-C1D-N1N-C6N
3	E	603	NAI	O4D-C1D-N1N-C6N
3	H	602	NAI	O4D-C1D-N1N-C6N
3	I	602	NAI	O4D-C1D-N1N-C6N
2	A	601	GTP	C3'-C4'-C5'-O5'
2	E	602	GTP	O4'-C4'-C5'-O5'
3	A	604	NAI	C3B-C4B-C5B-O5B
3	B	604	NAI	C3B-C4B-C5B-O5B
3	C	604	NAI	C3B-C4B-C5B-O5B
3	D	604	NAI	C3B-C4B-C5B-O5B
3	E	601	NAI	C3B-C4B-C5B-O5B
3	G	603	NAI	C3B-C4B-C5B-O5B
3	H	603	NAI	O4B-C4B-C5B-O5B
3	I	603	NAI	O4B-C4B-C5B-O5B
3	I	603	NAI	C3B-C4B-C5B-O5B
3	J	603	NAI	O4D-C4D-C5D-O5D
3	J	603	NAI	C3D-C4D-C5D-O5D
3	K	601	NAI	O4B-C4B-C5B-O5B
3	K	601	NAI	C3B-C4B-C5B-O5B
3	L	601	NAI	O4B-C4B-C5B-O5B
3	L	601	NAI	C3B-C4B-C5B-O5B
3	B	604	NAI	C2D-C1D-N1N-C6N
3	H	603	NAI	C3B-C4B-C5B-O5B
3	K	603	NAI	C3B-C4B-C5B-O5B
3	B	604	NAI	C2D-C1D-N1N-C2N
3	K	603	NAI	O4B-C4B-C5B-O5B
4	B	603	GGL	OXT-C-CA-N
2	K	602	GTP	C3'-C4'-C5'-O5'
3	G	602	NAI	C3D-C4D-C5D-O5D
3	L	601	NAI	O4D-C4D-C5D-O5D
3	L	601	NAI	C3D-C4D-C5D-O5D
3	L	603	NAI	C3D-C4D-C5D-O5D
4	B	603	GGL	CA-CB-CG-CD

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Mol	Chain	Res	Type	Atoms
3	F	603	NAI	O4D-C1D-N1N-C6N
3	C	602	NAI	O4B-C4B-C5B-O5B
3	H	602	NAI	O4B-C4B-C5B-O5B
3	I	602	NAI	O4B-C4B-C5B-O5B
3	J	602	NAI	O4B-C4B-C5B-O5B
2	J	601	GTP	PB-O3B-PG-O1G
3	C	604	NAI	C2B-C1B-N9A-C8A
3	F	601	NAI	C2B-C1B-N9A-C8A
2	D	601	GTP	PA-O3A-PB-O1B
3	I	603	NAI	PN-O3-PA-O1A
3	K	601	NAI	PN-O3-PA-O1A
3	C	602	NAI	C3B-C4B-C5B-O5B
3	D	602	NAI	O4B-C4B-C5B-O5B
3	G	602	NAI	O4B-C4B-C5B-O5B
3	H	602	NAI	C3B-C4B-C5B-O5B
3	I	602	NAI	C3B-C4B-C5B-O5B
3	J	602	NAI	C3B-C4B-C5B-O5B
3	D	604	NAI	C2B-C1B-N9A-C8A
2	E	602	GTP	C3'-C4'-C5'-O5'
3	D	602	NAI	C3B-C4B-C5B-O5B
3	C	602	NAI	PN-O3-PA-O5B
3	F	601	NAI	PN-O3-PA-O5B
3	H	602	NAI	PN-O3-PA-O5B
3	L	603	NAI	PN-O3-PA-O5B
4	C	603	GGL	OXT-C-CA-N
3	H	603	NAI	C2B-C1B-N9A-C8A
2	C	601	GTP	PB-O3B-PG-O2G
2	D	601	GTP	PB-O3B-PG-O3G
2	I	601	GTP	PB-O3B-PG-O2G
3	B	604	NAI	O4D-C1D-N1N-C2N
3	B	604	NAI	O4D-C1D-N1N-C6N
3	G	602	NAI	C3B-C4B-C5B-O5B
3	A	602	NAI	C2B-C1B-N9A-C8A
3	A	604	NAI	C2B-C1B-N9A-C8A
3	B	602	NAI	C2B-C1B-N9A-C8A
3	E	601	NAI	C2B-C1B-N9A-C8A
3	I	603	NAI	C2B-C1B-N9A-C8A
3	J	602	NAI	C2B-C1B-N9A-C8A
3	K	603	NAI	C2B-C1B-N9A-C8A
2	B	601	GTP	PB-O3A-PA-O2A
2	C	601	GTP	PB-O3A-PA-O2A
2	E	602	GTP	PB-O3A-PA-O2A

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Mol	Chain	Res	Type	Atoms
2	F	602	GTP	PB-O3A-PA-O2A
2	J	601	GTP	PB-O3A-PA-O2A
2	K	602	GTP	PB-O3A-PA-O2A
3	I	603	NAI	PN-O3-PA-O2A
3	K	601	NAI	PN-O3-PA-O2A
3	D	602	NAI	O4D-C1D-N1N-C6N
3	K	601	NAI	O4D-C1D-N1N-C2N
3	C	604	NAI	C2D-C1D-N1N-C2N
3	C	604	NAI	C2D-C1D-N1N-C6N
4	E	604	GGL	N-CA-CB-CG
4	F	604	GGL	N-CA-CB-CG
2	D	601	GTP	C5'-O5'-PA-O2A
2	E	602	GTP	C5'-O5'-PA-O1A
2	J	601	GTP	C5'-O5'-PA-O3A
2	J	601	GTP	C5'-O5'-PA-O2A
3	A	602	NAI	C5D-O5D-PN-O2N
3	A	604	NAI	C5B-O5B-PA-O1A
3	A	604	NAI	C5B-O5B-PA-O2A
3	A	604	NAI	C5B-O5B-PA-O3
3	B	602	NAI	C5D-O5D-PN-O3
3	B	602	NAI	C5D-O5D-PN-O1N
3	B	604	NAI	C5B-O5B-PA-O1A
3	B	604	NAI	C5B-O5B-PA-O2A
3	B	604	NAI	C5B-O5B-PA-O3
3	C	602	NAI	C5D-O5D-PN-O3
3	C	602	NAI	C5D-O5D-PN-O1N
3	C	604	NAI	C5B-O5B-PA-O1A
3	C	604	NAI	C5B-O5B-PA-O2A
3	C	604	NAI	C5B-O5B-PA-O3
3	D	602	NAI	C5D-O5D-PN-O1N
3	D	604	NAI	C5B-O5B-PA-O1A
3	D	604	NAI	C5B-O5B-PA-O2A
3	D	604	NAI	C5B-O5B-PA-O3
3	E	601	NAI	C5B-O5B-PA-O1A
3	E	601	NAI	C5B-O5B-PA-O3
3	E	601	NAI	C5D-O5D-PN-O3
3	E	601	NAI	C5D-O5D-PN-O2N
3	E	603	NAI	C5D-O5D-PN-O1N
3	G	602	NAI	C5B-O5B-PA-O2A
3	G	603	NAI	C5B-O5B-PA-O1A
3	G	603	NAI	C5B-O5B-PA-O2A
3	G	603	NAI	C5B-O5B-PA-O3

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Mol	Chain	Res	Type	Atoms
3	H	602	NAI	C5B-O5B-PA-O3
3	H	603	NAI	C5B-O5B-PA-O3
3	I	602	NAI	C5B-O5B-PA-O2A
3	I	603	NAI	C5B-O5B-PA-O1A
3	I	603	NAI	C5B-O5B-PA-O2A
3	I	603	NAI	C5B-O5B-PA-O3
3	I	603	NAI	C5D-O5D-PN-O2N
3	J	602	NAI	C5D-O5D-PN-O1N
3	J	603	NAI	C5B-O5B-PA-O1A
3	J	603	NAI	C5B-O5B-PA-O2A
3	J	603	NAI	C5B-O5B-PA-O3
3	K	601	NAI	C5B-O5B-PA-O1A
3	K	601	NAI	C5B-O5B-PA-O2A
3	K	601	NAI	C5B-O5B-PA-O3
3	K	603	NAI	C5B-O5B-PA-O2A
3	K	603	NAI	C5B-O5B-PA-O3
3	K	603	NAI	C5D-O5D-PN-O1N
3	L	601	NAI	C5B-O5B-PA-O1A
3	L	601	NAI	C5B-O5B-PA-O2A
3	L	601	NAI	C5B-O5B-PA-O3
3	L	603	NAI	C5B-O5B-PA-O2A
3	L	603	NAI	C5B-O5B-PA-O3
4	A	603	GGL	CA-CB-CG-CD
2	G	601	GTP	PB-O3A-PA-O2A
2	H	601	GTP	PB-O3A-PA-O2A
2	I	601	GTP	PB-O3A-PA-O2A
2	L	602	GTP	PB-O3A-PA-O2A
3	L	601	NAI	PN-O3-PA-O2A
3	A	602	NAI	C2B-C1B-N9A-C4A
3	C	604	NAI	C2B-C1B-N9A-C4A
3	D	604	NAI	C2B-C1B-N9A-C4A
3	E	601	NAI	C2B-C1B-N9A-C4A
3	F	601	NAI	C2B-C1B-N9A-C4A
3	H	603	NAI	C2B-C1B-N9A-C4A
3	E	603	NAI	C2B-C1B-N9A-C8A
3	J	603	NAI	O4D-C1D-N1N-C2N
3	F	601	NAI	O4B-C4B-C5B-O5B
4	E	604	GGL	CA-CB-CG-CD
3	E	601	NAI	C2D-C1D-N1N-C2N
3	C	602	NAI	O4D-C1D-N1N-C6N
3	C	604	NAI	O4D-C1D-N1N-C2N
3	E	601	NAI	O4D-C1D-N1N-C2N

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Mol	Chain	Res	Type	Atoms
3	J	602	NAI	O4D-C1D-N1N-C6N
3	A	604	NAI	C4D-C5D-O5D-PN
3	B	604	NAI	C4D-C5D-O5D-PN
3	J	603	NAI	C4B-C5B-O5B-PA
3	B	604	NAI	C2B-C1B-N9A-C8A
3	A	604	NAI	O4D-C1D-N1N-C2N
3	D	604	NAI	O4D-C1D-N1N-C2N
3	H	603	NAI	O4D-C1D-N1N-C2N
3	I	603	NAI	O4D-C1D-N1N-C2N
3	L	601	NAI	O4D-C1D-N1N-C2N
4	D	603	GGL	OE1-CD-CG-CB
4	F	604	GGL	OE2-CD-CG-CB
4	D	603	GGL	CA-CB-CG-CD
3	B	602	NAI	C2N-C3N-C7N-N7N
3	C	604	NAI	O4D-C1D-N1N-C6N
3	F	601	NAI	O4D-C1D-N1N-C2N
3	G	602	NAI	C2N-C3N-C7N-N7N
3	G	603	NAI	O4D-C1D-N1N-C2N
3	K	603	NAI	O4D-C1D-N1N-C6N
3	L	603	NAI	C2N-C3N-C7N-N7N
4	D	603	GGL	OE2-CD-CG-CB
3	A	604	NAI	PN-O3-PA-O2A
3	C	604	NAI	PN-O3-PA-O2A
4	F	604	GGL	OE1-CD-CG-CB
3	A	604	NAI	C2D-C1D-N1N-C2N
3	D	604	NAI	C2D-C1D-N1N-C2N
3	H	603	NAI	C2D-C1D-N1N-C2N
3	K	601	NAI	C2B-C1B-N9A-C8A
3	F	601	NAI	C4D-C5D-O5D-PN
3	G	603	NAI	C4D-C5D-O5D-PN
3	F	601	NAI	C2D-C1D-N1N-C2N
3	G	603	NAI	C2D-C1D-N1N-C2N
3	K	603	NAI	C2D-C1D-N1N-C6N
3	L	601	NAI	C2D-C1D-N1N-C2N
3	A	602	NAI	O4B-C1B-N9A-C8A
3	A	604	NAI	O4B-C1B-N9A-C8A
3	E	601	NAI	O4B-C1B-N9A-C8A
4	C	603	GGL	OE2-CD-CG-CB
2	A	601	GTP	PB-O3B-PG-O1G
2	C	601	GTP	PB-O3B-PG-O1G
2	E	602	GTP	PB-O3B-PG-O1G
2	G	601	GTP	PB-O3B-PG-O1G

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Mol	Chain	Res	Type	Atoms
2	G	601	GTP	PB-O3B-PG-O2G
2	K	602	GTP	PB-O3B-PG-O2G
4	C	603	GGL	OE1-CD-CG-CB
3	F	603	NAI	O4D-C4D-C5D-O5D
3	H	602	NAI	O4D-C4D-C5D-O5D
4	F	604	GGL	C-CA-CB-CG
3	C	604	NAI	O4B-C1B-N9A-C8A
3	D	604	NAI	O4B-C1B-N9A-C8A
3	F	601	NAI	O4B-C1B-N9A-C8A
3	H	603	NAI	O4B-C1B-N9A-C8A
3	I	603	NAI	O4B-C1B-N9A-C8A
3	J	602	NAI	O4B-C1B-N9A-C8A
3	E	601	NAI	C2D-C1D-N1N-C6N
3	I	603	NAI	C2D-C1D-N1N-C2N
3	C	604	NAI	C4D-C5D-O5D-PN
3	J	603	NAI	C4D-C5D-O5D-PN
2	A	601	GTP	PB-O3A-PA-O2A
3	A	604	NAI	PA-O3-PN-O2N
3	B	604	NAI	PN-O3-PA-O2A
3	D	604	NAI	PN-O3-PA-O2A
3	E	601	NAI	PN-O3-PA-O2A
3	G	603	NAI	PN-O3-PA-O2A
4	A	603	GGL	OE2-CD-CG-CB
3	K	603	NAI	O4B-C1B-N9A-C8A
3	L	603	NAI	O4B-C4B-C5B-O5B
3	I	603	NAI	C4B-C5B-O5B-PA
3	K	601	NAI	C4B-C5B-O5B-PA
4	A	603	GGL	OE1-CD-CG-CB
3	C	602	NAI	C2B-C1B-N9A-C8A
3	G	603	NAI	C2B-C1B-N9A-C8A
3	A	604	NAI	C2B-C1B-N9A-C4A
3	I	603	NAI	C2B-C1B-N9A-C4A
3	J	602	NAI	C2B-C1B-N9A-C4A
3	K	603	NAI	C2B-C1B-N9A-C4A
2	I	601	GTP	PB-O3B-PG-O1G
3	D	604	NAI	C4D-C5D-O5D-PN
3	I	603	NAI	C4D-C5D-O5D-PN
4	B	603	GGL	N-CA-CB-CG
3	J	603	NAI	C2D-C1D-N1N-C2N
3	B	602	NAI	O4B-C1B-N9A-C8A
4	B	603	GGL	O-C-CA-N
4	B	603	GGL	OE2-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
3	E	601	NAI	O4D-C1D-N1N-C6N
3	C	602	NAI	PA-O3-PN-O1N
3	E	603	NAI	PA-O3-PN-O1N
3	G	602	NAI	PA-O3-PN-O1N
3	H	602	NAI	PA-O3-PN-O1N
3	I	602	NAI	PA-O3-PN-O1N
3	J	602	NAI	PA-O3-PN-O1N
3	K	601	NAI	PA-O3-PN-O2N
3	K	603	NAI	PA-O3-PN-O1N
3	L	603	NAI	PA-O3-PN-O1N
4	E	604	GGL	OXT-C-CA-N
4	F	604	GGL	OXT-C-CA-N

There are no ring outliers.

33 monomers are involved in 51 short contacts:

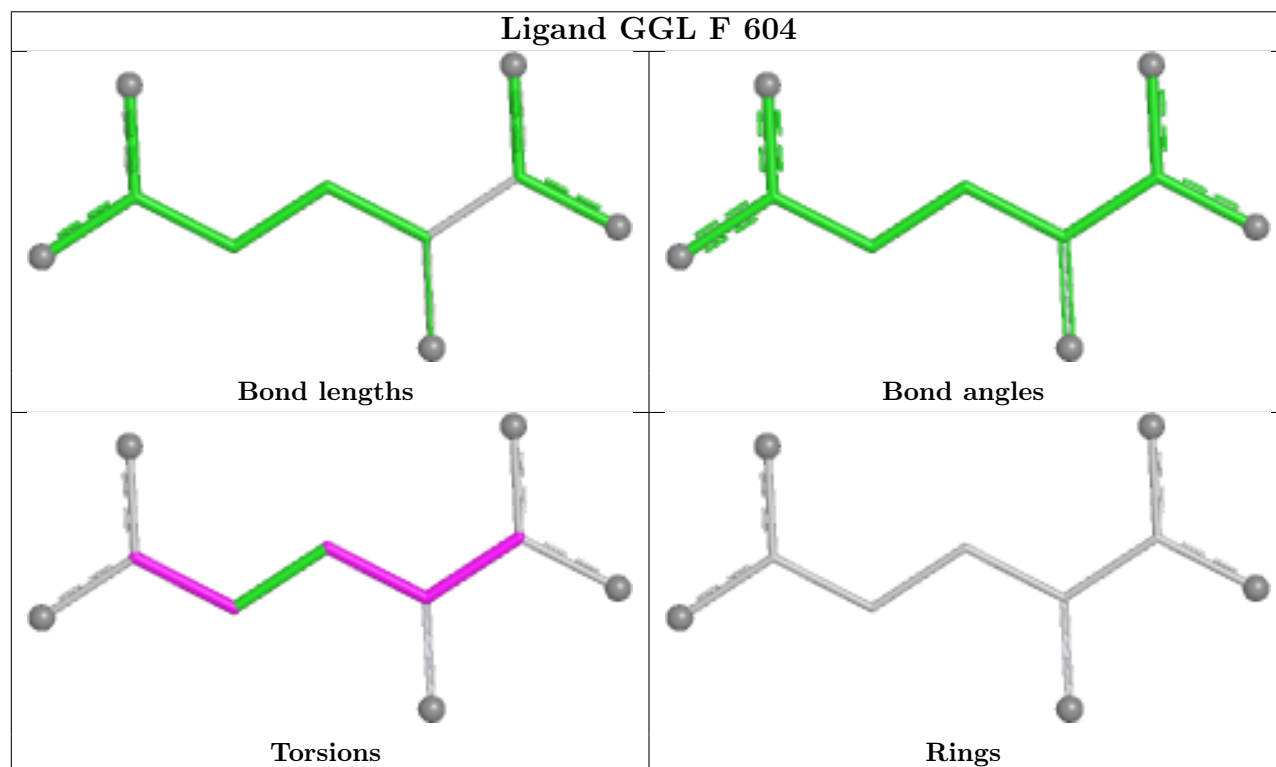
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	604	GGL	1	0
4	C	603	GGL	1	0
2	H	601	GTP	3	0
3	C	602	NAI	1	0
3	E	601	NAI	1	0
2	K	602	GTP	1	0
2	J	601	GTP	1	0
3	K	601	NAI	1	0
2	L	602	GTP	1	0
3	H	603	NAI	1	0
3	C	604	NAI	1	0
3	F	601	NAI	2	0
3	L	601	NAI	2	0
2	C	601	GTP	1	0
3	A	604	NAI	1	0
2	D	601	GTP	1	0
3	J	603	NAI	3	0
2	G	601	GTP	1	0
3	F	603	NAI	2	0
4	E	604	GGL	3	0
4	A	603	GGL	2	0
2	I	601	GTP	1	0
3	G	602	NAI	1	0
3	H	602	NAI	2	0
3	J	602	NAI	5	0

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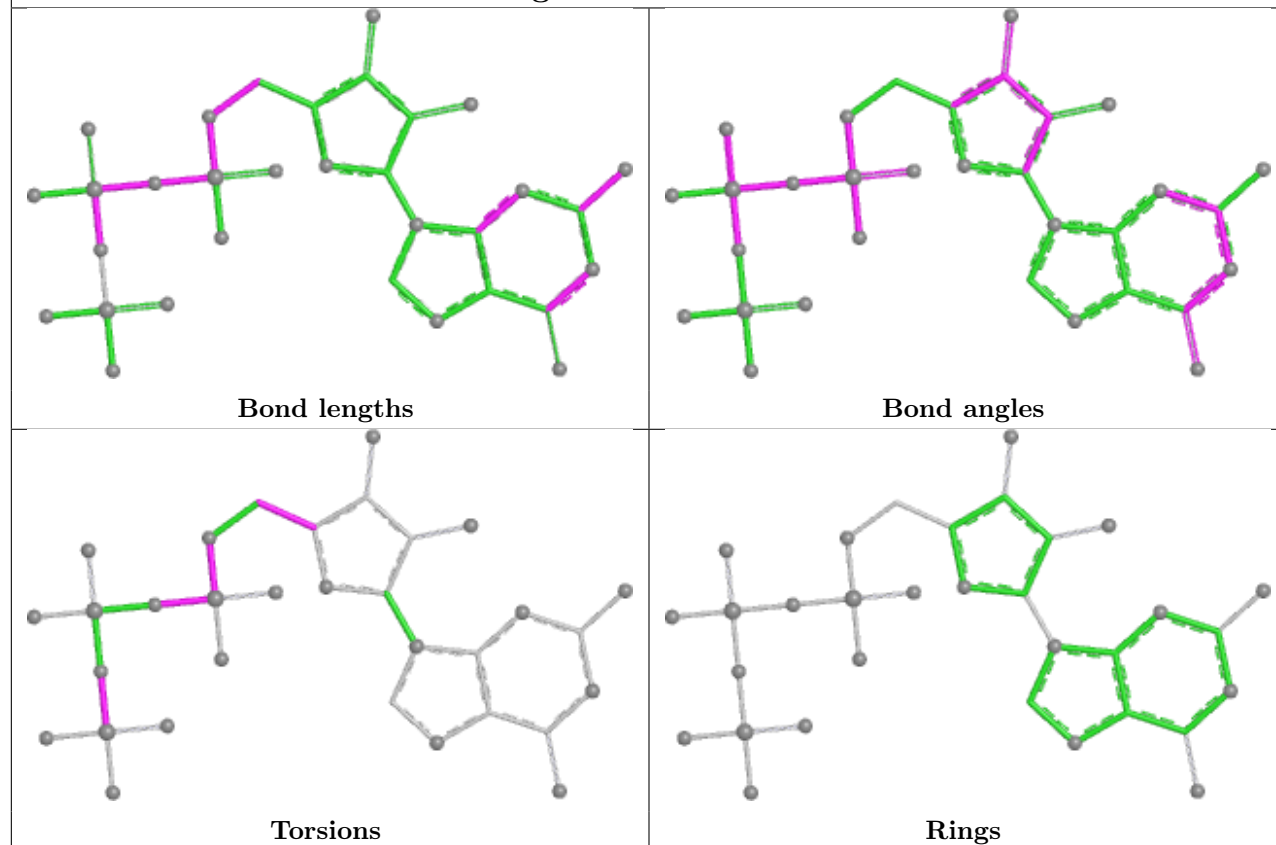
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	603	NAI	2	0
3	D	604	NAI	3	0
3	E	603	NAI	2	0
3	B	604	NAI	1	0
2	F	602	GTP	1	0
3	I	602	NAI	1	0
3	K	603	NAI	1	0
4	D	603	GGL	1	0

