



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:22 AM UTC

PDB ID : 3Q2K / pdb_00003q2k
Title : Crystal structure of the WlbA dehydrogenase from Bordetella pertussis in complex with NADH and UDP-GlcNAcA
Authors : Holden, H.M.; Thoden, J.B.
Deposited on : 2010-12-20
Resolution : 2.13 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

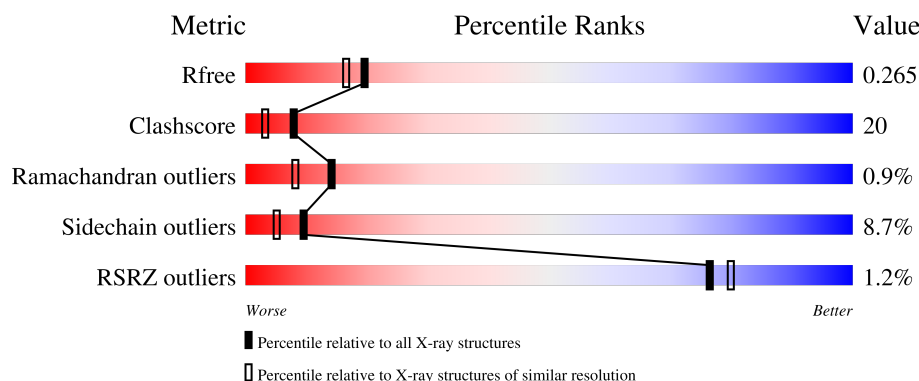
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	370	
1	B	370	
1	C	370	
1	D	370	
1	E	370	

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Mol	Chain	Length	Quality of chain
1	F	370	% 61% 25% • 12%
1	G	370	% 65% 22% 5% 8%
1	H	370	% 60% 27% 5% 8%
1	I	370	% 61% 27% 5% 8%
1	J	370	% 60% 28% • • 6%
1	K	370	2% 54% 28% • • 13%
1	L	370	3% 50% 28% 8% 13%
1	M	370	% 61% 26% 6% 6%
1	N	370	63% 23% 6% 8%
1	O	370	63% 22% 5% • 10%
1	P	370	2% 57% 25% • • 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 43985 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	0	0
			2707	1699	492	504	12			
1	B	329	Total	C	N	O	S	0	2	0
			2587	1625	476	474	12			
1	C	347	Total	C	N	O	S	0	0	0
			2712	1702	493	505	12			
1	D	343	Total	C	N	O	S	0	1	0
			2693	1689	492	500	12			
1	E	321	Total	C	N	O	S	0	0	0
			2501	1572	457	460	12			
1	F	327	Total	C	N	O	S	0	0	0
			2552	1600	468	472	12			
1	G	342	Total	C	N	O	S	0	0	0
			2677	1680	488	497	12			
1	H	342	Total	C	N	O	S	0	1	0
			2681	1684	488	497	12			
1	I	342	Total	C	N	O	S	0	0	0
			2677	1680	488	497	12			
1	J	346	Total	C	N	O	S	0	0	0
			2707	1699	492	504	12			
1	K	322	Total	C	N	O	S	0	0	0
			2511	1577	461	461	12			
1	L	321	Total	C	N	O	S	0	1	0
			2514	1579	463	460	12			
1	M	346	Total	C	N	O	S	0	0	0
			2707	1699	492	504	12			
1	N	342	Total	C	N	O	S	0	0	0
			2677	1680	488	497	12			
1	O	334	Total	C	N	O	S	0	0	0
			2610	1637	479	482	12			
1	P	322	Total	C	N	O	S	0	0	0
			2511	1577	461	461	12			