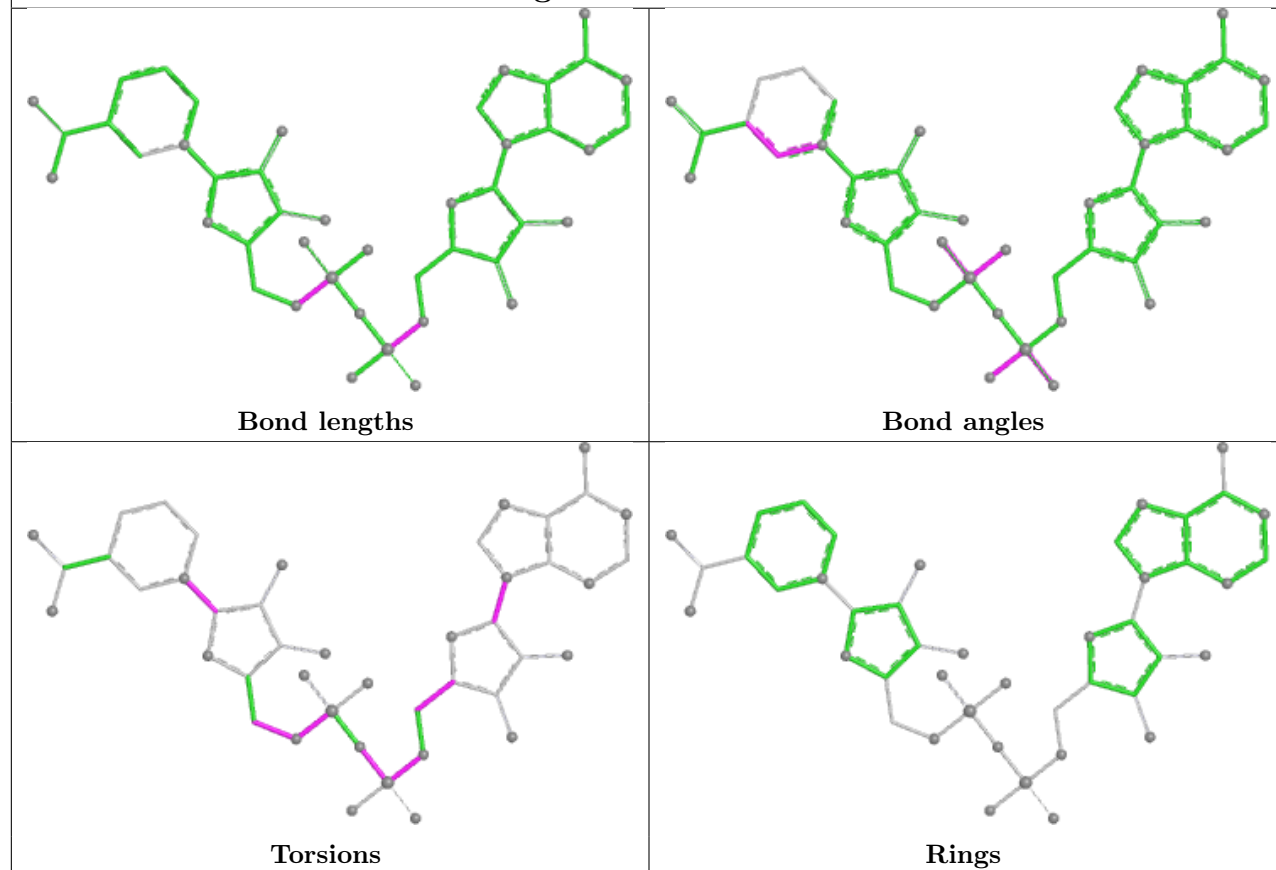
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

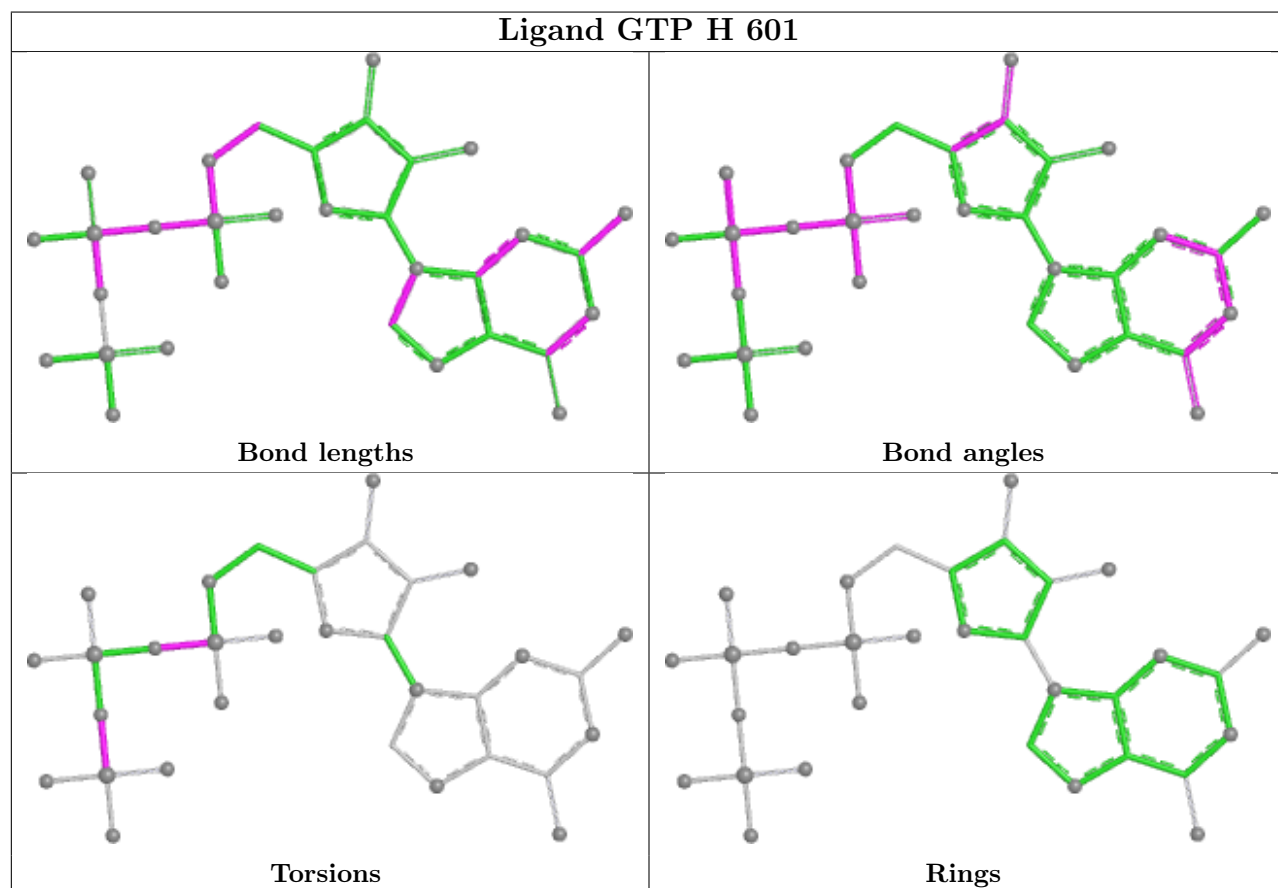
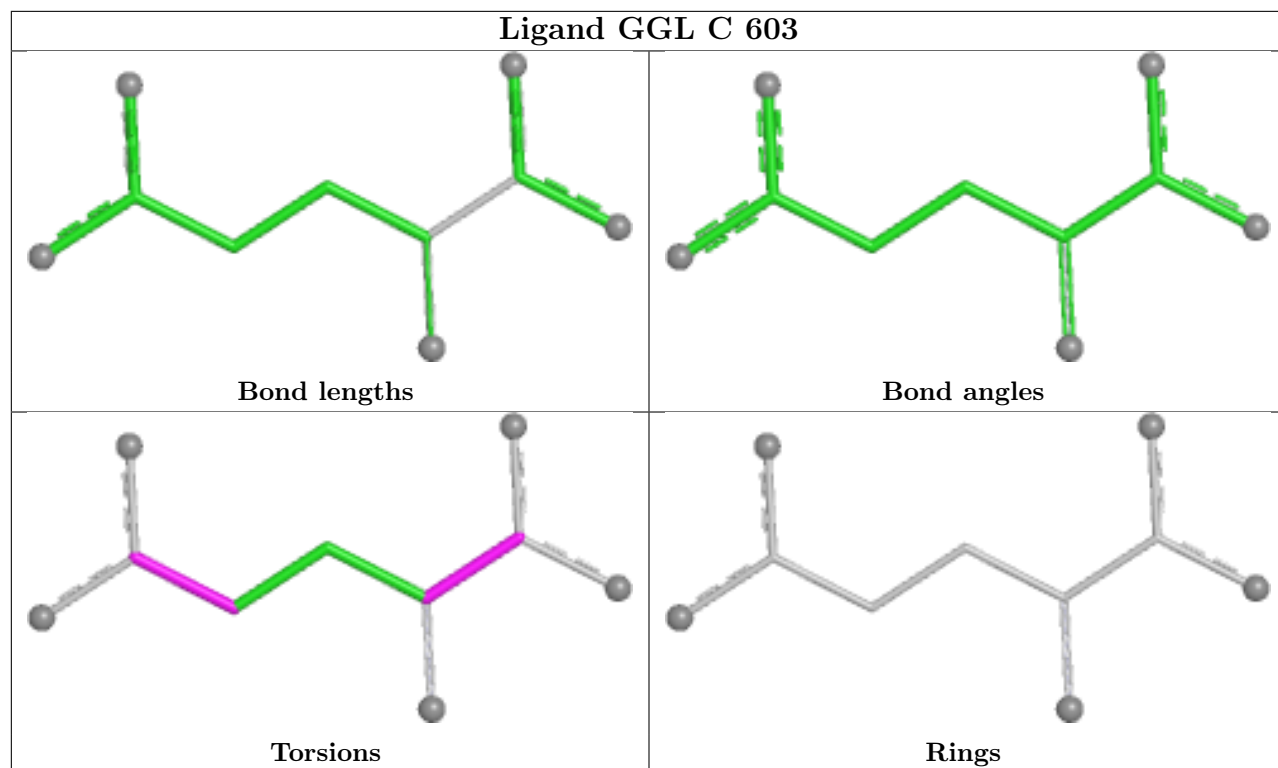