There are 320 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q79H45
A	-18	GLY	-	expression tag	UNP Q79H45
A	-17	SER	-	expression tag	UNP Q79H45
A	-16	SER	-	expression tag	UNP Q79H45
A	-15	HIS	-	expression tag	UNP Q79H45
A	-14	HIS	-	expression tag	UNP Q79H45
A	-13	HIS	-	expression tag	UNP Q79H45
A	-12	HIS	-	expression tag	UNP Q79H45
A	-11	HIS	-	expression tag	UNP Q79H45
A	-10	HIS	-	expression tag	UNP Q79H45
A	-9	SER	-	expression tag	UNP Q79H45
A	-8	SER	-	expression tag	UNP Q79H45
A	-7	GLU	-	expression tag	UNP Q79H45
A	-6	ASN	-	expression tag	UNP Q79H45
A	-5	LEU	-	expression tag	UNP Q79H45
A	-4	TYR	-	expression tag	UNP Q79H45
A	-3	PHE	-	expression tag	UNP Q79H45
A	-2	GLN	-	expression tag	UNP Q79H45
A	-1	GLY	-	expression tag	UNP Q79H45
A	0	HIS	-	expression tag	UNP Q79H45
B	-19	MET	-	expression tag	UNP Q79H45
B	-18	GLY	-	expression tag	UNP Q79H45
B	-17	SER	-	expression tag	UNP Q79H45
B	-16	SER	-	expression tag	UNP Q79H45
B	-15	HIS	-	expression tag	UNP Q79H45
B	-14	HIS	-	expression tag	UNP Q79H45
B	-13	HIS	-	expression tag	UNP Q79H45
B	-12	HIS	-	expression tag	UNP Q79H45
B	-11	HIS	-	expression tag	UNP Q79H45
B	-10	HIS	-	expression tag	UNP Q79H45
B	-9	SER	-	expression tag	UNP Q79H45
B	-8	SER	-	expression tag	UNP Q79H45
B	-7	GLU	-	expression tag	UNP Q79H45
B	-6	ASN	-	expression tag	UNP Q79H45
B	-5	LEU	-	expression tag	UNP Q79H45
B	-4	TYR	-	expression tag	UNP Q79H45
B	-3	PHE	-	expression tag	UNP Q79H45
B	-2	GLN	-	expression tag	UNP Q79H45
B	-1	GLY	-	expression tag	UNP Q79H45
B	0	HIS	-	expression tag	UNP Q79H45
C	-19	MET	-	expression tag	UNP Q79H45
C	-18	GLY	-	expression tag	UNP Q79H45

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	SER	-	expression tag	UNP Q79H45
C	-16	SER	-	expression tag	UNP Q79H45
C	-15	HIS	-	expression tag	UNP Q79H45
C	-14	HIS	-	expression tag	UNP Q79H45
C	-13	HIS	-	expression tag	UNP Q79H45
C	-12	HIS	-	expression tag	UNP Q79H45
C	-11	HIS	-	expression tag	UNP Q79H45
C	-10	HIS	-	expression tag	UNP Q79H45
C	-9	SER	-	expression tag	UNP Q79H45
C	-8	SER	-	expression tag	UNP Q79H45
C	-7	GLU	-	expression tag	UNP Q79H45
C	-6	ASN	-	expression tag	UNP Q79H45
C	-5	LEU	-	expression tag	UNP Q79H45
C	-4	TYR	-	expression tag	UNP Q79H45
C	-3	PHE	-	expression tag	UNP Q79H45
C	-2	GLN	-	expression tag	UNP Q79H45
C	-1	GLY	-	expression tag	UNP Q79H45
C	0	HIS	-	expression tag	UNP Q79H45
D	-19	MET	-	expression tag	UNP Q79H45
D	-18	GLY	-	expression tag	UNP Q79H45
D	-17	SER	-	expression tag	UNP Q79H45
D	-16	SER	-	expression tag	UNP Q79H45
D	-15	HIS	-	expression tag	UNP Q79H45
D	-14	HIS	-	expression tag	UNP Q79H45
D	-13	HIS	-	expression tag	UNP Q79H45
D	-12	HIS	-	expression tag	UNP Q79H45
D	-11	HIS	-	expression tag	UNP Q79H45
D	-10	HIS	-	expression tag	UNP Q79H45
D	-9	SER	-	expression tag	UNP Q79H45
D	-8	SER	-	expression tag	UNP Q79H45
D	-7	GLU	-	expression tag	UNP Q79H45
D	-6	ASN	-	expression tag	UNP Q79H45
D	-5	LEU	-	expression tag	UNP Q79H45
D	-4	TYR	-	expression tag	UNP Q79H45
D	-3	PHE	-	expression tag	UNP Q79H45
D	-2	GLN	-	expression tag	UNP Q79H45
D	-1	GLY	-	expression tag	UNP Q79H45
D	0	HIS	-	expression tag	UNP Q79H45
E	-19	MET	-	expression tag	UNP Q79H45
E	-18	GLY	-	expression tag	UNP Q79H45
E	-17	SER	-	expression tag	UNP Q79H45
E	-16	SER	-	expression tag	UNP Q79H45

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-15	HIS	-	expression tag	UNP Q79H45
E	-14	HIS	-	expression tag	UNP Q79H45
E	-13	HIS	-	expression tag	UNP Q79H45
E	-12	HIS	-	expression tag	UNP Q79H45
E	-11	HIS	-	expression tag	UNP Q79H45
E	-10	HIS	-	expression tag	UNP Q79H45
E	-9	SER	-	expression tag	UNP Q79H45
E	-8	SER	-	expression tag	UNP Q79H45
E	-7	GLU	-	expression tag	UNP Q79H45
E	-6	ASN	-	expression tag	UNP Q79H45
E	-5	LEU	-	expression tag	UNP Q79H45
E	-4	TYR	-	expression tag	UNP Q79H45
E	-3	PHE	-	expression tag	UNP Q79H45
E	-2	GLN	-	expression tag	UNP Q79H45
E	-1	GLY	-	expression tag	UNP Q79H45
E	0	HIS	-	expression tag	UNP Q79H45
F	-19	MET	-	expression tag	UNP Q79H45
F	-18	GLY	-	expression tag	UNP Q79H45
F	-17	SER	-	expression tag	UNP Q79H45
F	-16	SER	-	expression tag	UNP Q79H45
F	-15	HIS	-	expression tag	UNP Q79H45
F	-14	HIS	-	expression tag	UNP Q79H45
F	-13	HIS	-	expression tag	UNP Q79H45
F	-12	HIS	-	expression tag	UNP Q79H45
F	-11	HIS	-	expression tag	UNP Q79H45
F	-10	HIS	-	expression tag	UNP Q79H45
F	-9	SER	-	expression tag	UNP Q79H45
F	-8	SER	-	expression tag	UNP Q79H45
F	-7	GLU	-	expression tag	UNP Q79H45
F	-6	ASN	-	expression tag	UNP Q79H45
F	-5	LEU	-	expression tag	UNP Q79H45
F	-4	TYR	-	expression tag	UNP Q79H45
F	-3	PHE	-	expression tag	UNP Q79H45
F	-2	GLN	-	expression tag	UNP Q79H45
F	-1	GLY	-	expression tag	UNP Q79H45
F	0	HIS	-	expression tag	UNP Q79H45
G	-19	MET	-	expression tag	UNP Q79H45
G	-18	GLY	-	expression tag	UNP Q79H45
G	-17	SER	-	expression tag	UNP Q79H45
G	-16	SER	-	expression tag	UNP Q79H45
G	-15	HIS	-	expression tag	UNP Q79H45
G	-14	HIS	-	expression tag	UNP Q79H45

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-13	HIS	-	expression tag	UNP Q79H45
G	-12	HIS	-	expression tag	UNP Q79H45
G	-11	HIS	-	expression tag	UNP Q79H45
G	-10	HIS	-	expression tag	UNP Q79H45
G	-9	SER	-	expression tag	UNP Q79H45
G	-8	SER	-	expression tag	UNP Q79H45
G	-7	GLU	-	expression tag	UNP Q79H45
G	-6	ASN	-	expression tag	UNP Q79H45
G	-5	LEU	-	expression tag	UNP Q79H45
G	-4	TYR	-	expression tag	UNP Q79H45
G	-3	PHE	-	expression tag	UNP Q79H45
G	-2	GLN	-	expression tag	UNP Q79H45
G	-1	GLY	-	expression tag	UNP Q79H45
G	0	HIS	-	expression tag	UNP Q79H45
H	-19	MET	-	expression tag	UNP Q79H45
H	-18	GLY	-	expression tag	UNP Q79H45
H	-17	SER	-	expression tag	UNP Q79H45
H	-16	SER	-	expression tag	UNP Q79H45
H	-15	HIS	-	expression tag	UNP Q79H45
H	-14	HIS	-	expression tag	UNP Q79H45
H	-13	HIS	-	expression tag	UNP Q79H45
H	-12	HIS	-	expression tag	UNP Q79H45
H	-11	HIS	-	expression tag	UNP Q79H45
H	-10	HIS	-	expression tag	UNP Q79H45
H	-9	SER	-	expression tag	UNP Q79H45
H	-8	SER	-	expression tag	UNP Q79H45
H	-7	GLU	-	expression tag	UNP Q79H45
H	-6	ASN	-	expression tag	UNP Q79H45
H	-5	LEU	-	expression tag	UNP Q79H45
H	-4	TYR	-	expression tag	UNP Q79H45
H	-3	PHE	-	expression tag	UNP Q79H45
H	-2	GLN	-	expression tag	UNP Q79H45
H	-1	GLY	-	expression tag	UNP Q79H45
H	0	HIS	-	expression tag	UNP Q79H45
I	-19	MET	-	expression tag	UNP Q79H45
I	-18	GLY	-	expression tag	UNP Q79H45
I	-17	SER	-	expression tag	UNP Q79H45
I	-16	SER	-	expression tag	UNP Q79H45
I	-15	HIS	-	expression tag	UNP Q79H45
I	-14	HIS	-	expression tag	UNP Q79H45
I	-13	HIS	-	expression tag	UNP Q79H45
I	-12	HIS	-	expression tag	UNP Q79H45