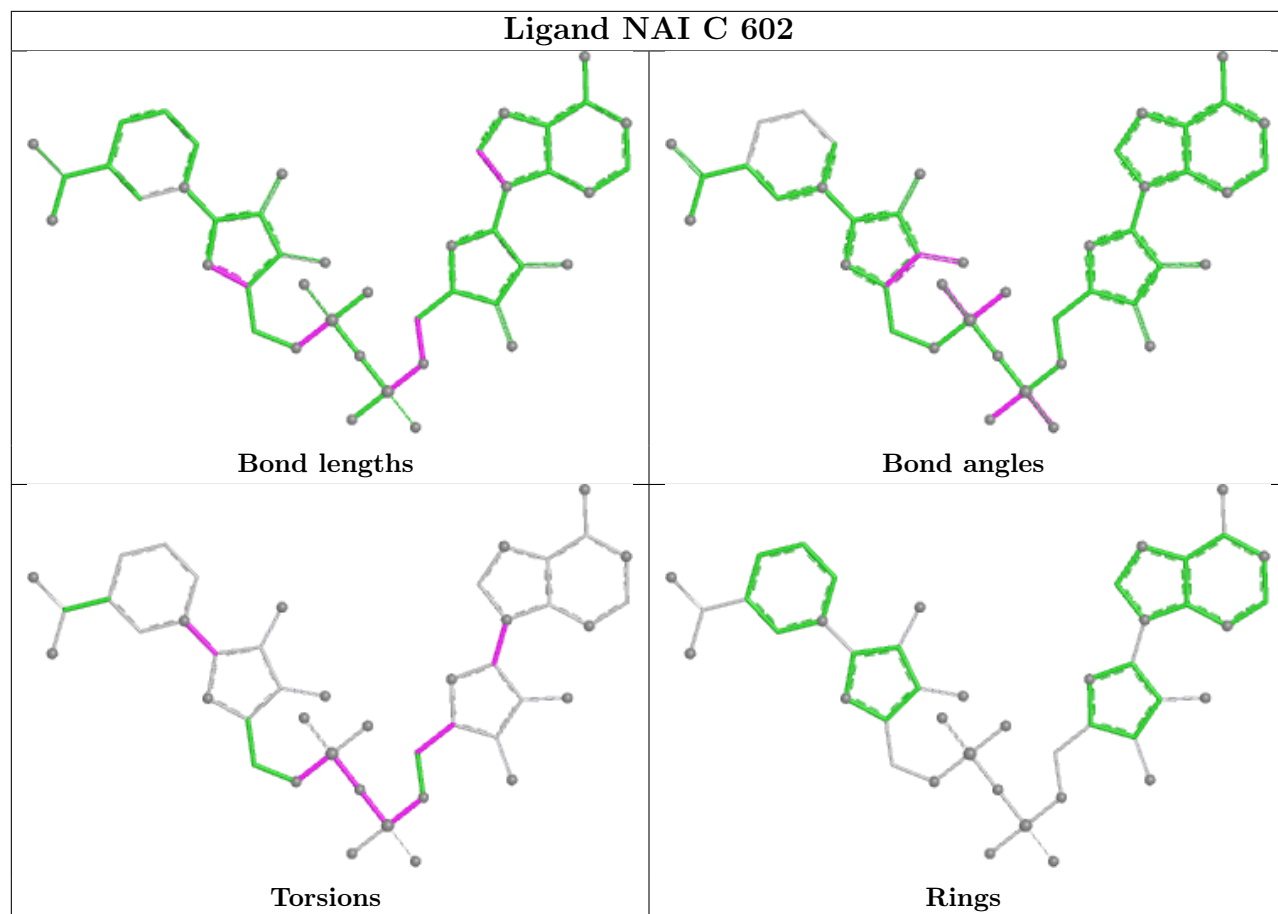
Ligand GTP E 602



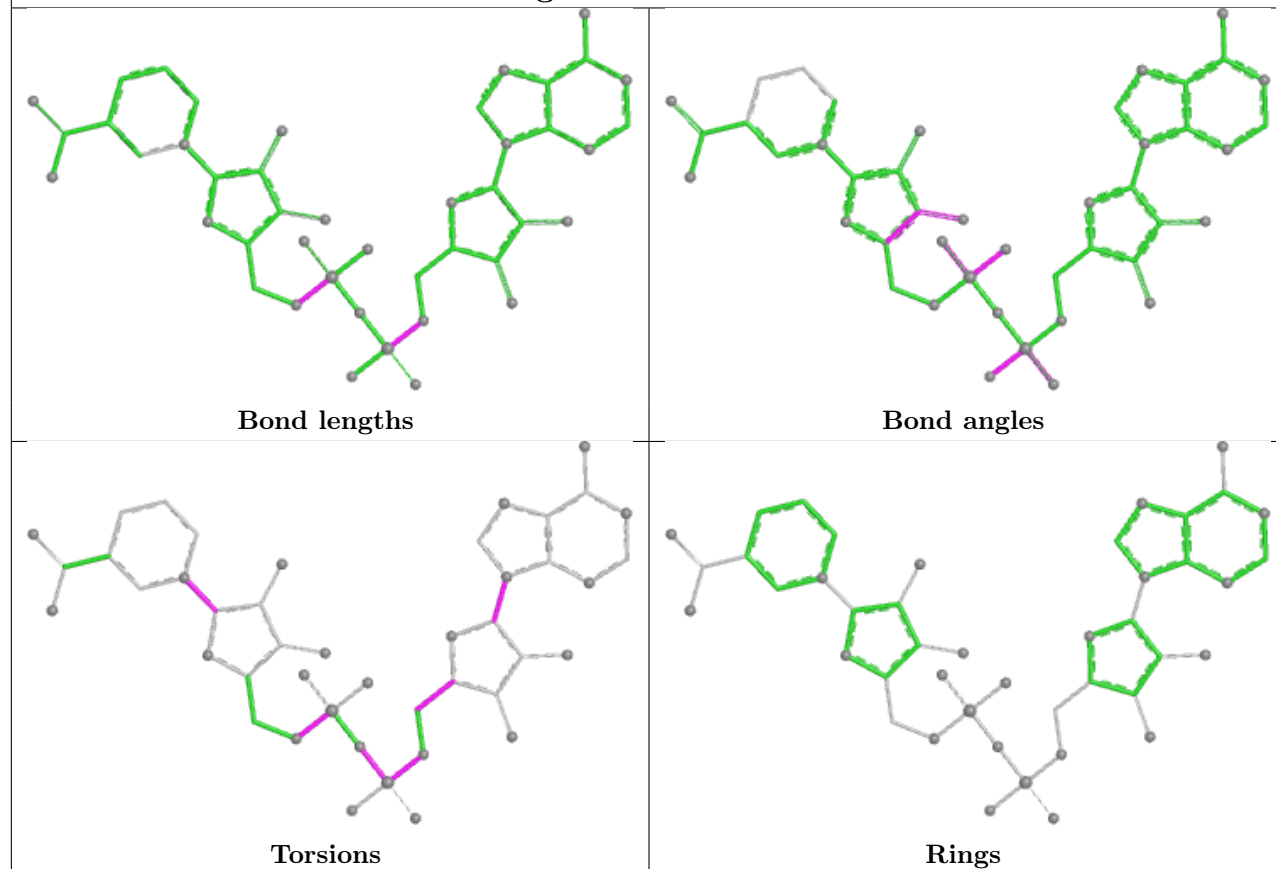
Ligand NAI G 603



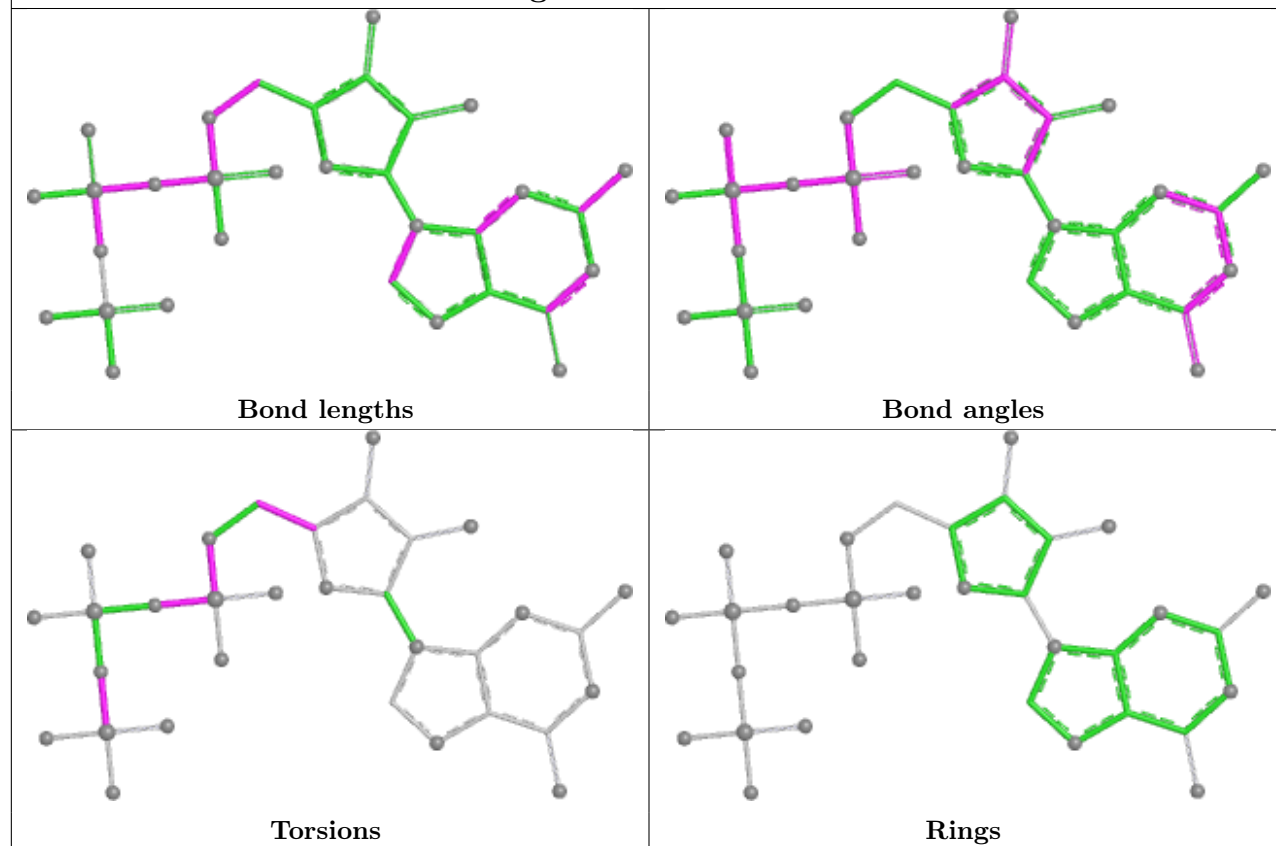




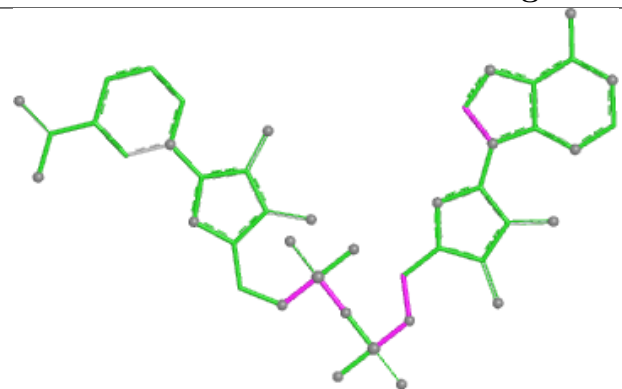
Ligand NAI E 601



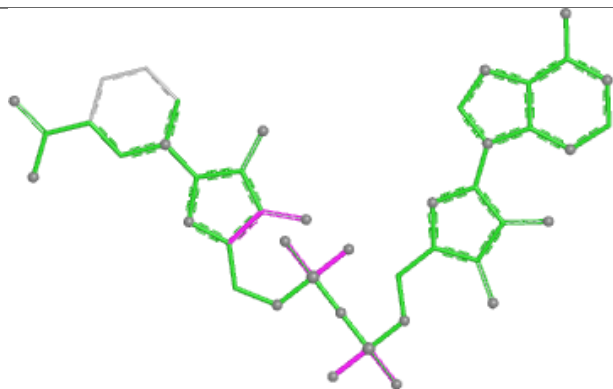
Ligand GTP K 602



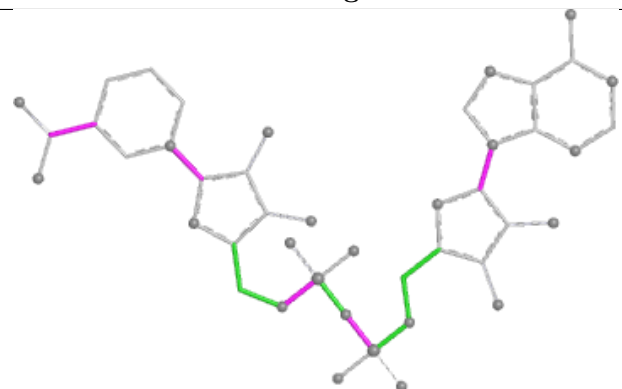
Ligand NAI B 602



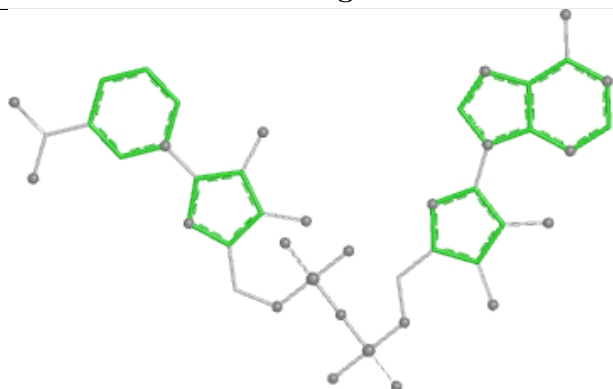
Bond lengths



Bond angles

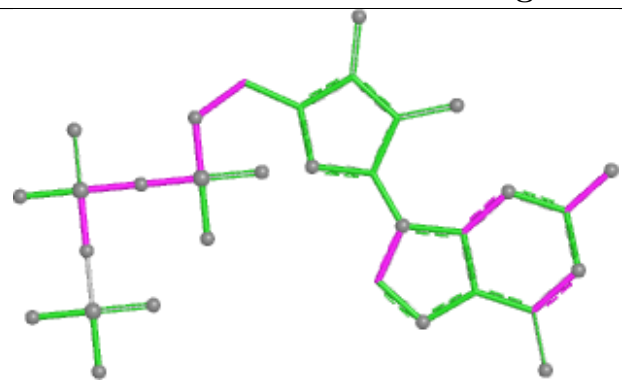


Torsions

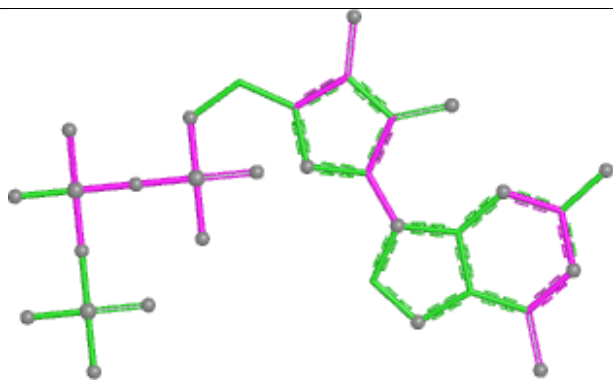


Rings

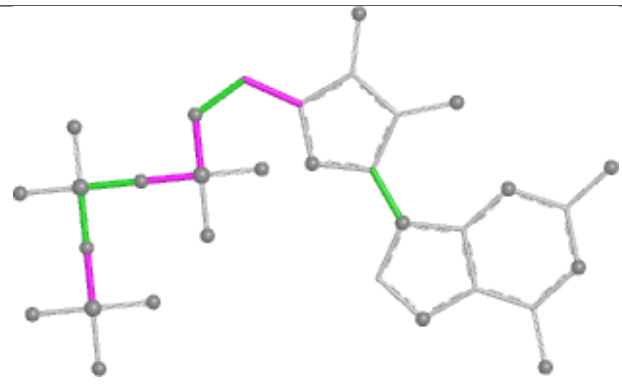
Ligand GTP A 601



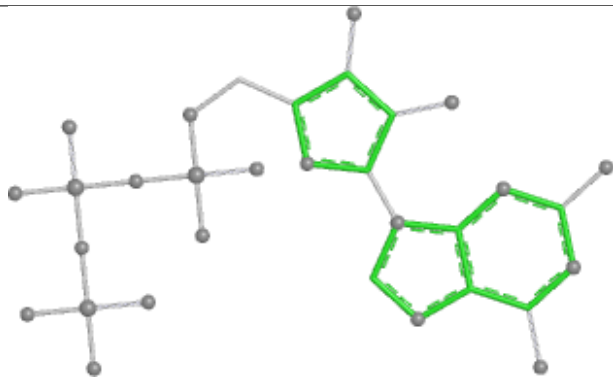
Bond lengths



Bond angles

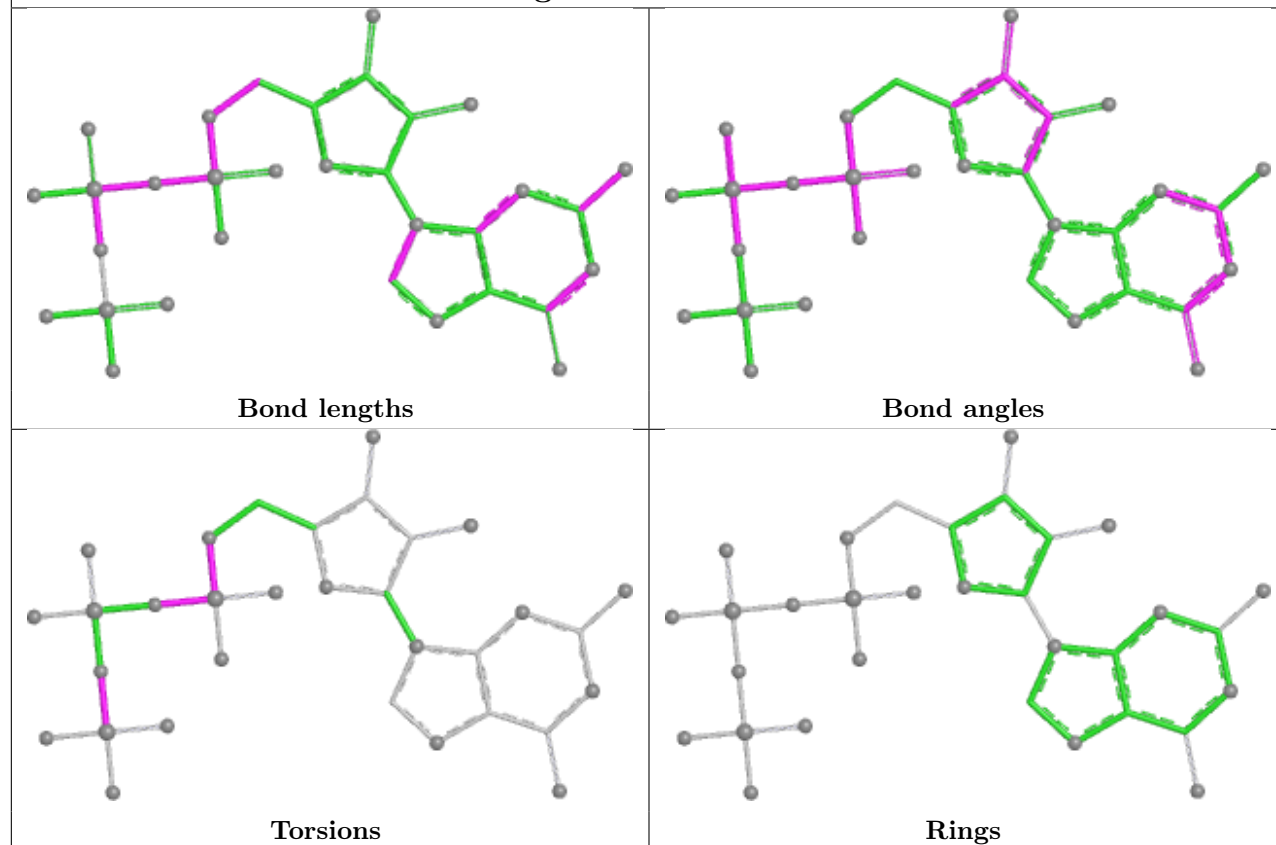


Torsions

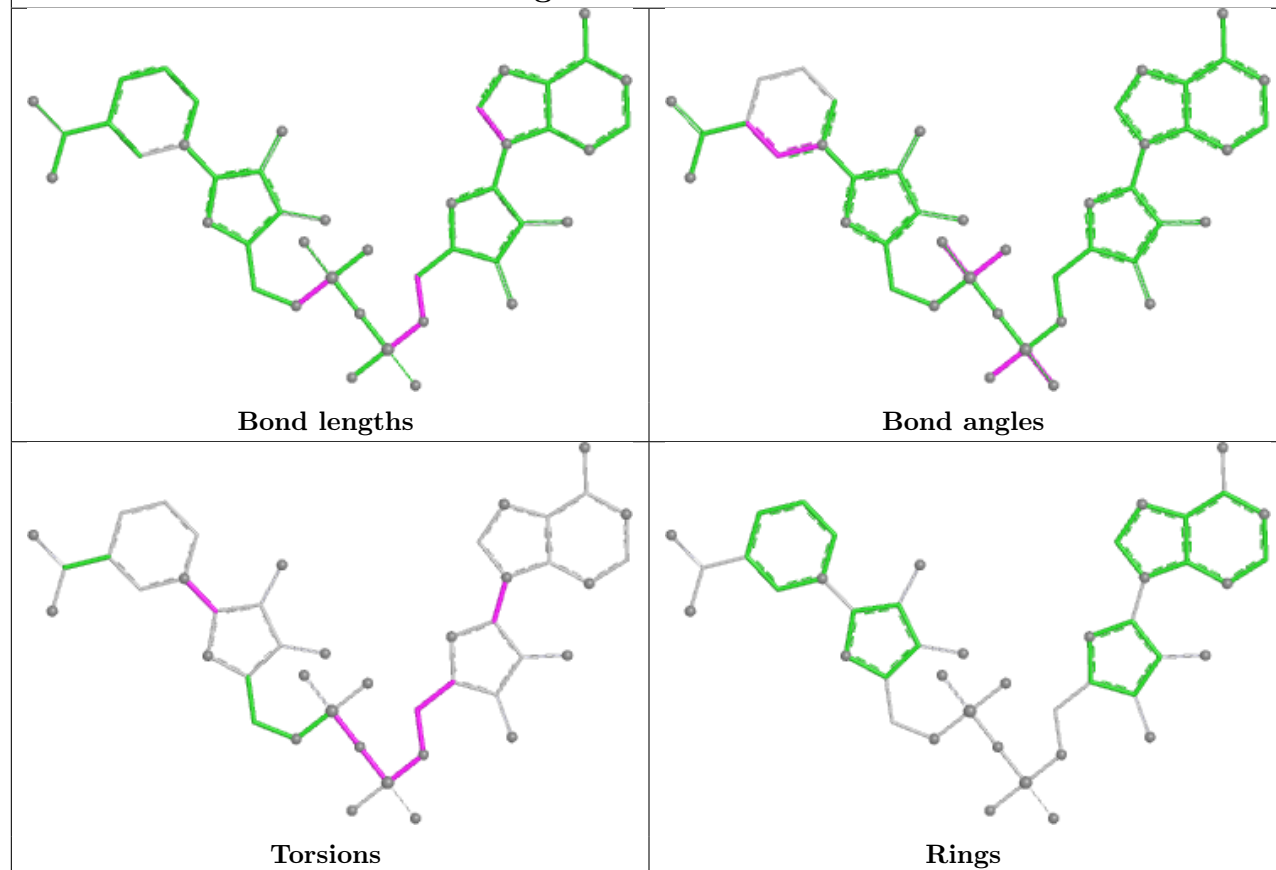


Rings

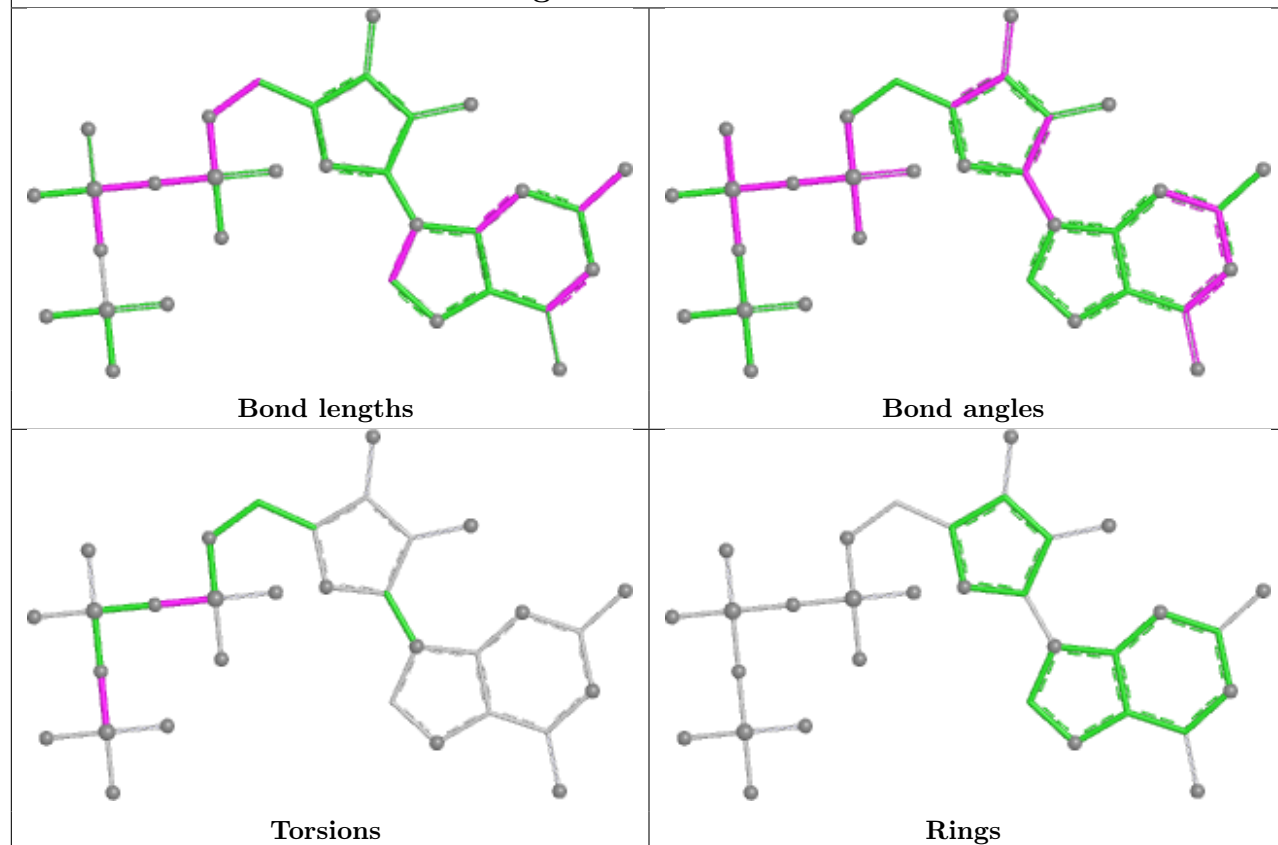
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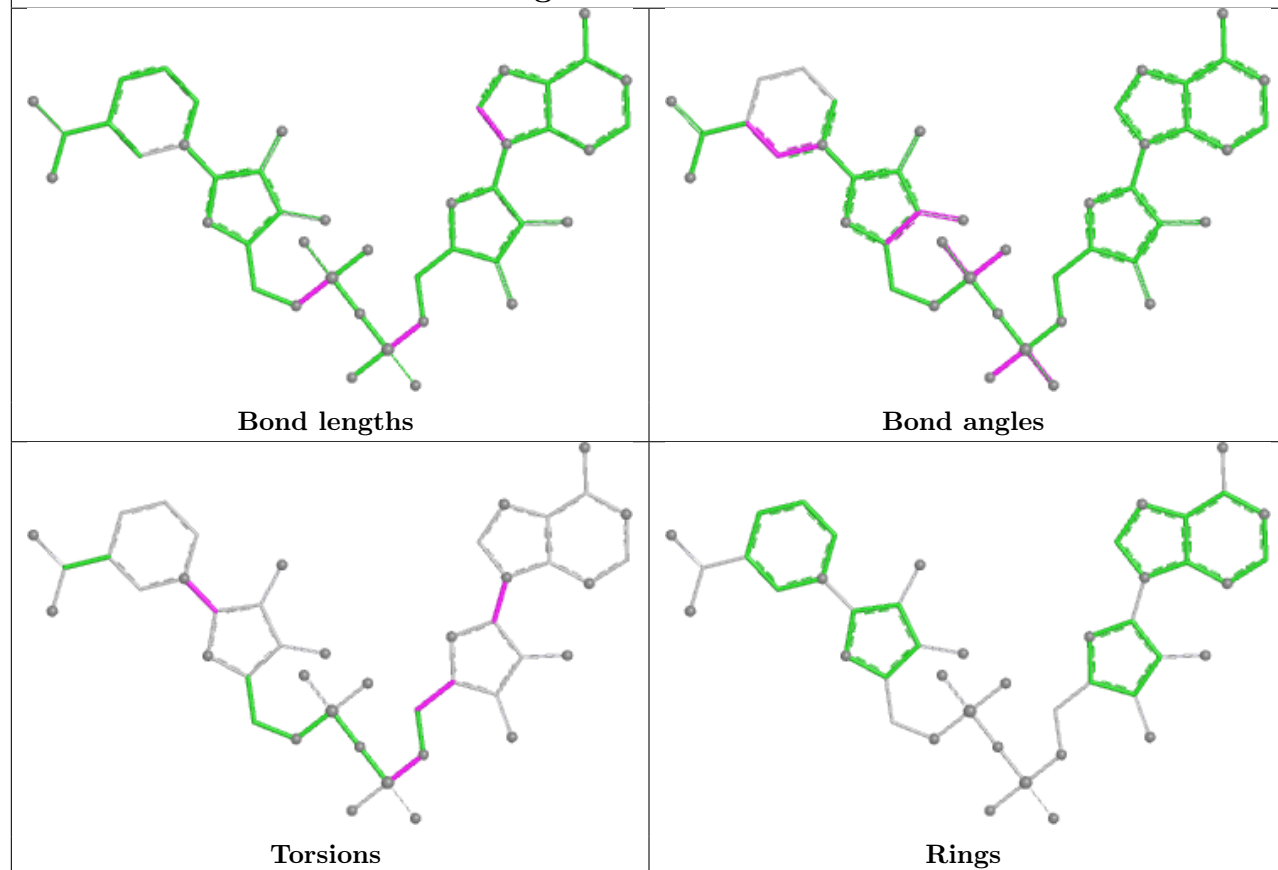
Ligand NAI K 601

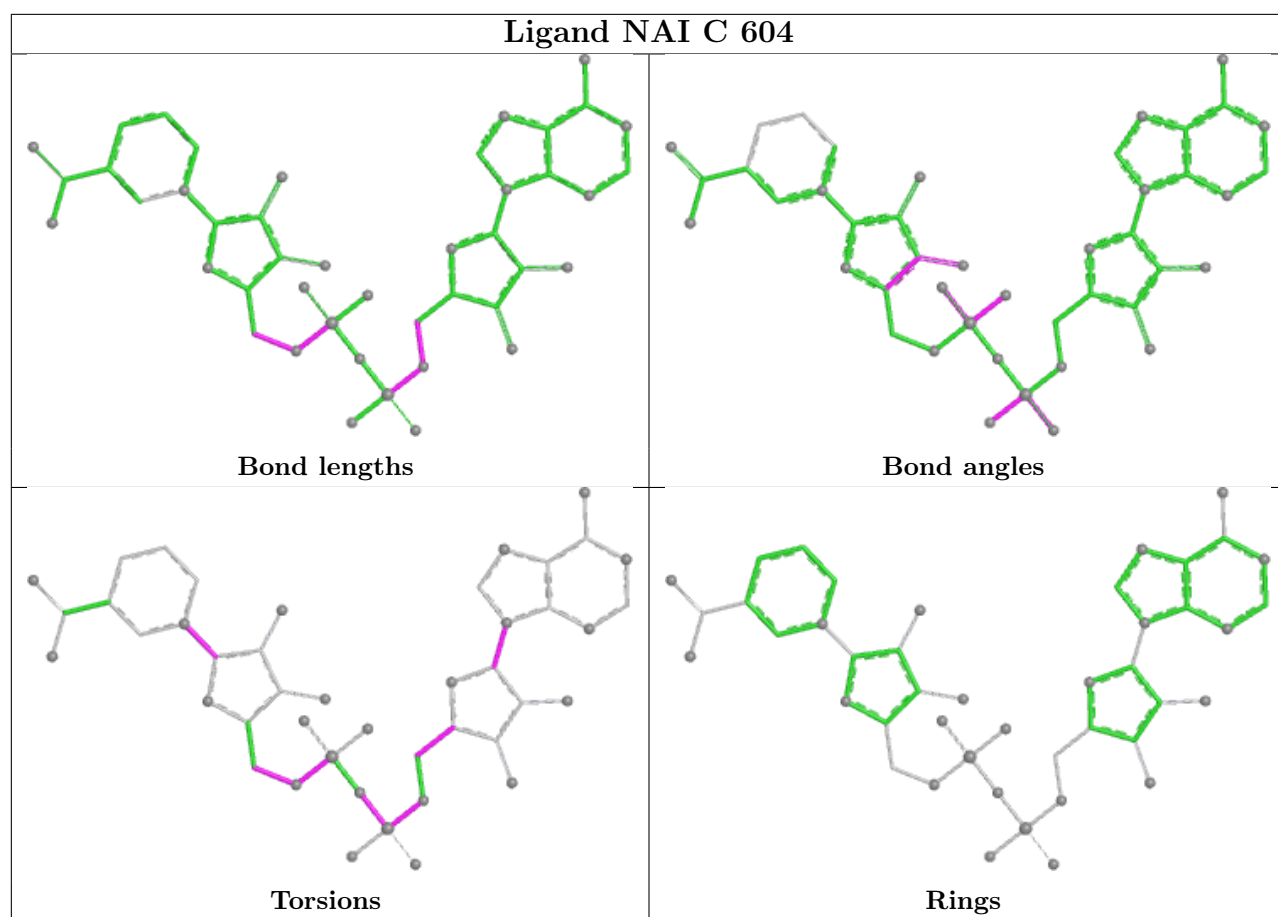


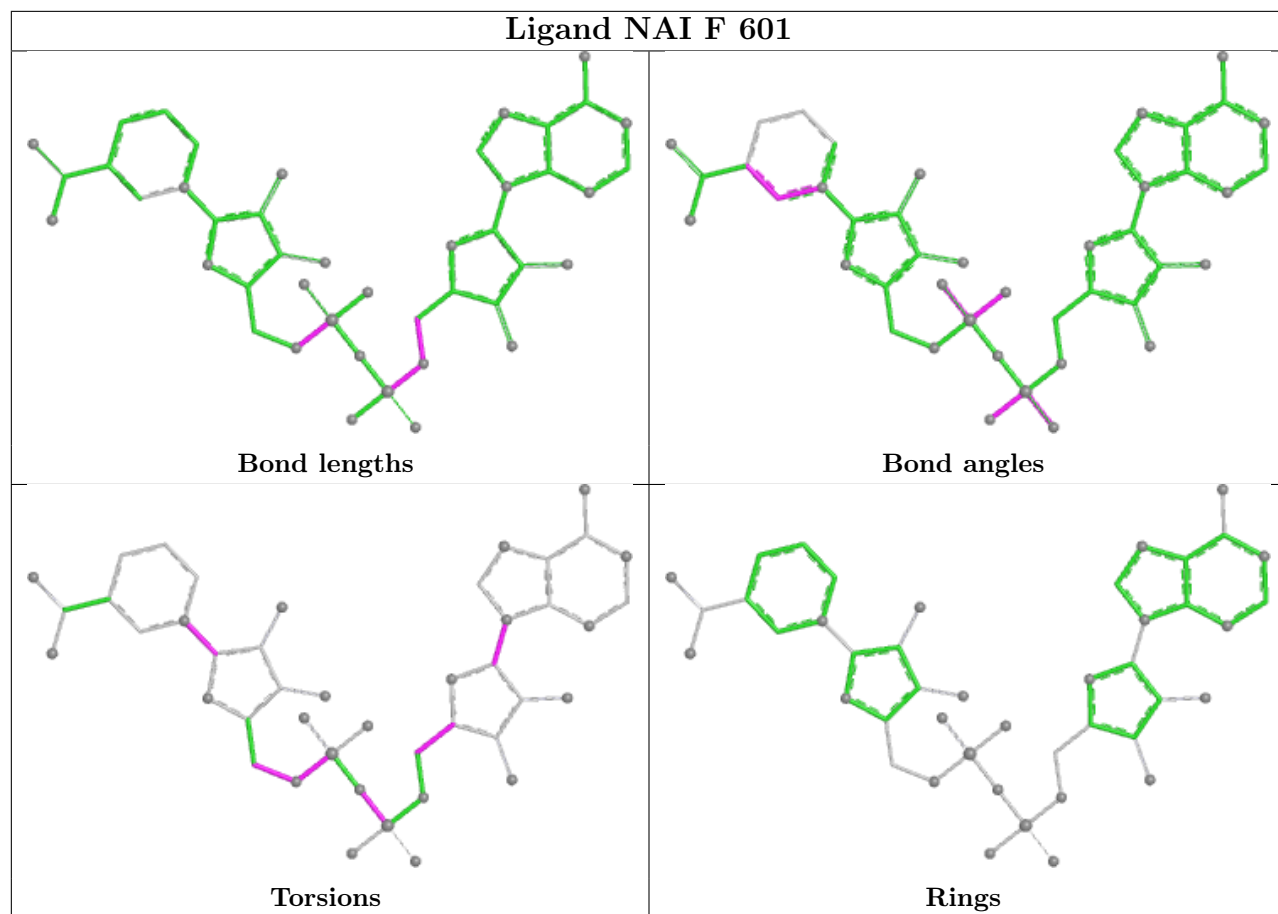
Ligand GTP L 602



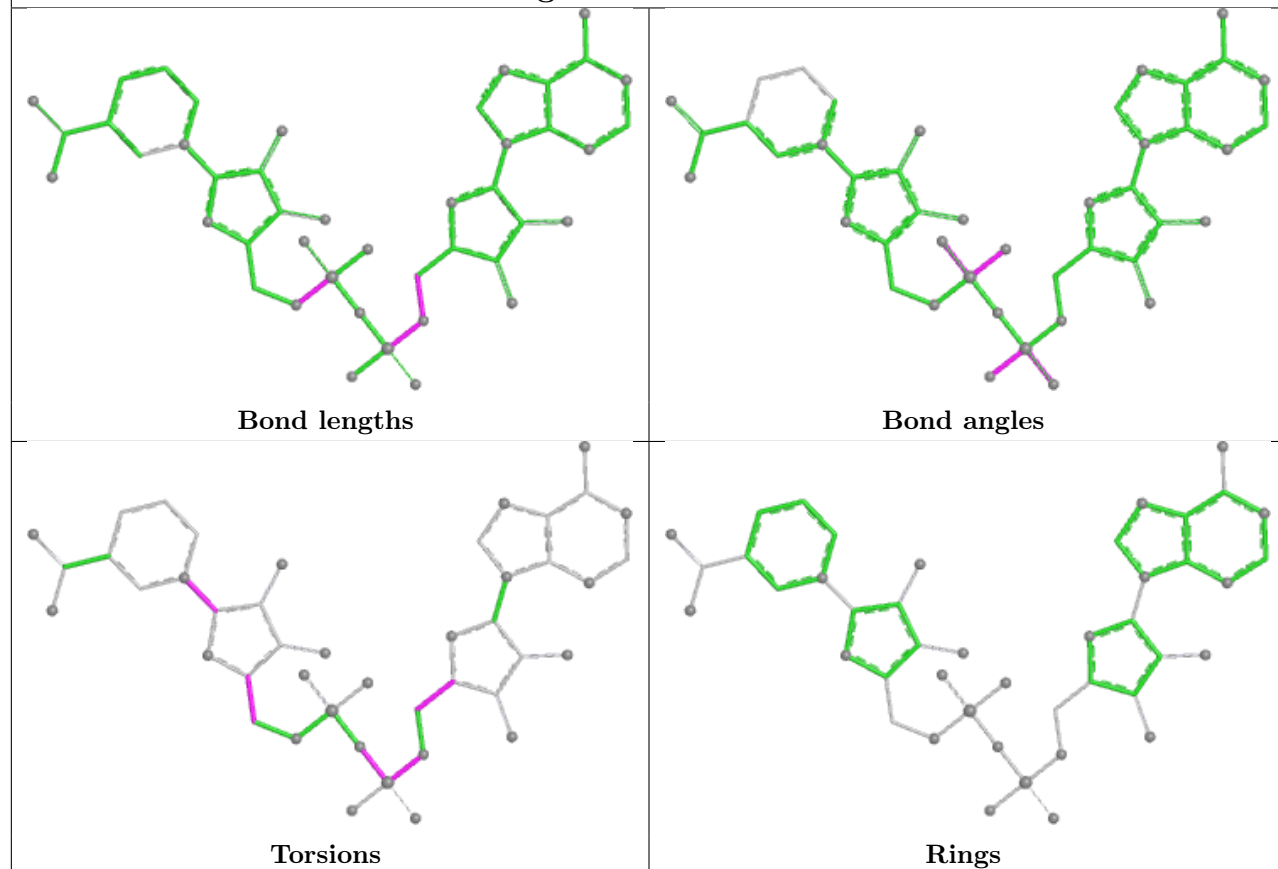
Ligand NAI H 603



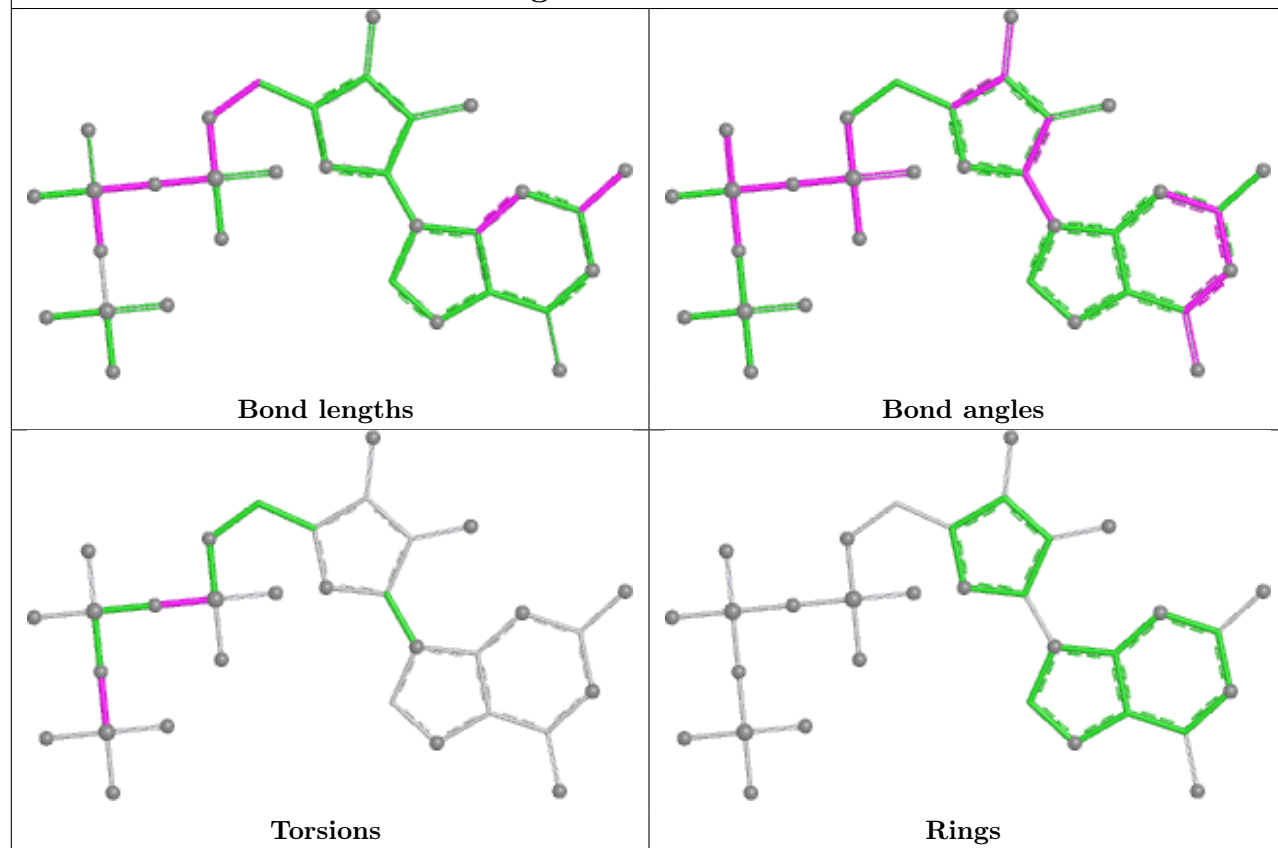




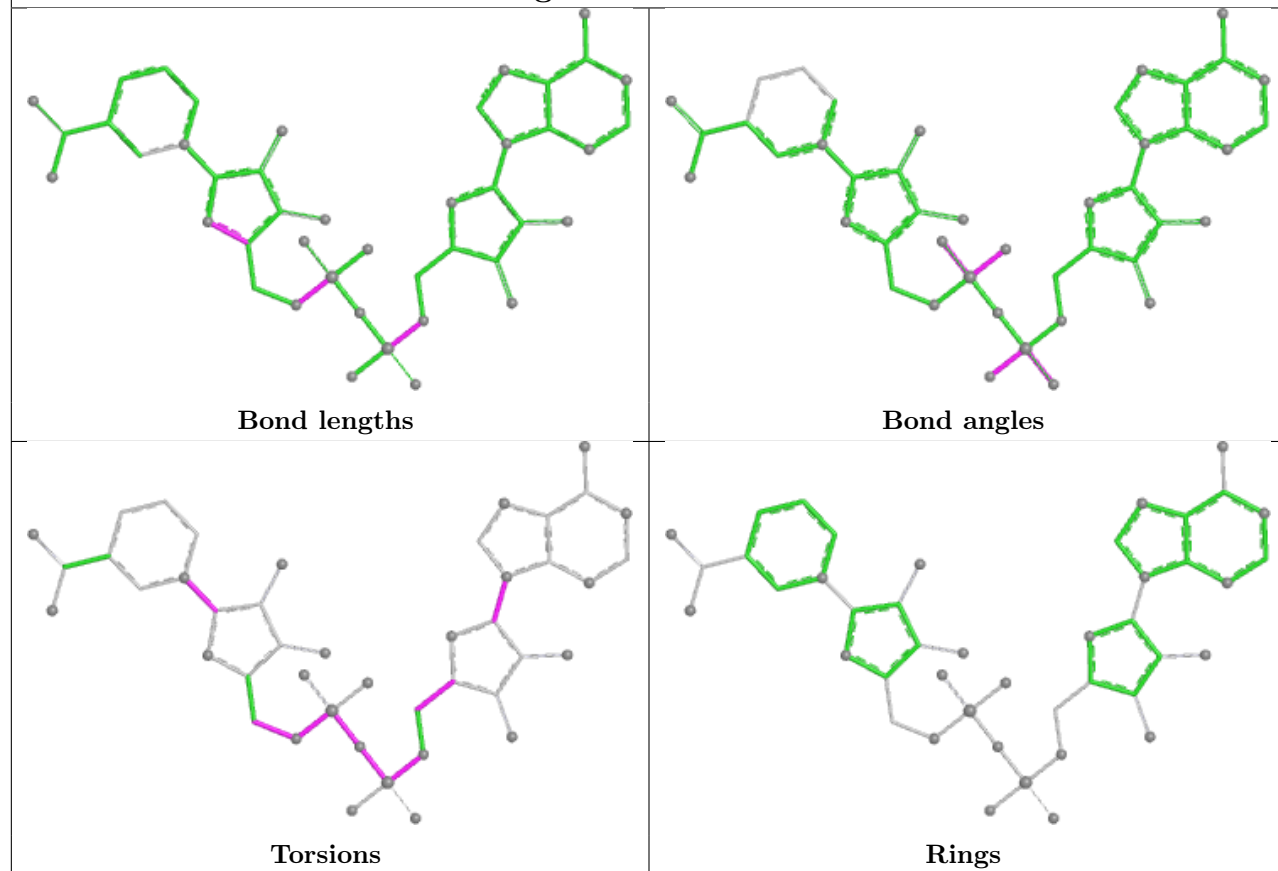
Ligand NAI L 601



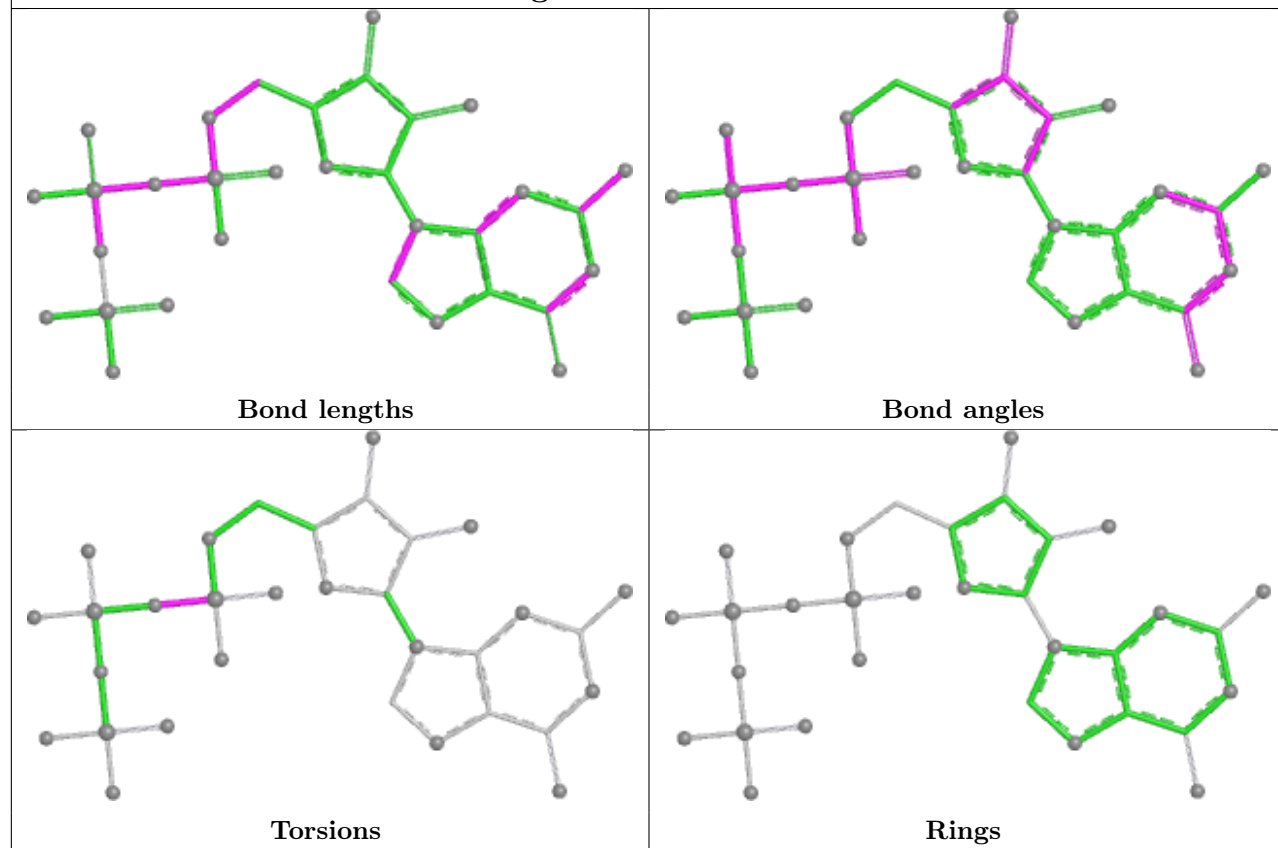
Ligand GTP C 601

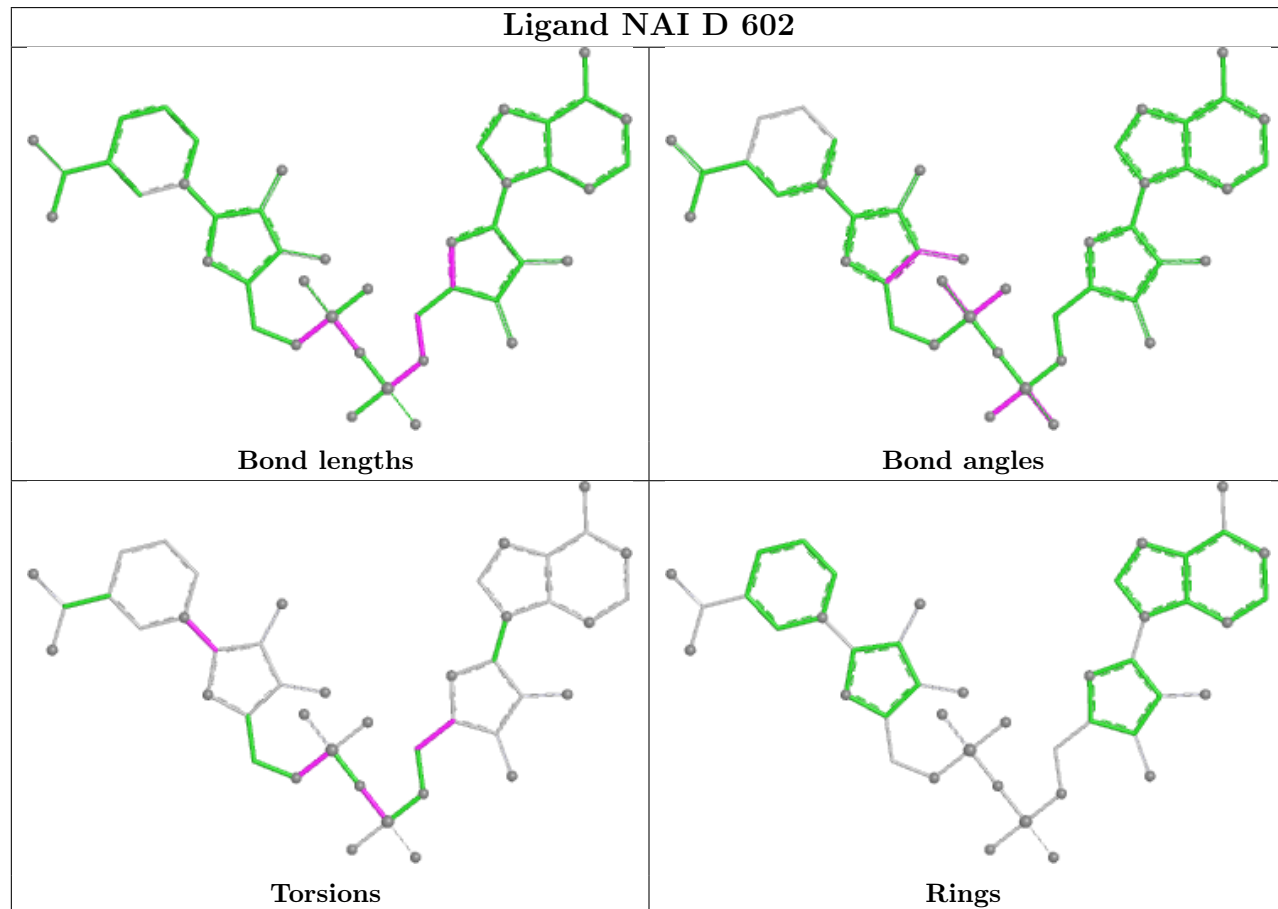
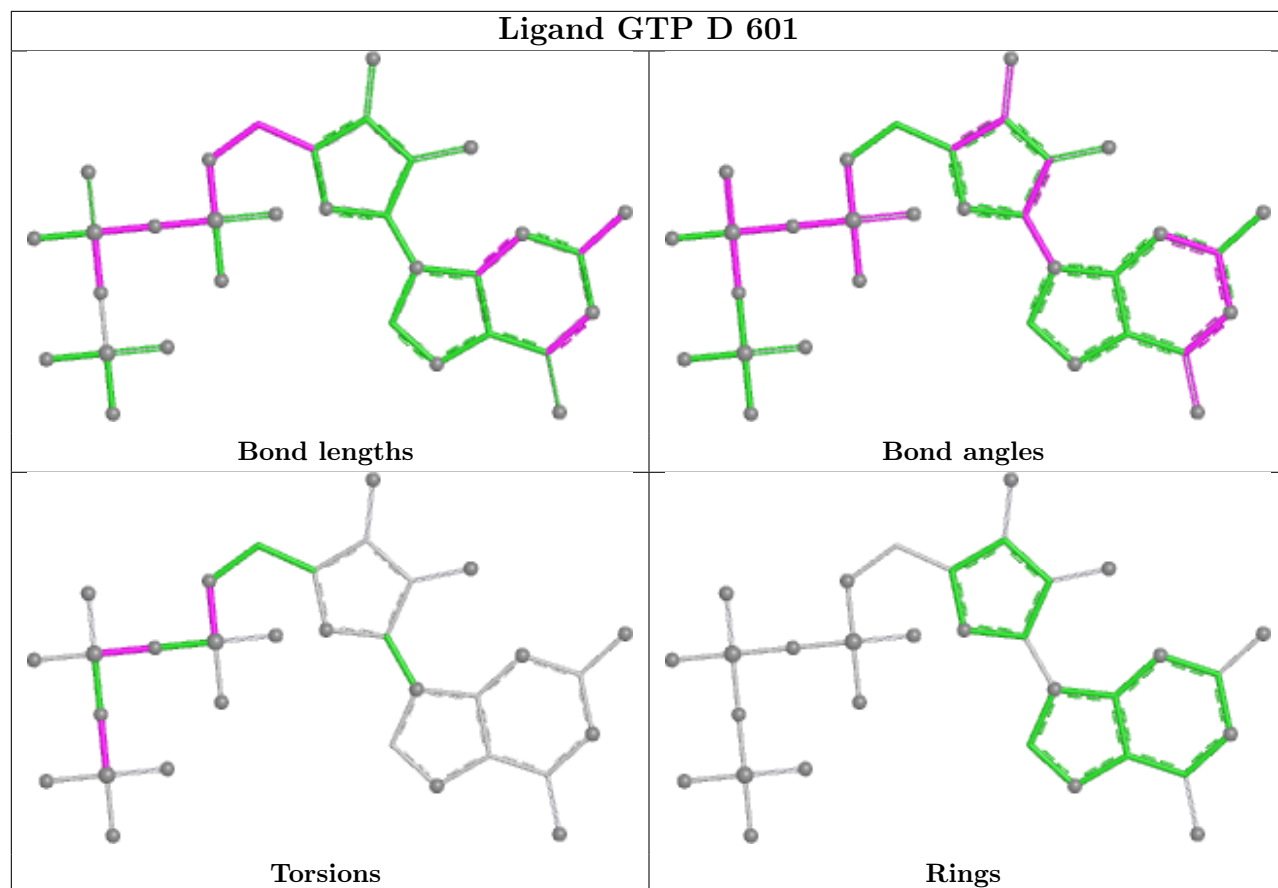