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-11	HIS	-	expression tag	UNP Q79H45
I	-10	HIS	-	expression tag	UNP Q79H45
I	-9	SER	-	expression tag	UNP Q79H45
I	-8	SER	-	expression tag	UNP Q79H45
I	-7	GLU	-	expression tag	UNP Q79H45
I	-6	ASN	-	expression tag	UNP Q79H45
I	-5	LEU	-	expression tag	UNP Q79H45
I	-4	TYR	-	expression tag	UNP Q79H45
I	-3	PHE	-	expression tag	UNP Q79H45
I	-2	GLN	-	expression tag	UNP Q79H45
I	-1	GLY	-	expression tag	UNP Q79H45
I	0	HIS	-	expression tag	UNP Q79H45
J	-19	MET	-	expression tag	UNP Q79H45
J	-18	GLY	-	expression tag	UNP Q79H45
J	-17	SER	-	expression tag	UNP Q79H45
J	-16	SER	-	expression tag	UNP Q79H45
J	-15	HIS	-	expression tag	UNP Q79H45
J	-14	HIS	-	expression tag	UNP Q79H45
J	-13	HIS	-	expression tag	UNP Q79H45
J	-12	HIS	-	expression tag	UNP Q79H45
J	-11	HIS	-	expression tag	UNP Q79H45
J	-10	HIS	-	expression tag	UNP Q79H45
J	-9	SER	-	expression tag	UNP Q79H45
J	-8	SER	-	expression tag	UNP Q79H45
J	-7	GLU	-	expression tag	UNP Q79H45
J	-6	ASN	-	expression tag	UNP Q79H45
J	-5	LEU	-	expression tag	UNP Q79H45
J	-4	TYR	-	expression tag	UNP Q79H45
J	-3	PHE	-	expression tag	UNP Q79H45
J	-2	GLN	-	expression tag	UNP Q79H45
J	-1	GLY	-	expression tag	UNP Q79H45
J	0	HIS	-	expression tag	UNP Q79H45
K	-19	MET	-	expression tag	UNP Q79H45
K	-18	GLY	-	expression tag	UNP Q79H45
K	-17	SER	-	expression tag	UNP Q79H45
K	-16	SER	-	expression tag	UNP Q79H45
K	-15	HIS	-	expression tag	UNP Q79H45
K	-14	HIS	-	expression tag	UNP Q79H45
K	-13	HIS	-	expression tag	UNP Q79H45
K	-12	HIS	-	expression tag	UNP Q79H45
K	-11	HIS	-	expression tag	UNP Q79H45
K	-10	HIS	-	expression tag	UNP Q79H45

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-9	SER	-	expression tag	UNP Q79H45
K	-8	SER	-	expression tag	UNP Q79H45
K	-7	GLU	-	expression tag	UNP Q79H45
K	-6	ASN	-	expression tag	UNP Q79H45
K	-5	LEU	-	expression tag	UNP Q79H45
K	-4	TYR	-	expression tag	UNP Q79H45
K	-3	PHE	-	expression tag	UNP Q79H45
K	-2	GLN	-	expression tag	UNP Q79H45
K	-1	GLY	-	expression tag	UNP Q79H45
K	0	HIS	-	expression tag	UNP Q79H45
L	-19	MET	-	expression tag	UNP Q79H45
L	-18	GLY	-	expression tag	UNP Q79H45
L	-17	SER	-	expression tag	UNP Q79H45
L	-16	SER	-	expression tag	UNP Q79H45
L	-15	HIS	-	expression tag	UNP Q79H45
L	-14	HIS	-	expression tag	UNP Q79H45
L	-13	HIS	-	expression tag	UNP Q79H45
L	-12	HIS	-	expression tag	UNP Q79H45
L	-11	HIS	-	expression tag	UNP Q79H45
L	-10	HIS	-	expression tag	UNP Q79H45
L	-9	SER	-	expression tag	UNP Q79H45
L	-8	SER	-	expression tag	UNP Q79H45
L	-7	GLU	-	expression tag	UNP Q79H45
L	-6	ASN	-	expression tag	UNP Q79H45
L	-5	LEU	-	expression tag	UNP Q79H45
L	-4	TYR	-	expression tag	UNP Q79H45
L	-3	PHE	-	expression tag	UNP Q79H45
L	-2	GLN	-	expression tag	UNP Q79H45
L	-1	GLY	-	expression tag	UNP Q79H45
L	0	HIS	-	expression tag	UNP Q79H45
M	-19	MET	-	expression tag	UNP Q79H45
M	-18	GLY	-	expression tag	UNP Q79H45
M	-17	SER	-	expression tag	UNP Q79H45
M	-16	SER	-	expression tag	UNP Q79H45
M	-15	HIS	-	expression tag	UNP Q79H45
M	-14	HIS	-	expression tag	UNP Q79H45
M	-13	HIS	-	expression tag	UNP Q79H45
M	-12	HIS	-	expression tag	UNP Q79H45
M	-11	HIS	-	expression tag	UNP Q79H45
M	-10	HIS	-	expression tag	UNP Q79H45
M	-9	SER	-	expression tag	UNP Q79H45
M	-8	SER	-	expression tag	UNP Q79H45

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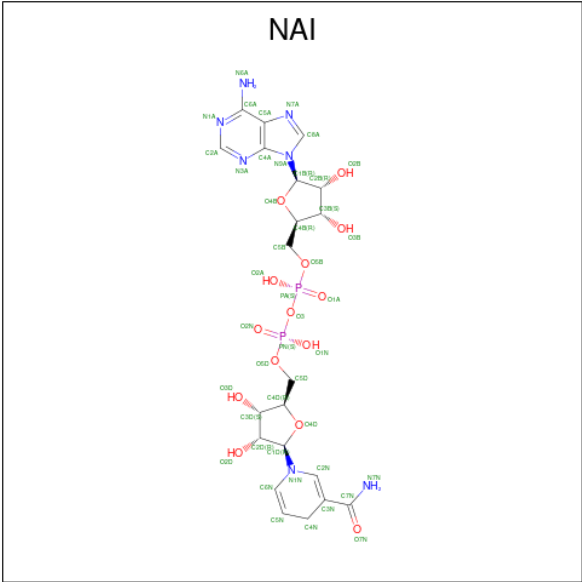
Chain	Residue	Modelled	Actual	Comment	Reference
M	-7	GLU	-	expression tag	UNP Q79H45
M	-6	ASN	-	expression tag	UNP Q79H45
M	-5	LEU	-	expression tag	UNP Q79H45
M	-4	TYR	-	expression tag	UNP Q79H45
M	-3	PHE	-	expression tag	UNP Q79H45
M	-2	GLN	-	expression tag	UNP Q79H45
M	-1	GLY	-	expression tag	UNP Q79H45
M	0	HIS	-	expression tag	UNP Q79H45
N	-19	MET	-	expression tag	UNP Q79H45
N	-18	GLY	-	expression tag	UNP Q79H45
N	-17	SER	-	expression tag	UNP Q79H45
N	-16	SER	-	expression tag	UNP Q79H45
N	-15	HIS	-	expression tag	UNP Q79H45
N	-14	HIS	-	expression tag	UNP Q79H45
N	-13	HIS	-	expression tag	UNP Q79H45
N	-12	HIS	-	expression tag	UNP Q79H45
N	-11	HIS	-	expression tag	UNP Q79H45
N	-10	HIS	-	expression tag	UNP Q79H45
N	-9	SER	-	expression tag	UNP Q79H45
N	-8	SER	-	expression tag	UNP Q79H45
N	-7	GLU	-	expression tag	UNP Q79H45
N	-6	ASN	-	expression tag	UNP Q79H45
N	-5	LEU	-	expression tag	UNP Q79H45
N	-4	TYR	-	expression tag	UNP Q79H45
N	-3	PHE	-	expression tag	UNP Q79H45
N	-2	GLN	-	expression tag	UNP Q79H45
N	-1	GLY	-	expression tag	UNP Q79H45
N	0	HIS	-	expression tag	UNP Q79H45
O	-19	MET	-	expression tag	UNP Q79H45
O	-18	GLY	-	expression tag	UNP Q79H45
O	-17	SER	-	expression tag	UNP Q79H45
O	-16	SER	-	expression tag	UNP Q79H45
O	-15	HIS	-	expression tag	UNP Q79H45
O	-14	HIS	-	expression tag	UNP Q79H45
O	-13	HIS	-	expression tag	UNP Q79H45
O	-12	HIS	-	expression tag	UNP Q79H45
O	-11	HIS	-	expression tag	UNP Q79H45
O	-10	HIS	-	expression tag	UNP Q79H45
O	-9	SER	-	expression tag	UNP Q79H45
O	-8	SER	-	expression tag	UNP Q79H45
O	-7	GLU	-	expression tag	UNP Q79H45
O	-6	ASN	-	expression tag	UNP Q79H45