Ligand NAI A 604

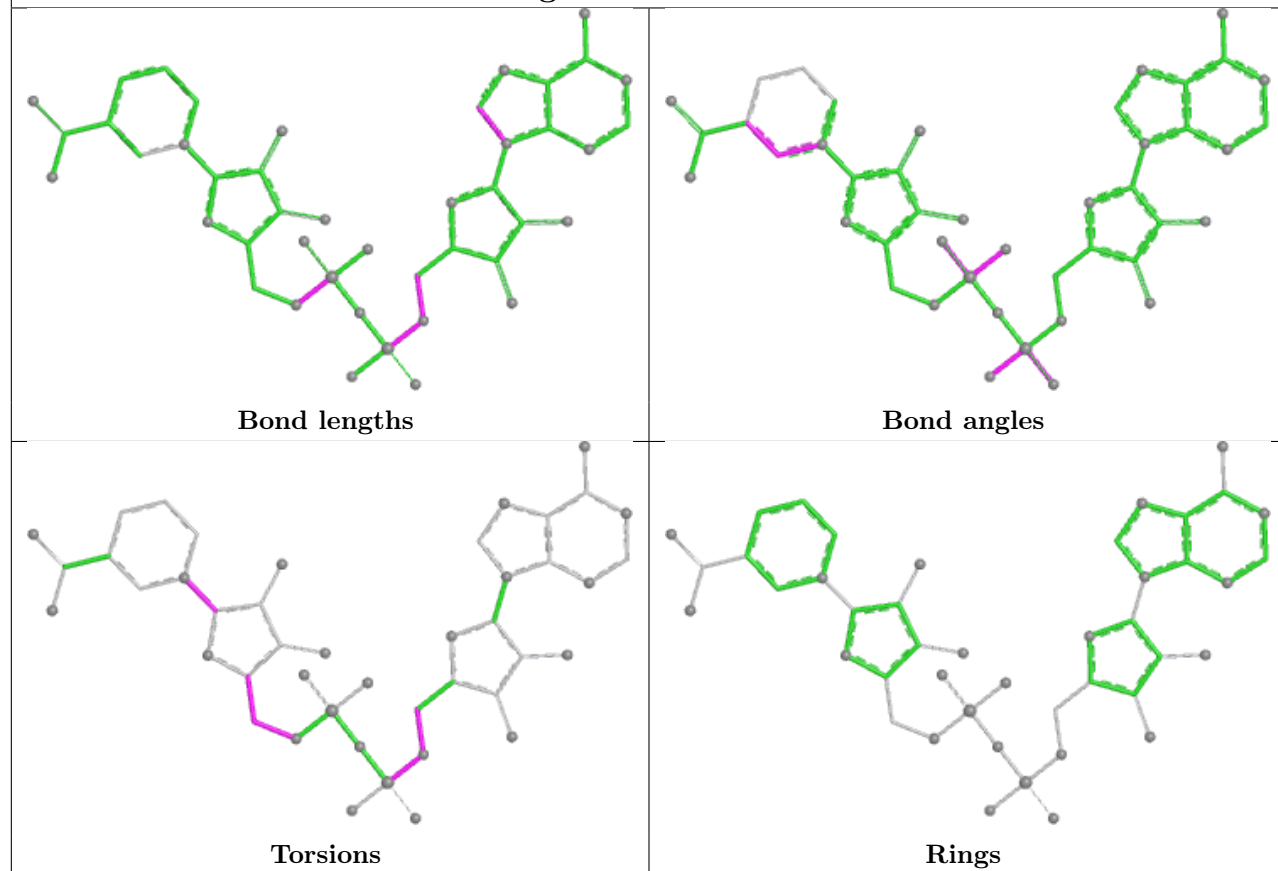


Ligand GTP B 601

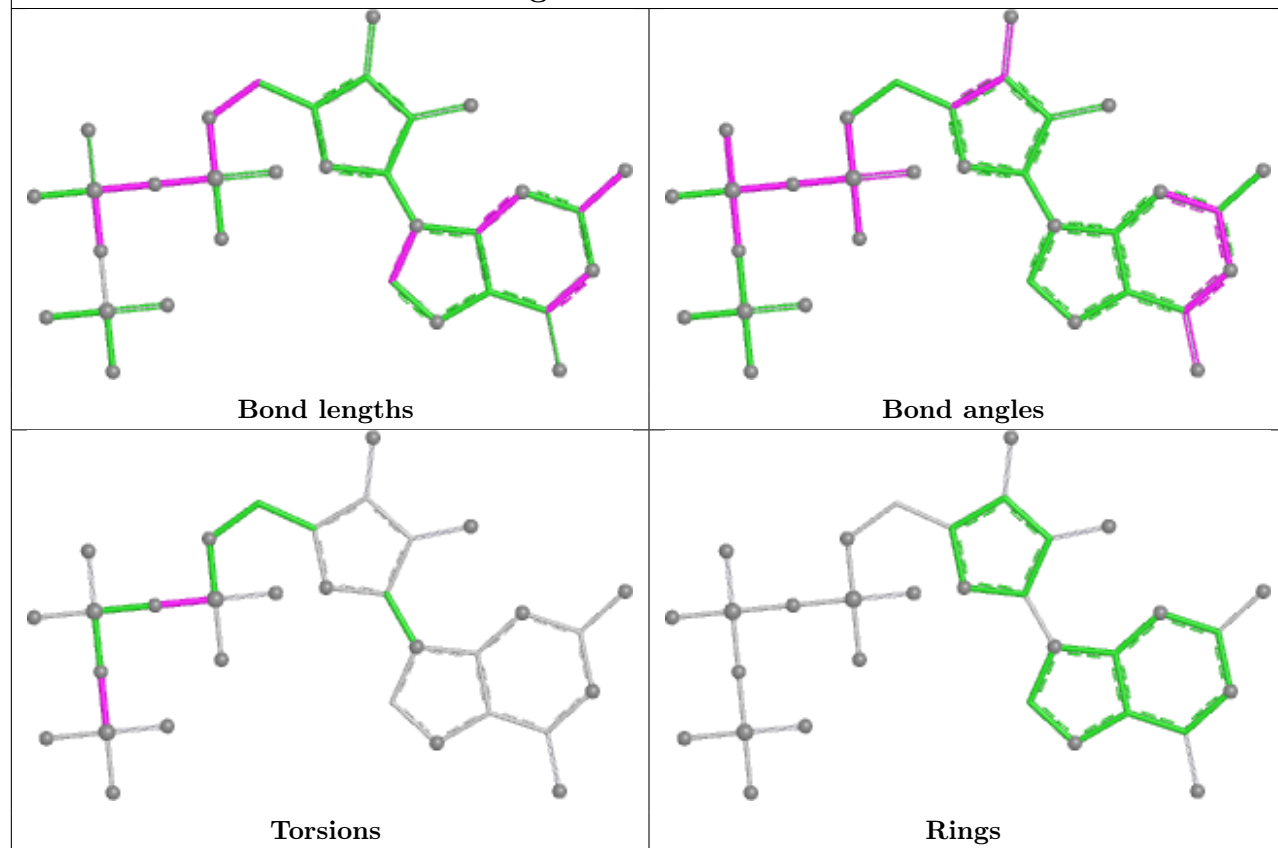


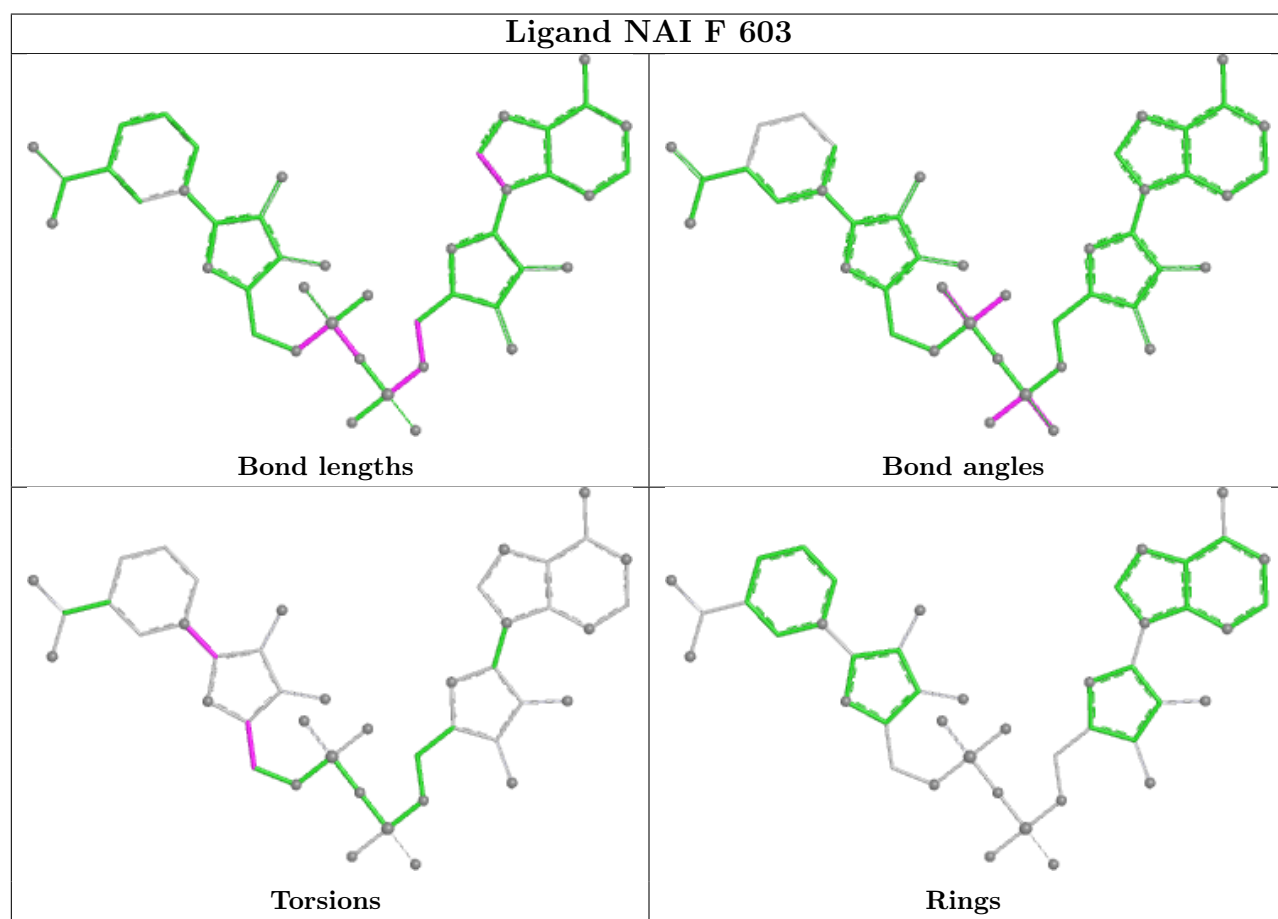
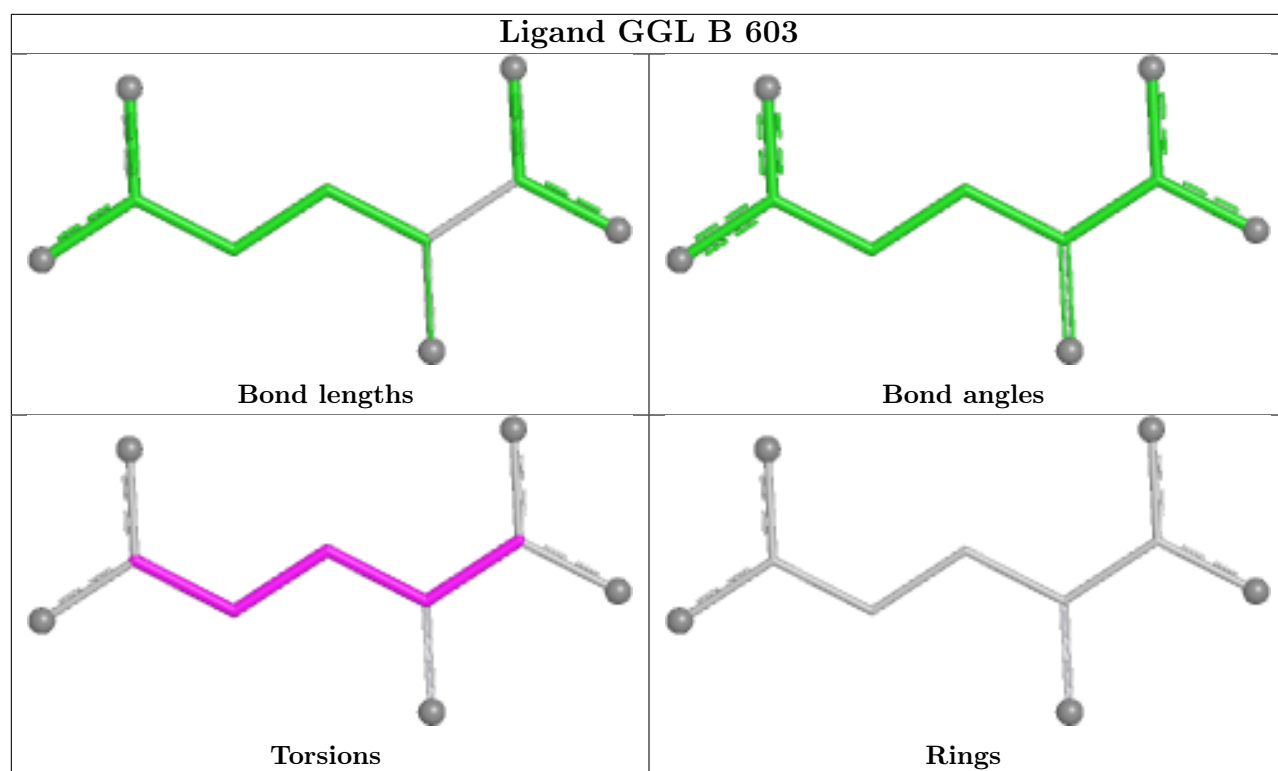


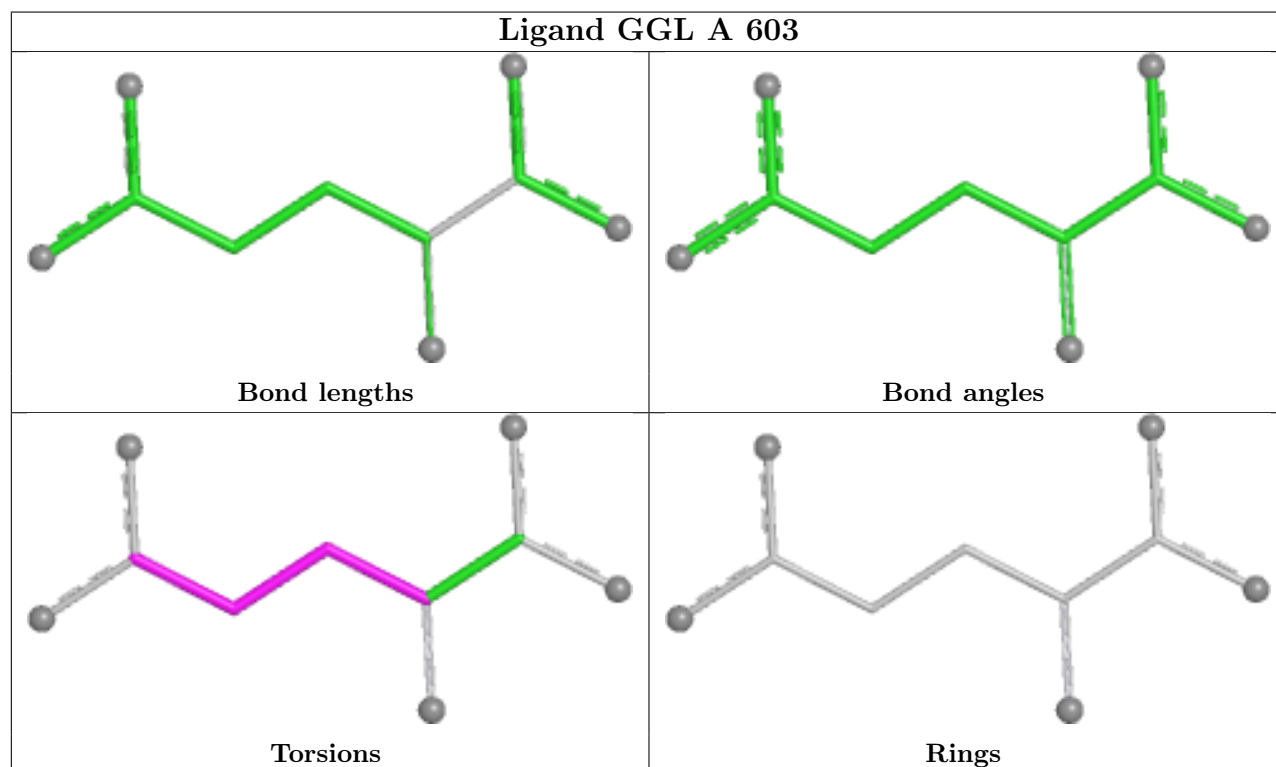
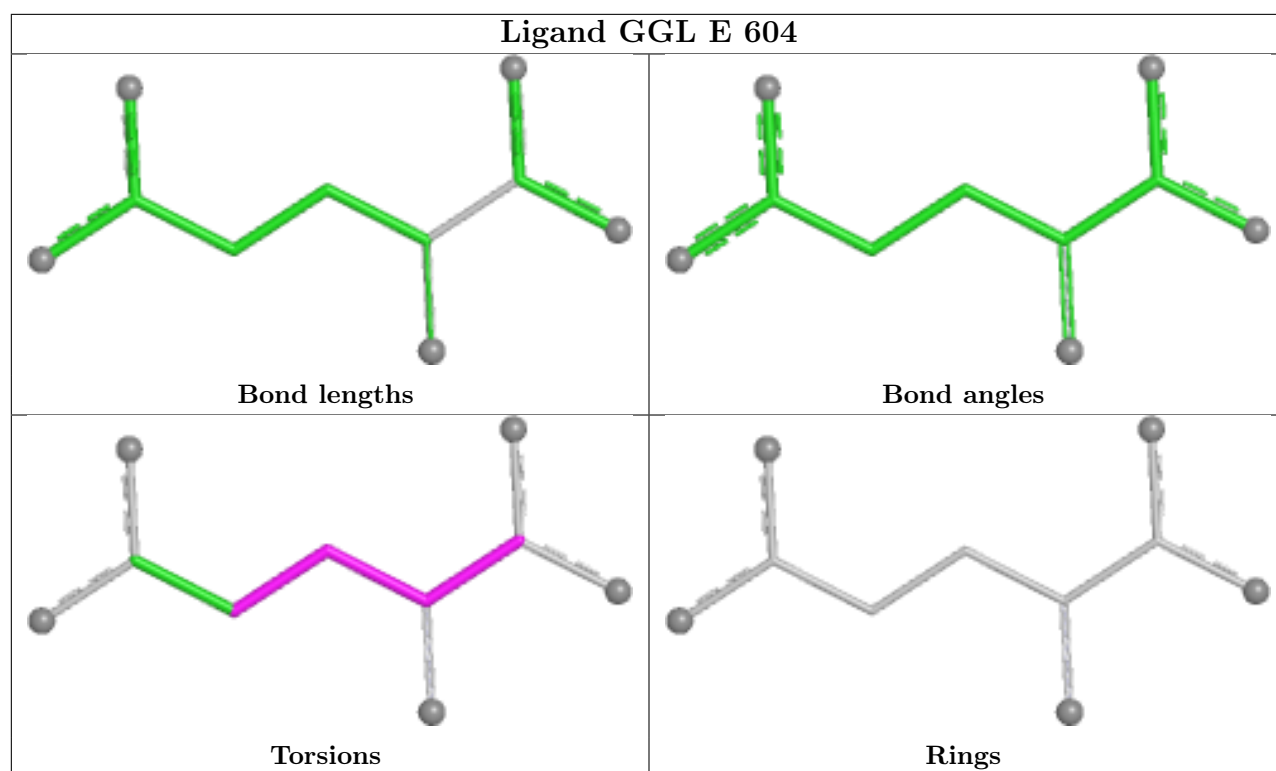
Ligand NAI J 603



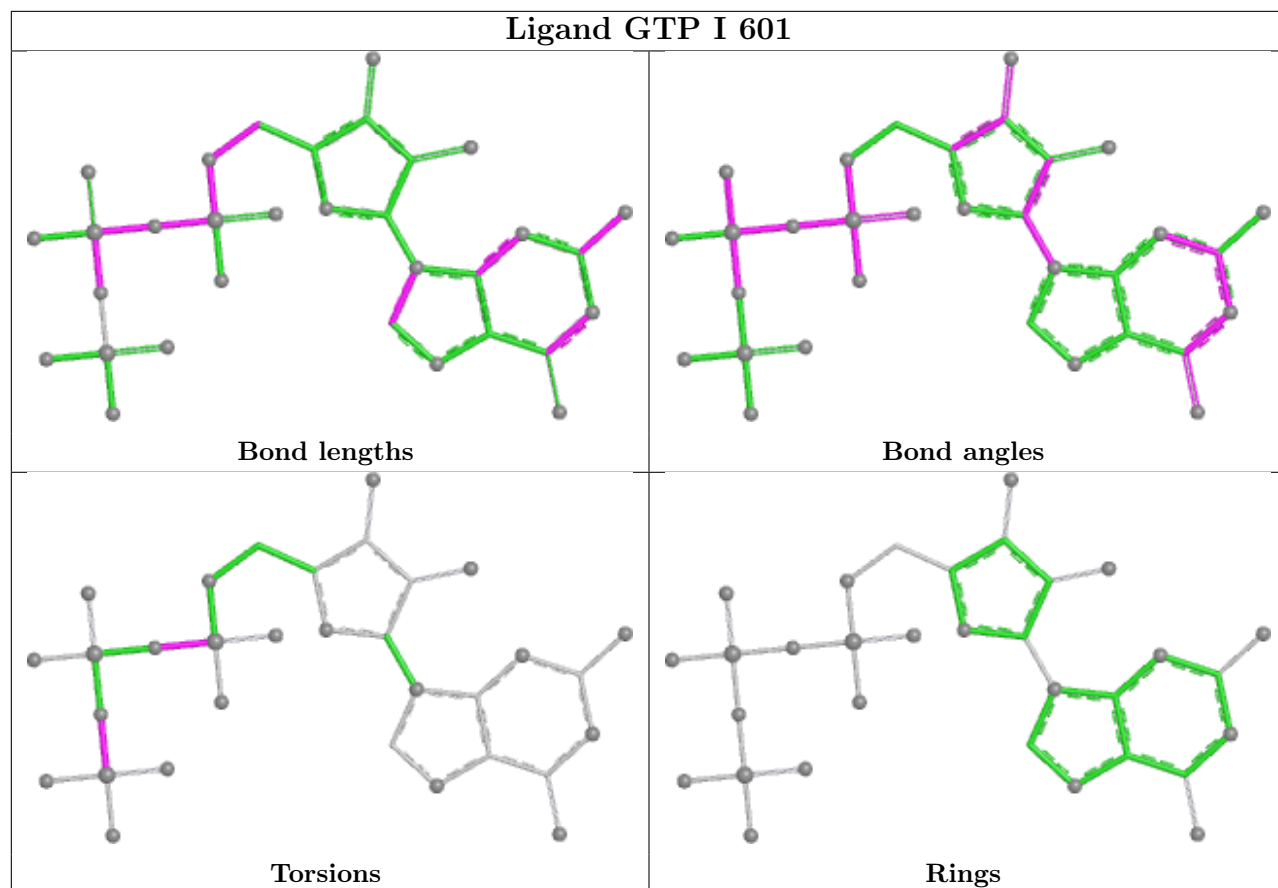
Ligand GTP G 601



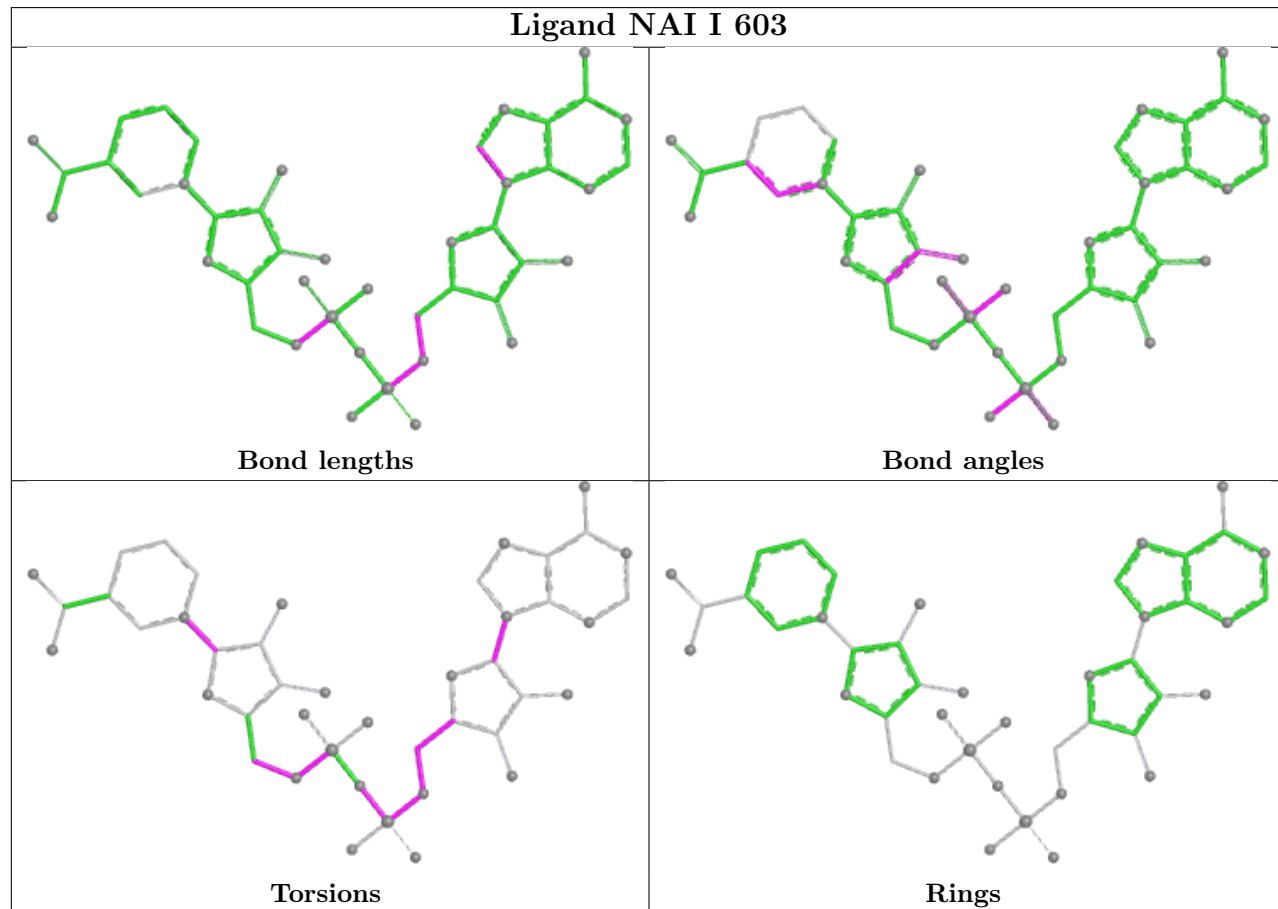


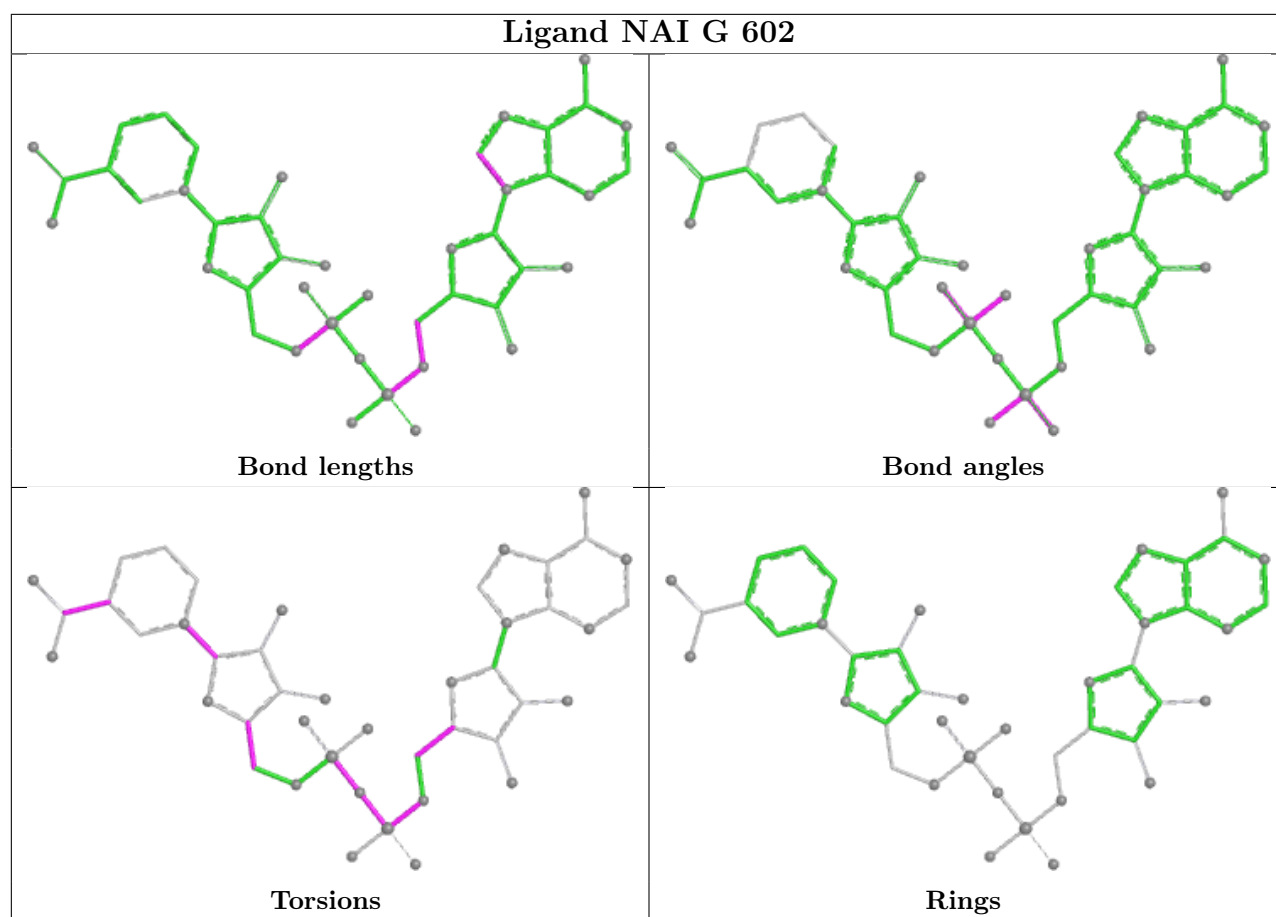


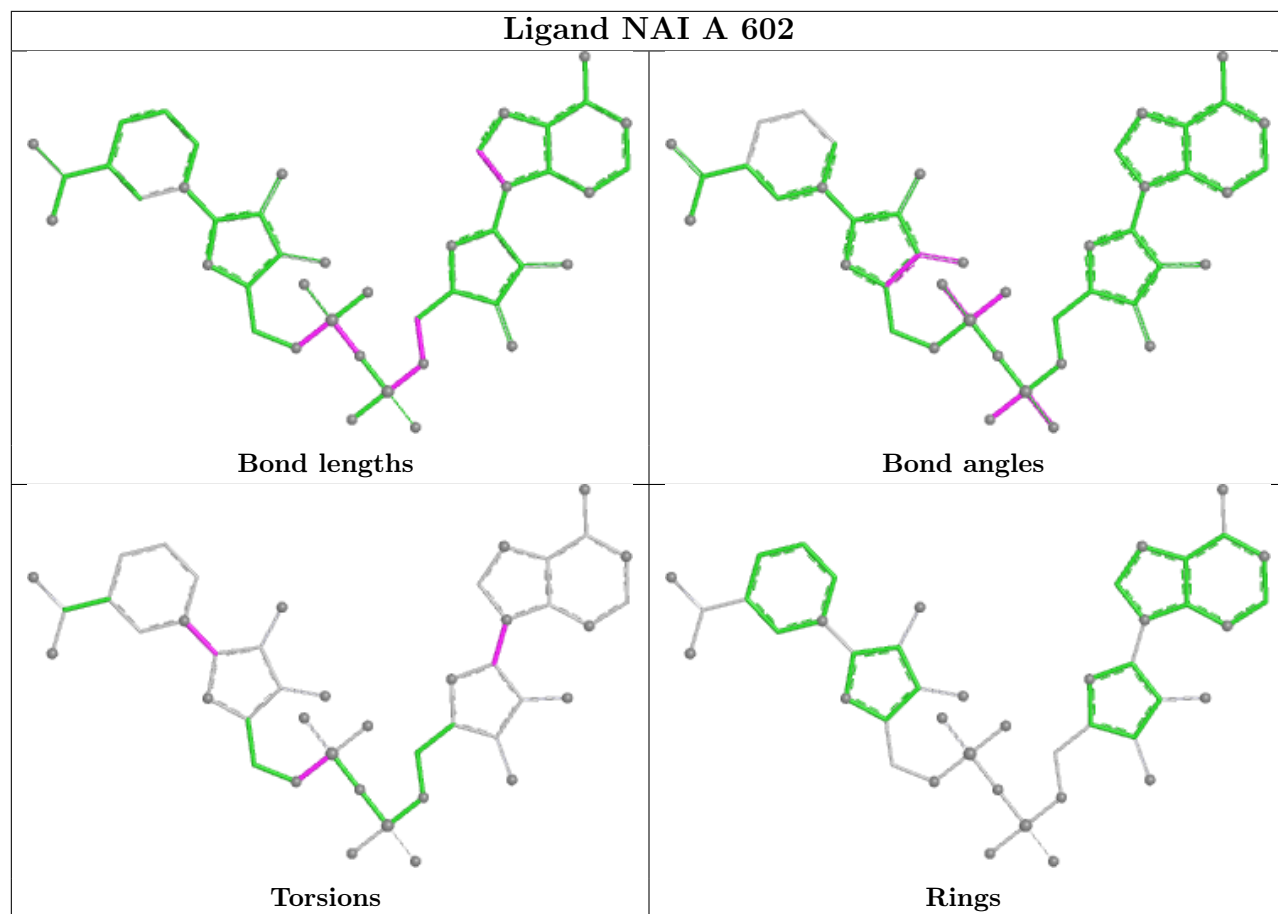
Ligand GTP I 601

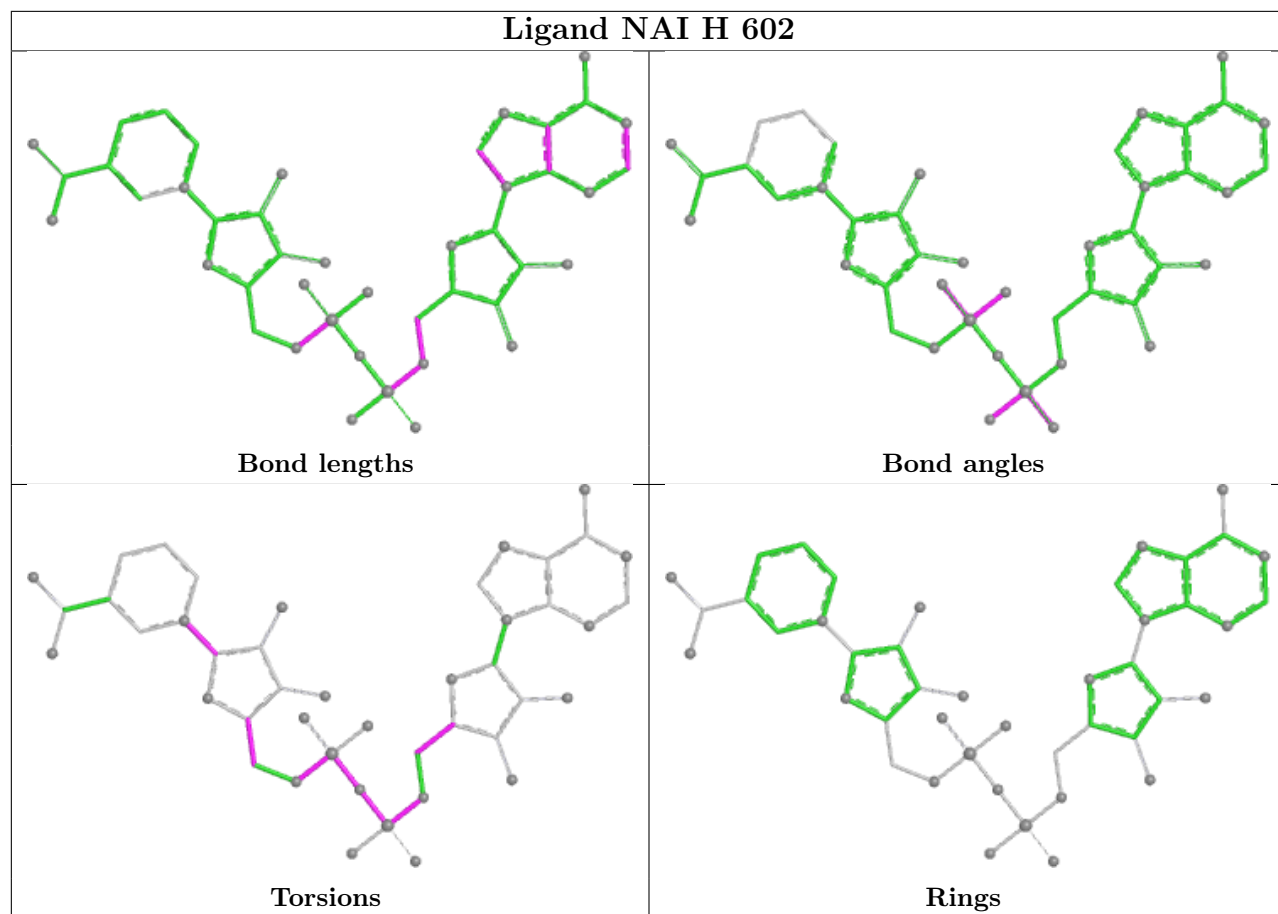


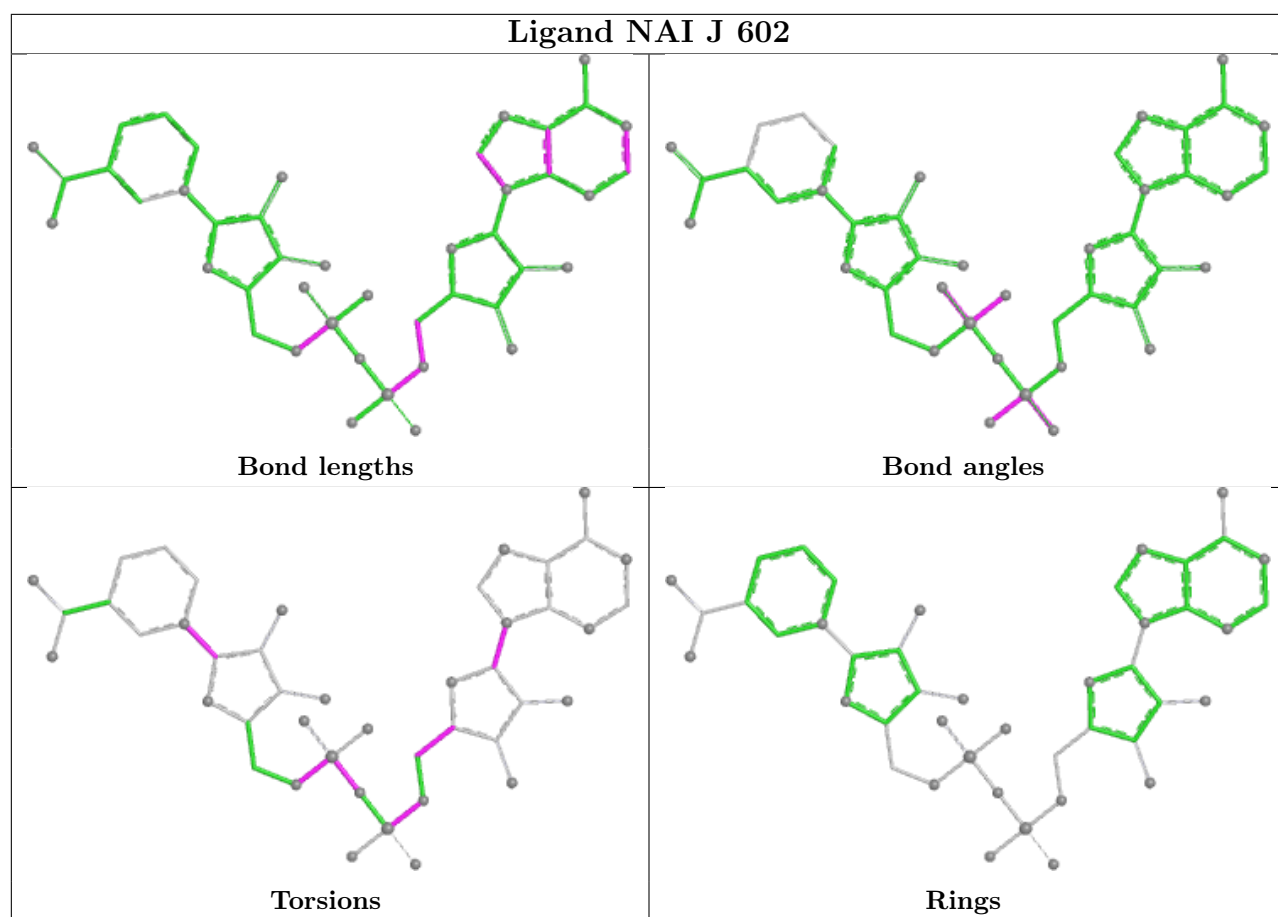
Ligand NAI I 603

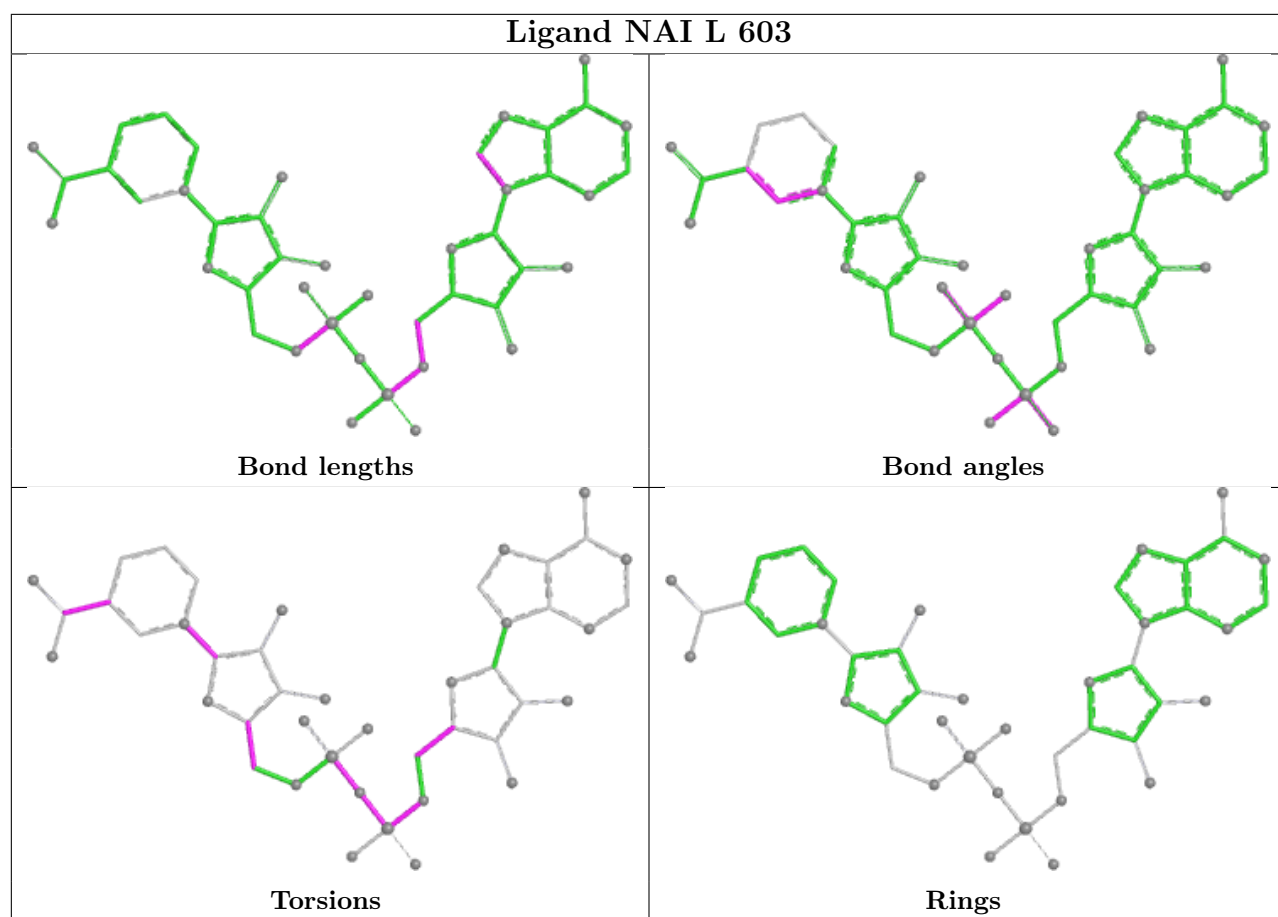


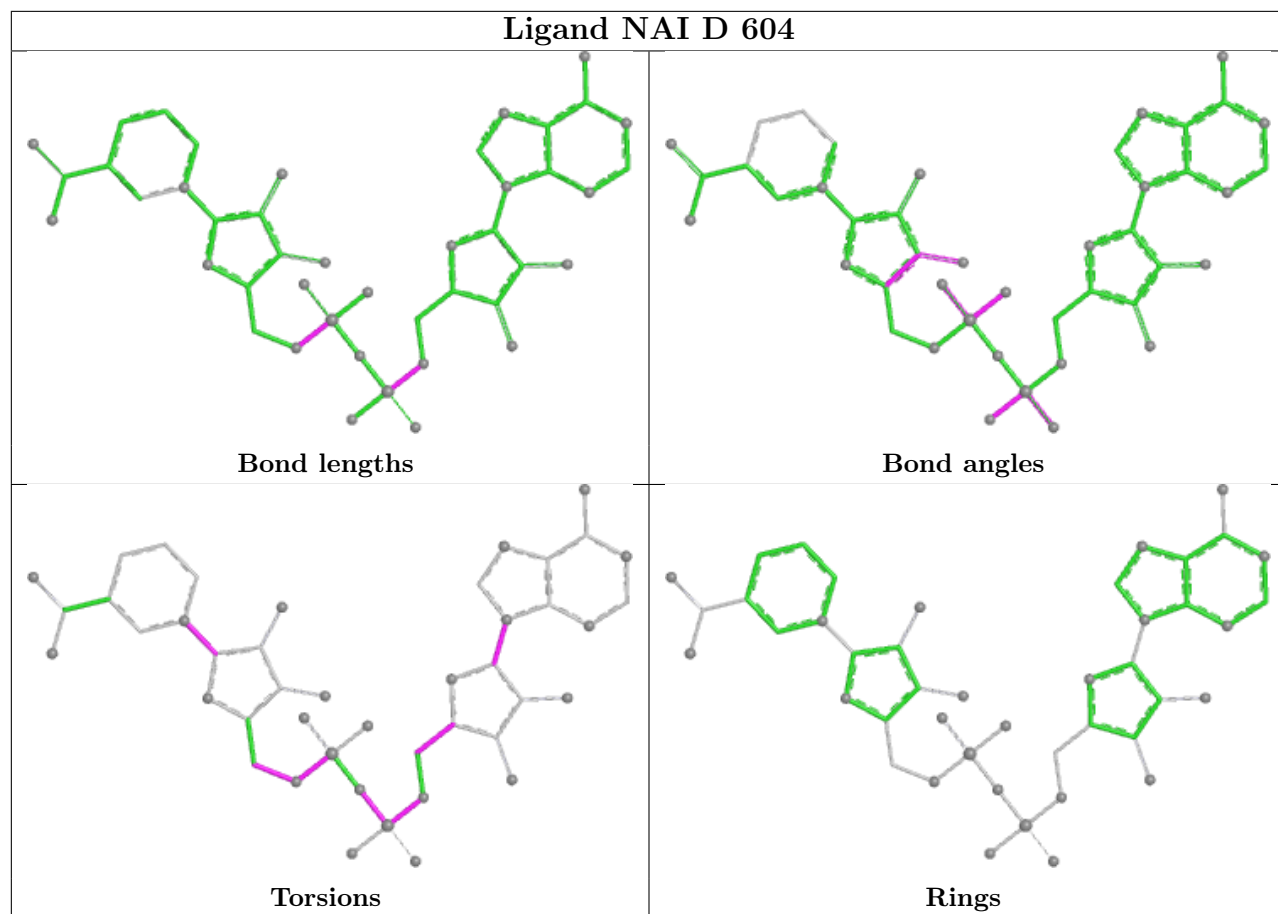


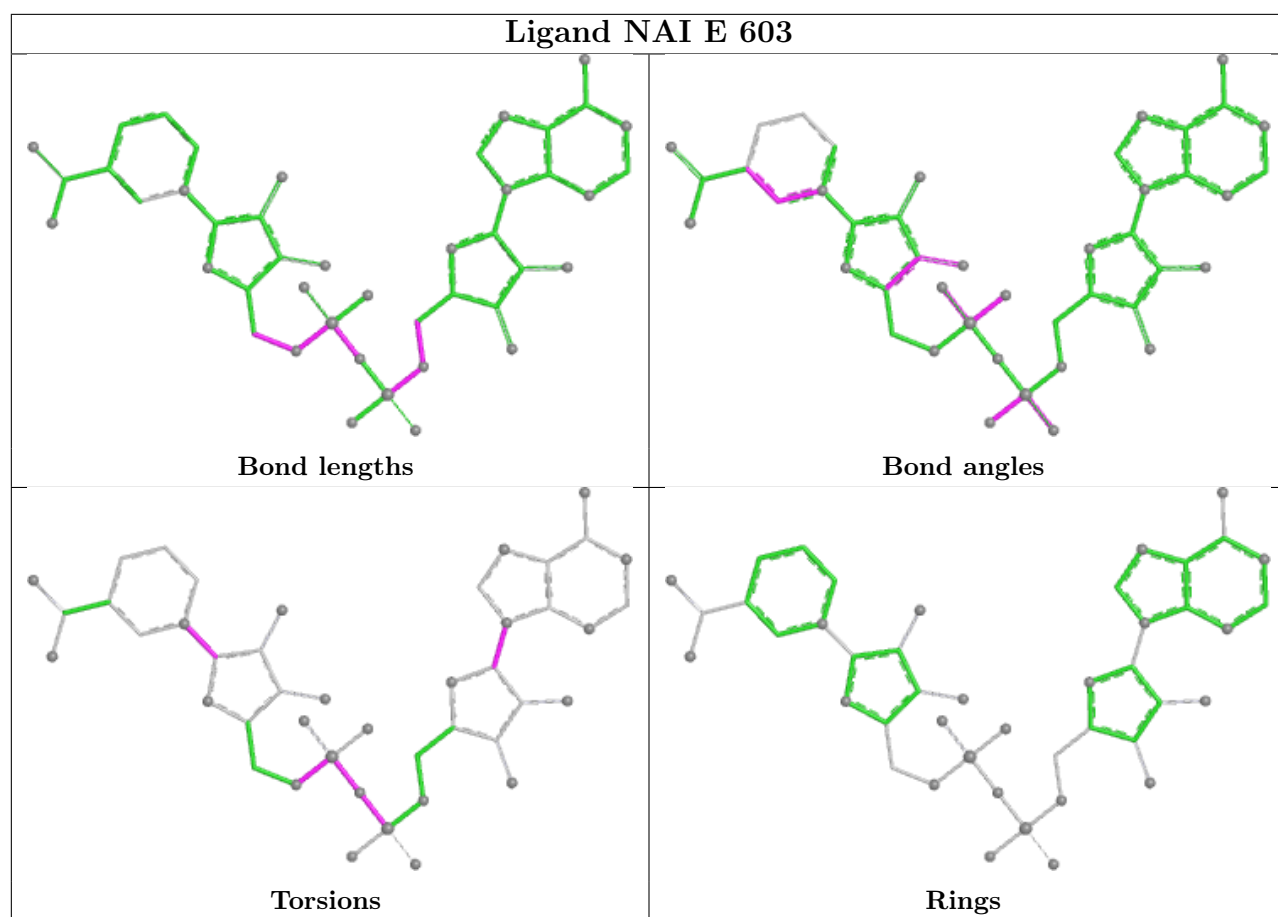




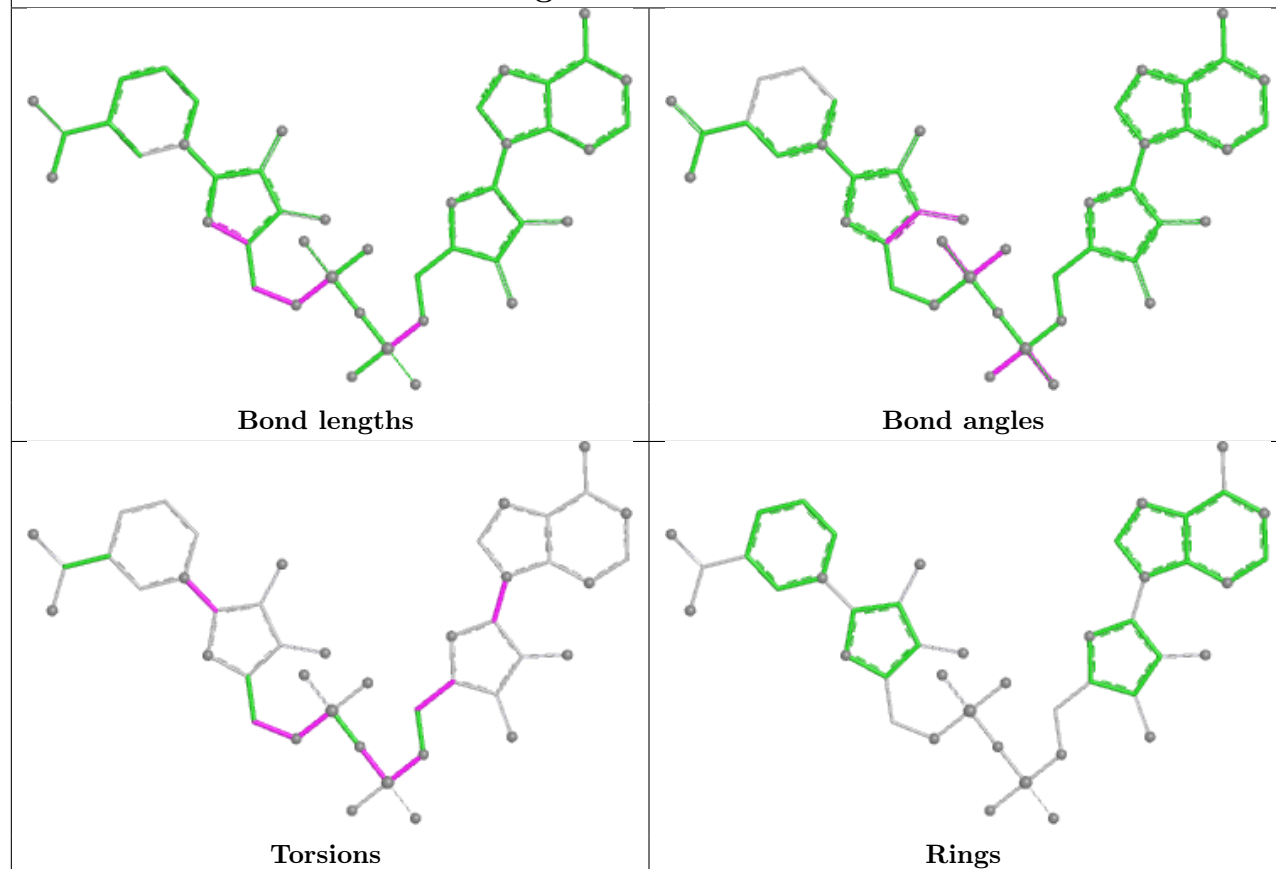




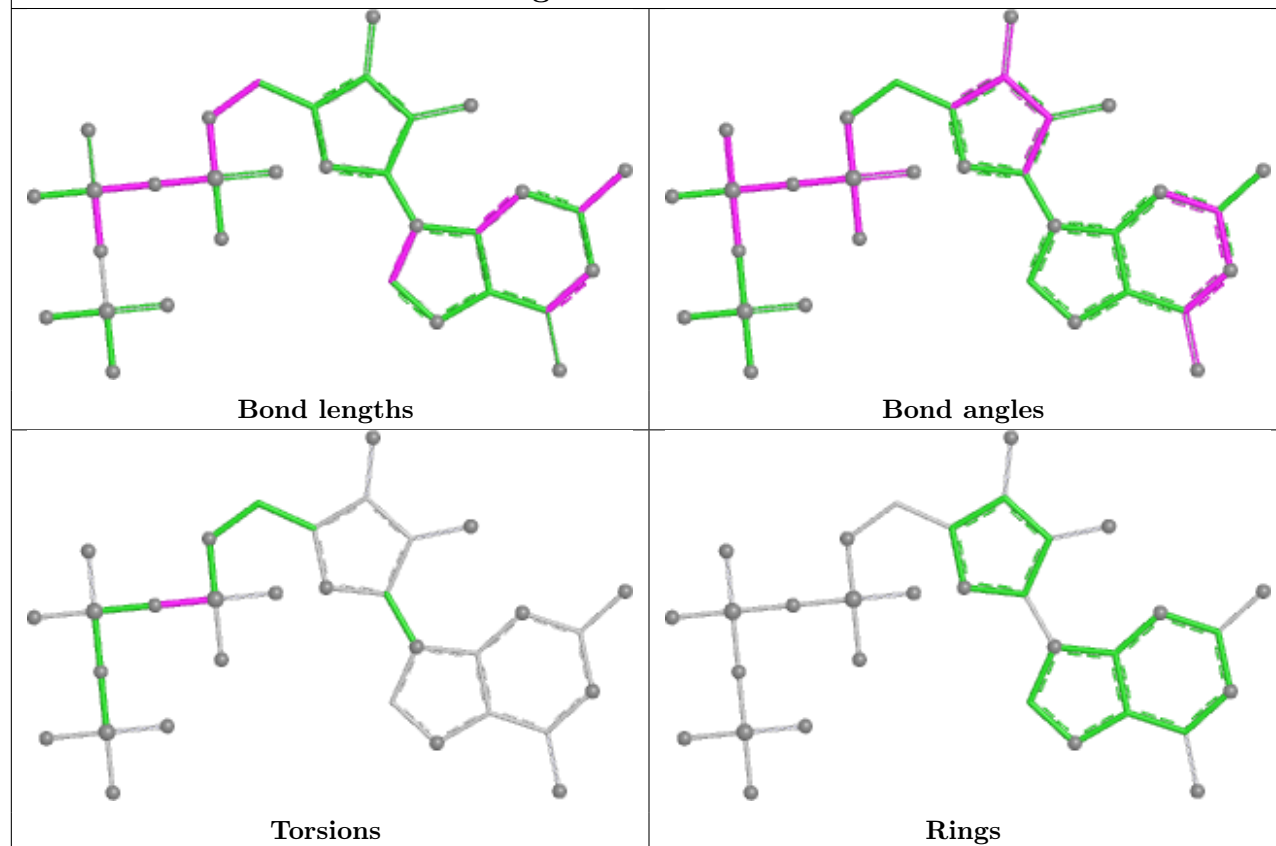


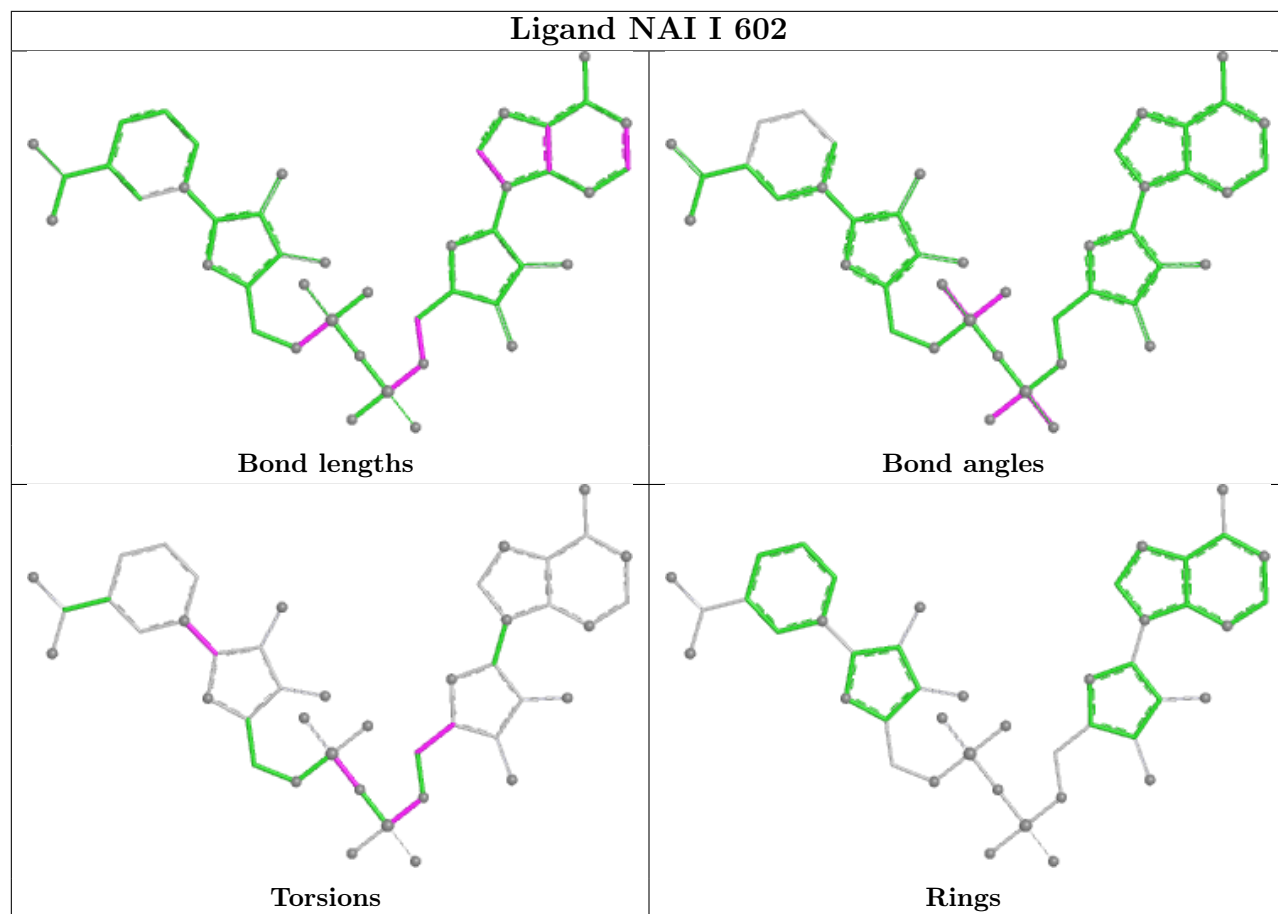


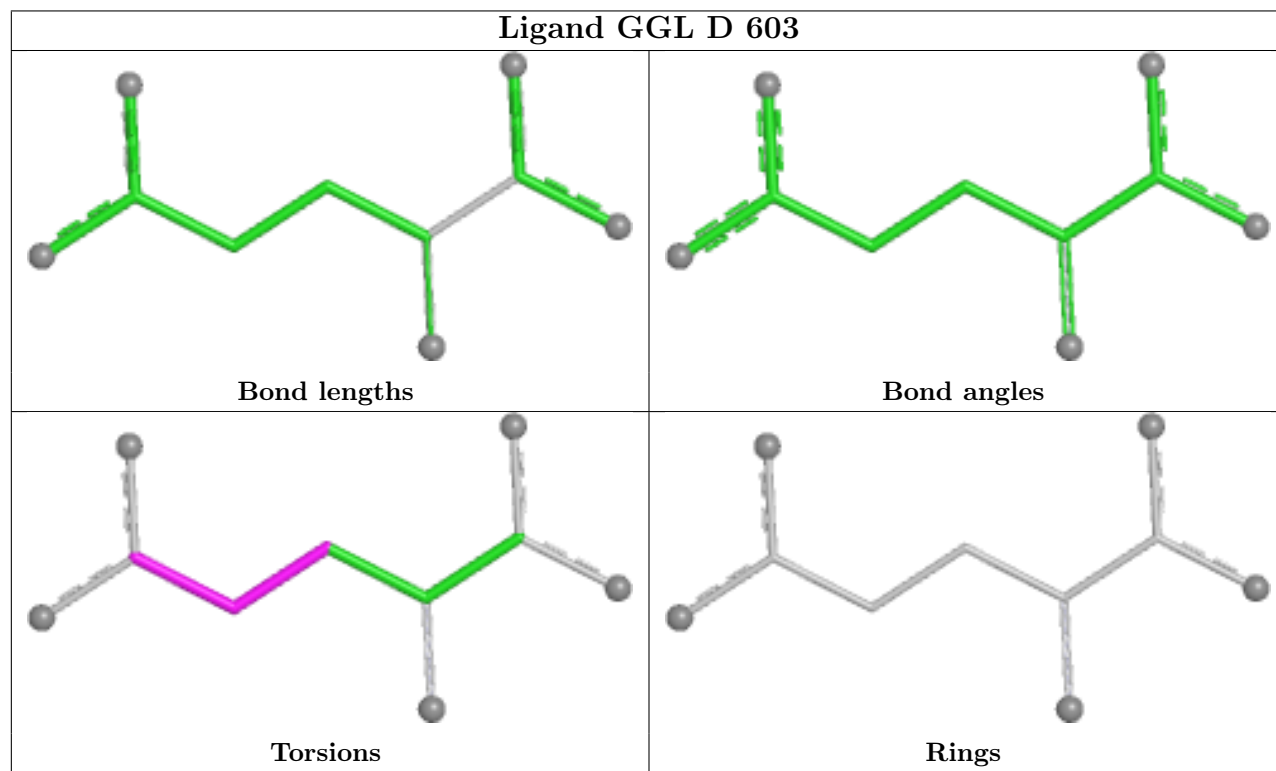
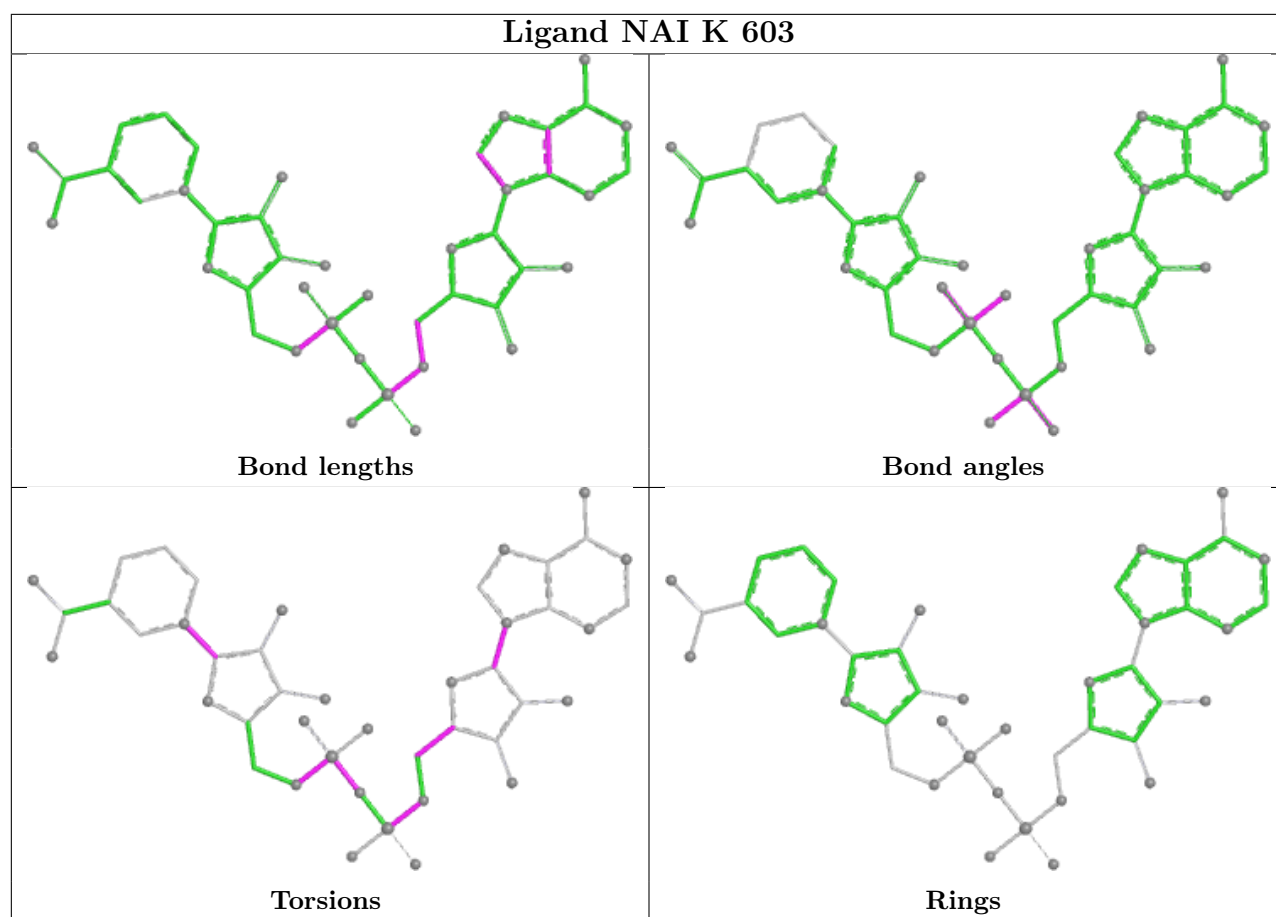
Ligand NAI B 604



Ligand GTP F 602







5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

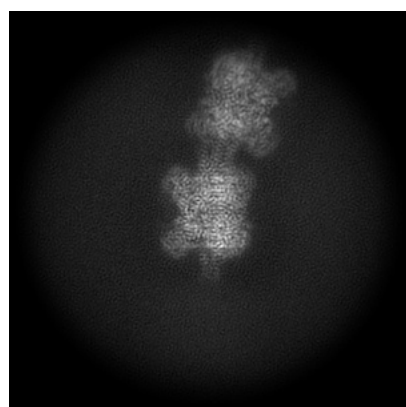
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74581. These allow visual inspection of the internal detail of the map and identification of artifacts.