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-5	LEU	-	expression tag	UNP Q79H45
O	-4	TYR	-	expression tag	UNP Q79H45
O	-3	PHE	-	expression tag	UNP Q79H45
O	-2	GLN	-	expression tag	UNP Q79H45
O	-1	GLY	-	expression tag	UNP Q79H45
O	0	HIS	-	expression tag	UNP Q79H45
P	-19	MET	-	expression tag	UNP Q79H45
P	-18	GLY	-	expression tag	UNP Q79H45
P	-17	SER	-	expression tag	UNP Q79H45
P	-16	SER	-	expression tag	UNP Q79H45
P	-15	HIS	-	expression tag	UNP Q79H45
P	-14	HIS	-	expression tag	UNP Q79H45
P	-13	HIS	-	expression tag	UNP Q79H45
P	-12	HIS	-	expression tag	UNP Q79H45
P	-11	HIS	-	expression tag	UNP Q79H45
P	-10	HIS	-	expression tag	UNP Q79H45
P	-9	SER	-	expression tag	UNP Q79H45
P	-8	SER	-	expression tag	UNP Q79H45
P	-7	GLU	-	expression tag	UNP Q79H45
P	-6	ASN	-	expression tag	UNP Q79H45
P	-5	LEU	-	expression tag	UNP Q79H45
P	-4	TYR	-	expression tag	UNP Q79H45
P	-3	PHE	-	expression tag	UNP Q79H45
P	-2	GLN	-	expression tag	UNP Q79H45
P	-1	GLY	-	expression tag	UNP Q79H45
P	0	HIS	-	expression tag	UNP Q79H45

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂).



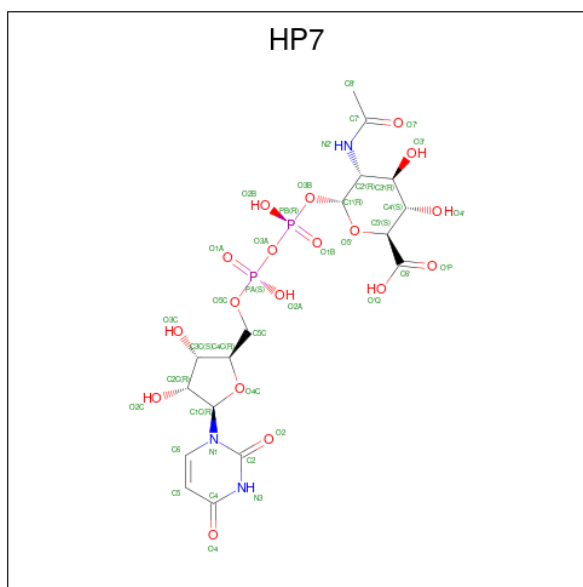
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	I	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	J	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	K	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	L	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	M	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	N	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	O	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	P	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is (2S,3S,4R,5R,6R)-5-acetamido-6-[[[(2R,3S,4R,5R)-5-(2,4-dioxypyrimidin-1-yl)-3,4-dihydroxy-oxolan-2-yl]methoxy-hydroxy-phosphoryl]oxy-hydroxy-phosphoryl]oxy-3,4-dihydroxy-oxane-2-carboxylic acid (CCD ID: HP7) (formula: C₁₇H₂₅N₃O₁₈P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	B	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	C	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	D	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	E	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	F	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	G	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	H	1	Total	C	N	O	P	0	0
			40	17	3	18	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	I	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	J	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	K	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	L	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	M	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	N	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	O	1	Total	C	N	O	P	0	0
			40	17	3	18	2		
3	P	1	Total	C	N	O	P	0	0
			40	17	3	18	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	85	Total	O	0	0
			85	85		
4	B	54	Total	O	0	0
			54	54		
4	C	58	Total	O	0	0
			58	58		
4	D	51	Total	O	0	0
			51	51		
4	E	21	Total	O	0	0
			21	21		
4	F	24	Total	O	0	0
			24	24		
4	G	49	Total	O	0	0
			49	49		
4	H	35	Total	O	0	0
			35	35		
4	I	36	Total	O	0	0
			36	36		
4	J	30	Total	O	0	0
			30	30		
4	K	26	Total	O	0	0
			26	26		