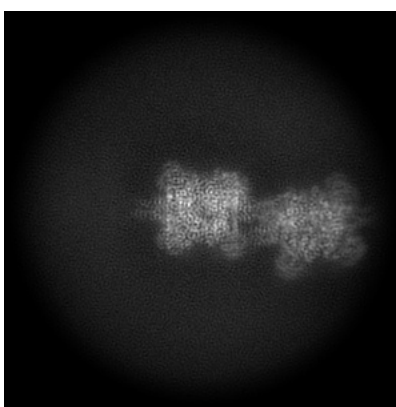
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

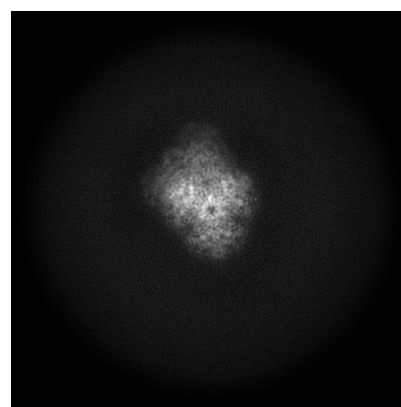
6.1.1 Primary map



X



Y

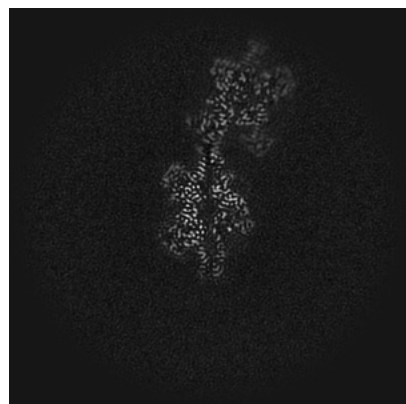


Z

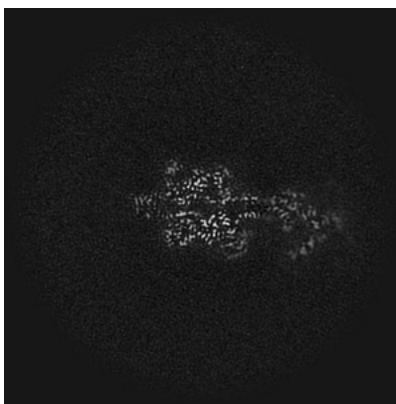
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

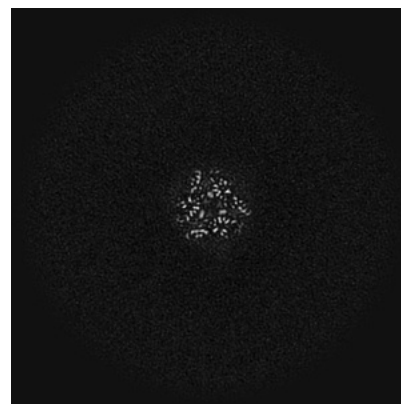
6.2.1 Primary map



X Index: 160



Y Index: 160

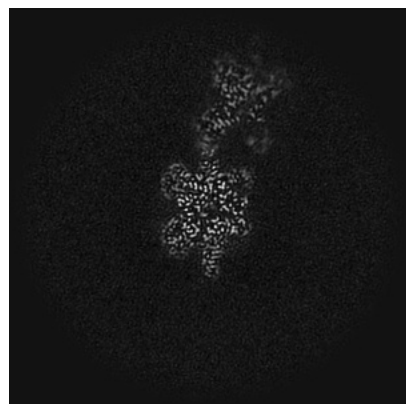


Z Index: 160

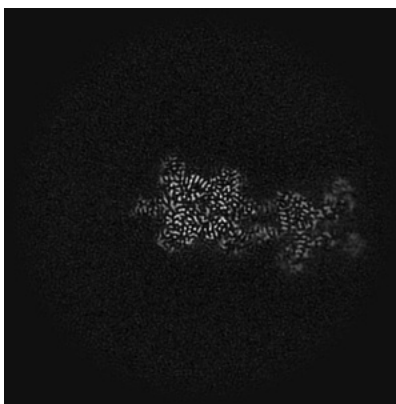
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

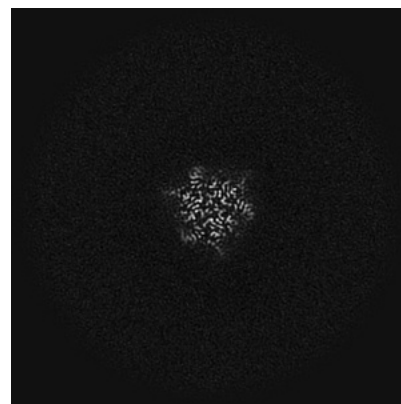
6.3.1 Primary map



X Index: 166



Y Index: 167

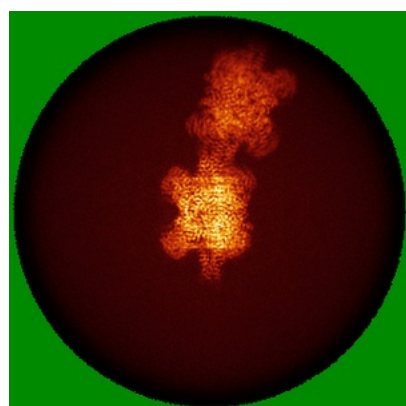


Z Index: 169

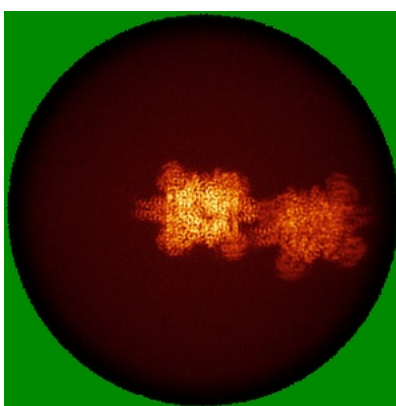
The images above show the largest variance slices of the map in three orthogonal directions.

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

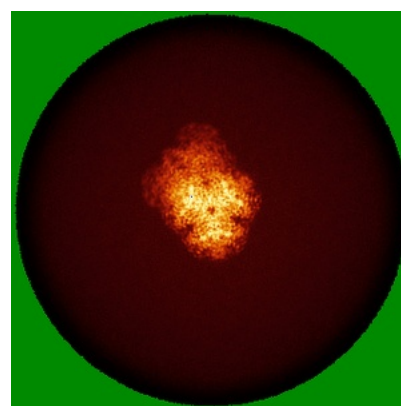
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

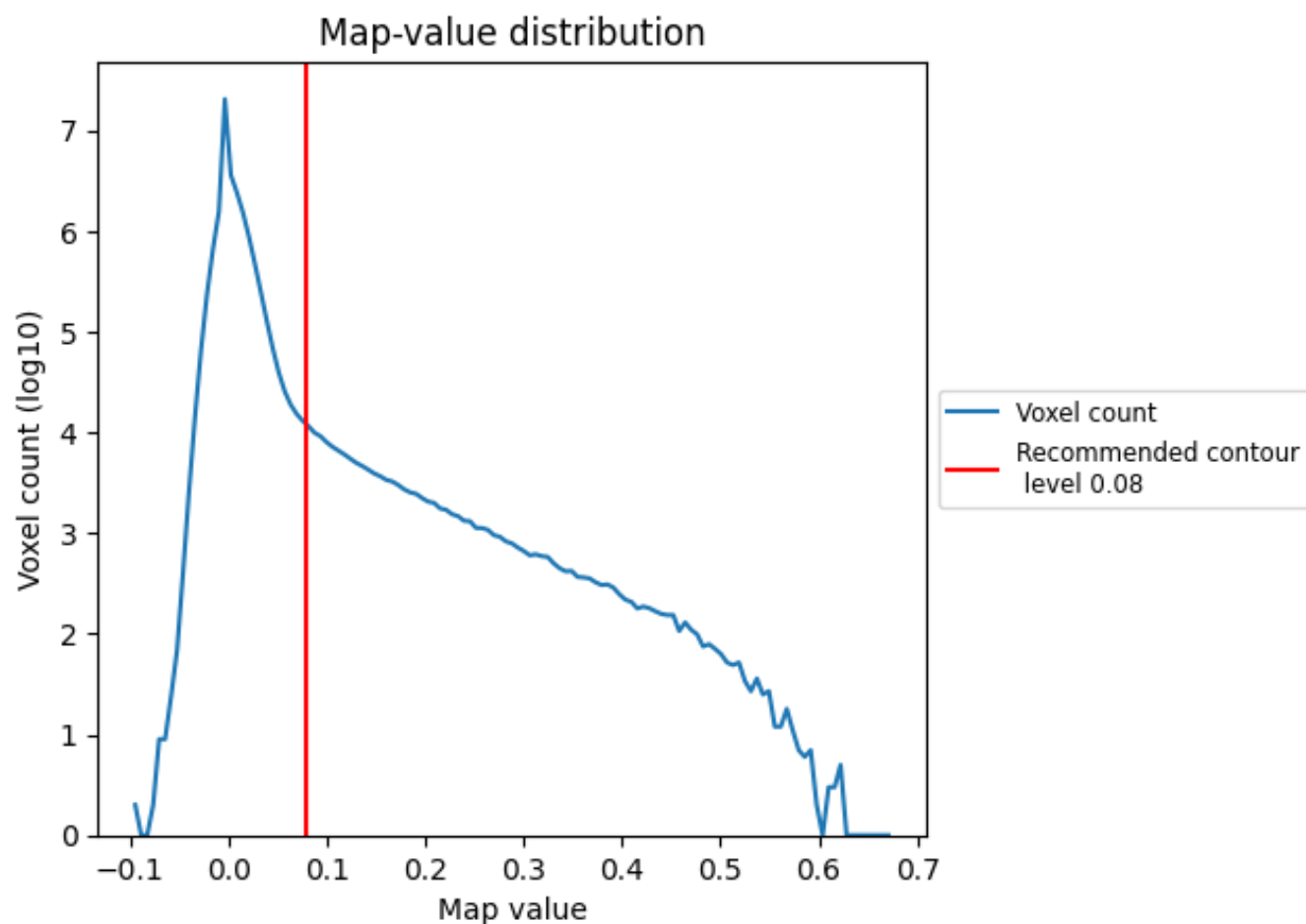
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

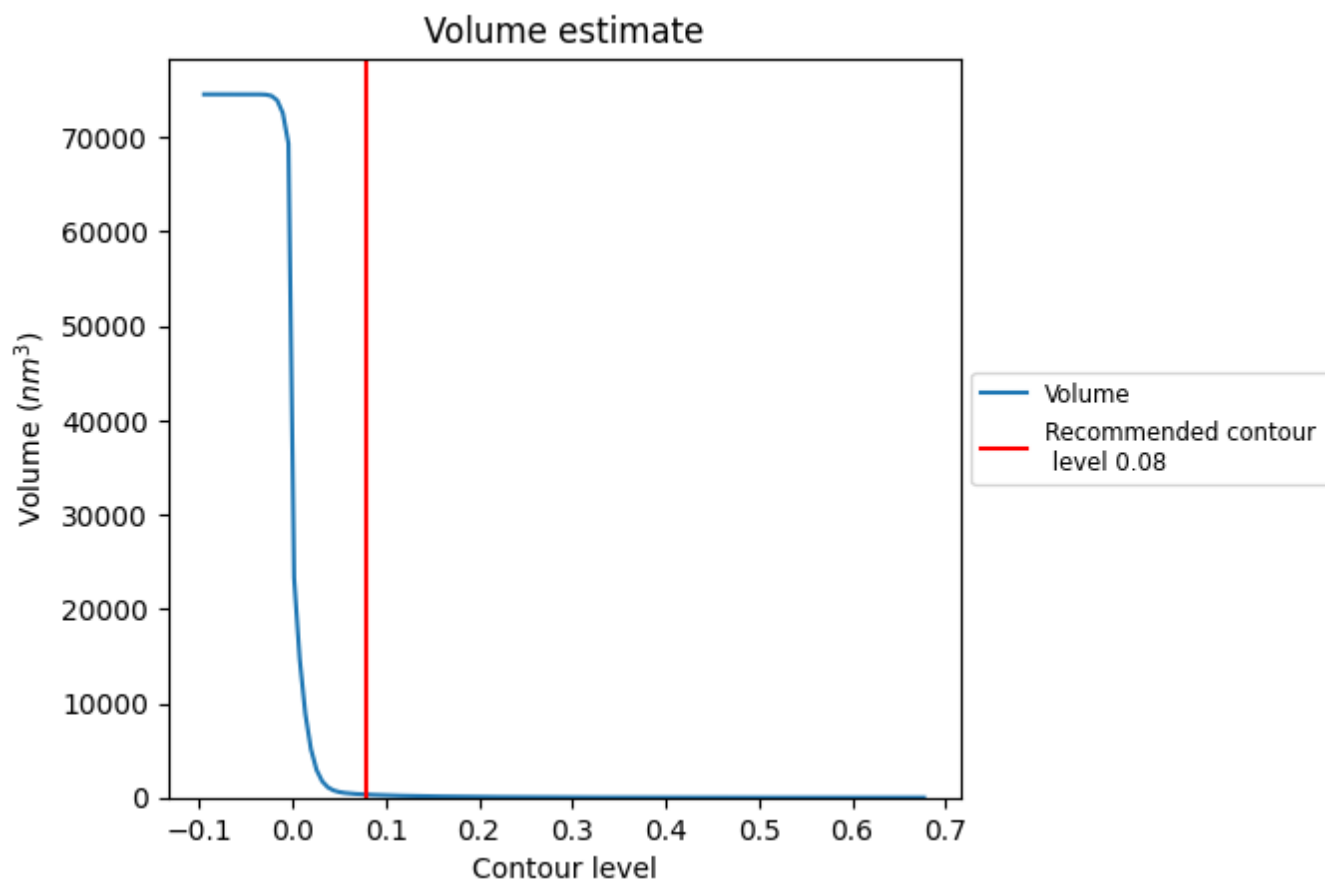
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

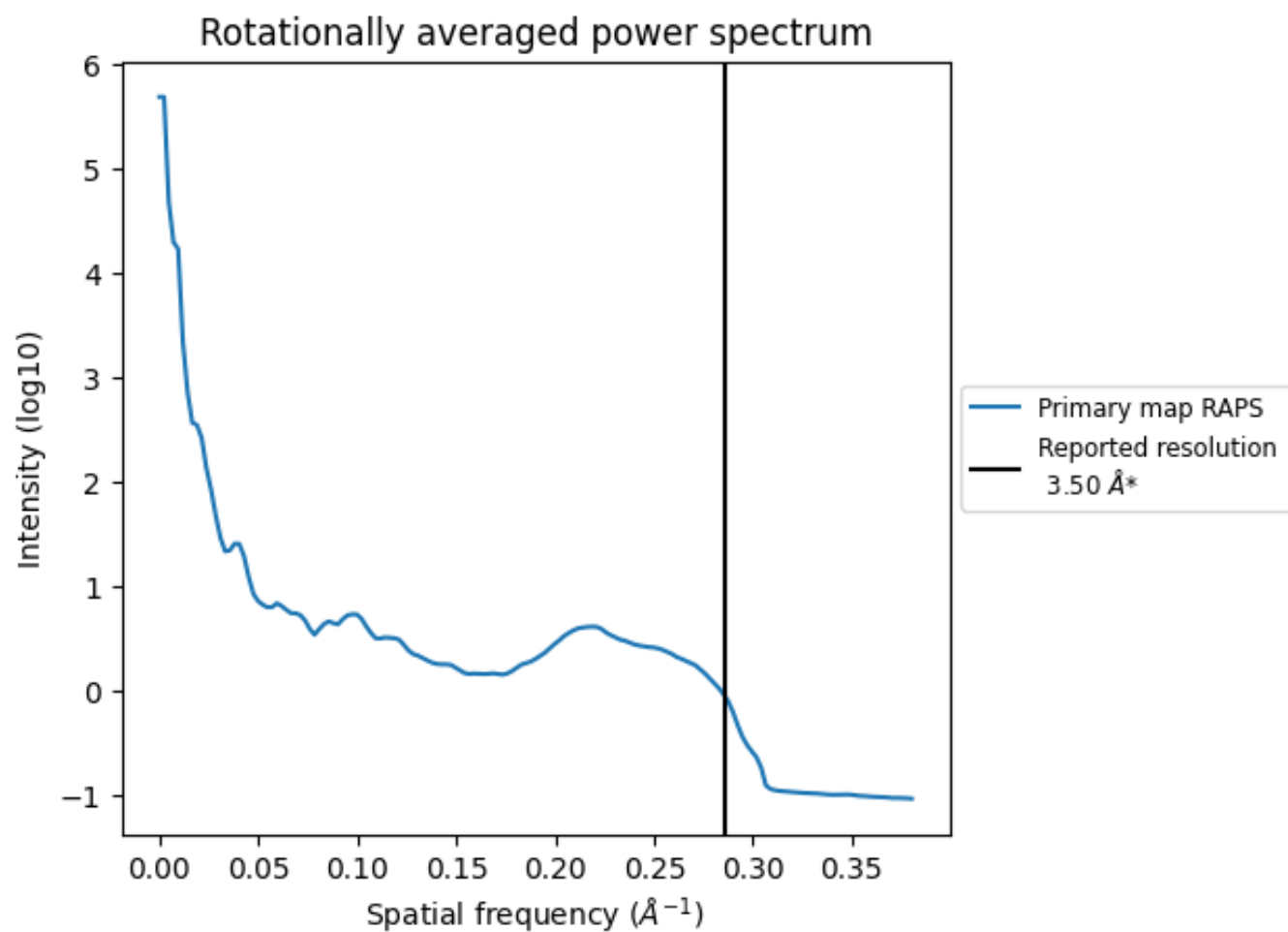
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 318 nm³; this corresponds to an approximate mass of 287 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 0.286 Å⁻¹

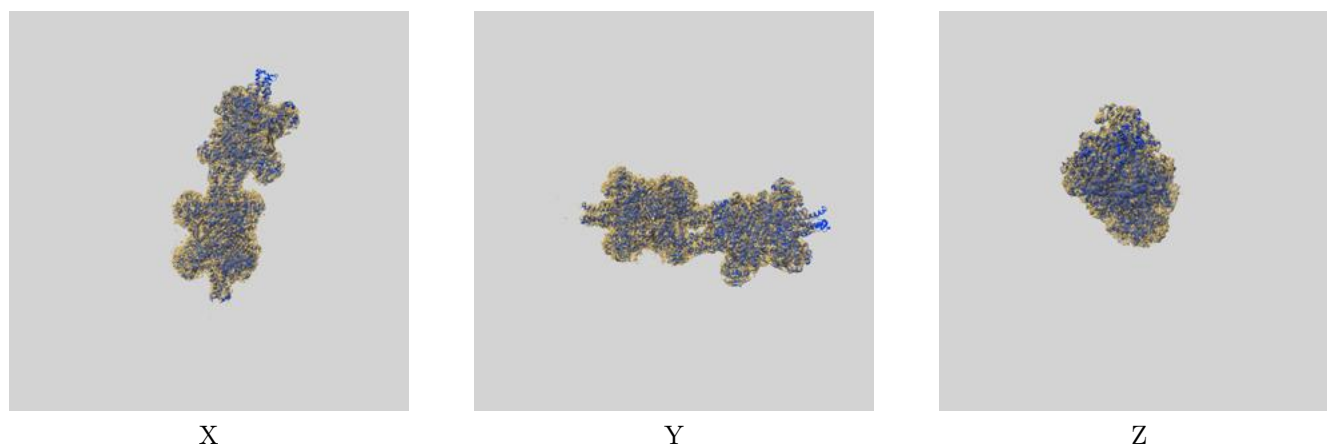
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

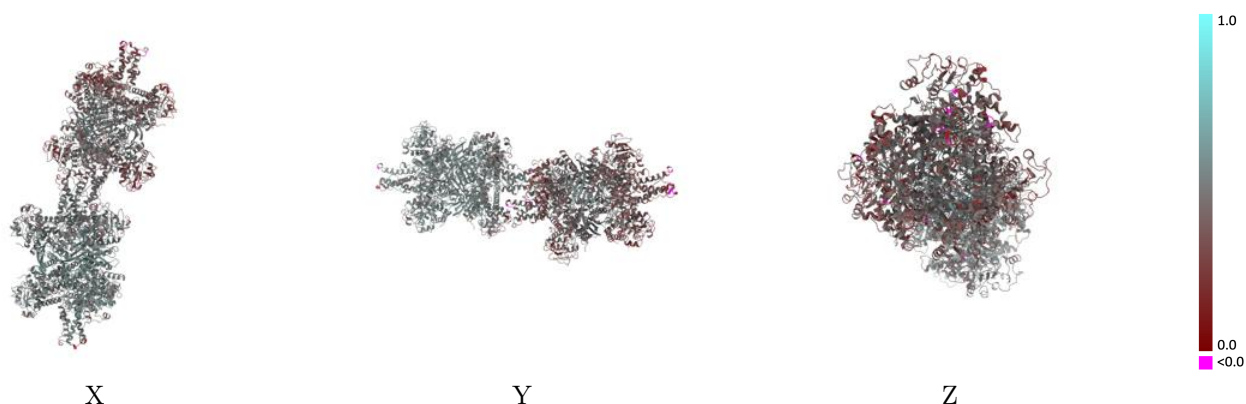
This section contains information regarding the fit between EMDB map EMD-74581 and PDB model 9ZQT. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



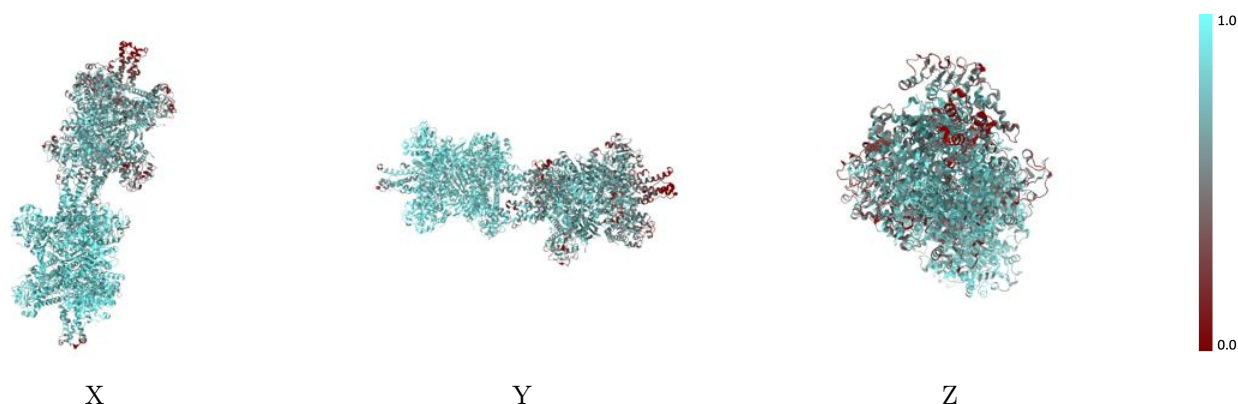
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



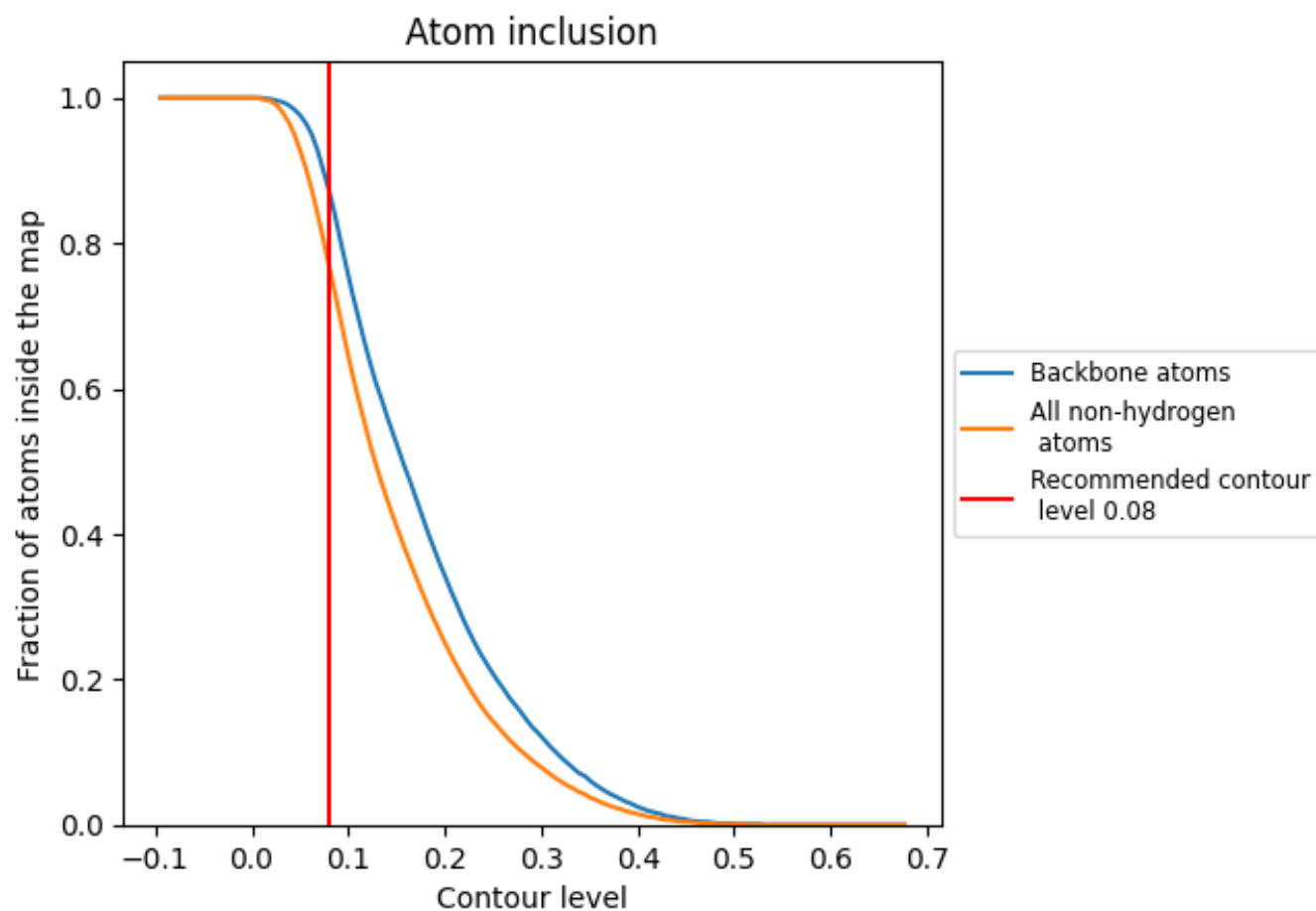
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7700	0.4590
A	0.8730	0.4940
B	0.8810	0.5050
C	0.8970	0.5240
D	0.8940	0.5200
E	0.8870	0.5170
F	0.8660	0.4980
G	0.6660	0.4030
H	0.7470	0.4320
I	0.6150	0.4050
J	0.5900	0.3820
K	0.6290	0.4050
L	0.6970	0.4240