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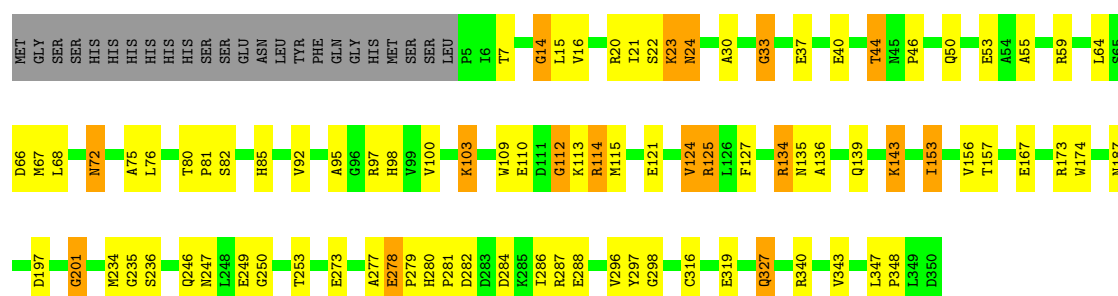
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	37	Total 37	O 37	0	0
4	M	36	Total 36	O 36	0	0
4	N	34	Total 34	O 34	0	0
4	O	17	Total 17	O 17	0	0
4	P	24	Total 24	O 24	0	0

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

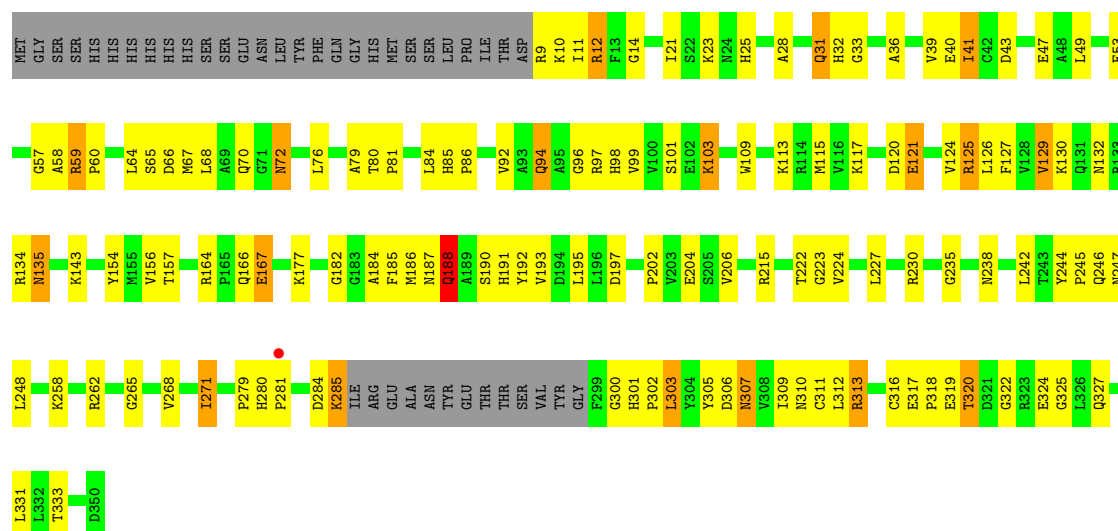
• Molecule 1: oxidoreductase

Chain A: 



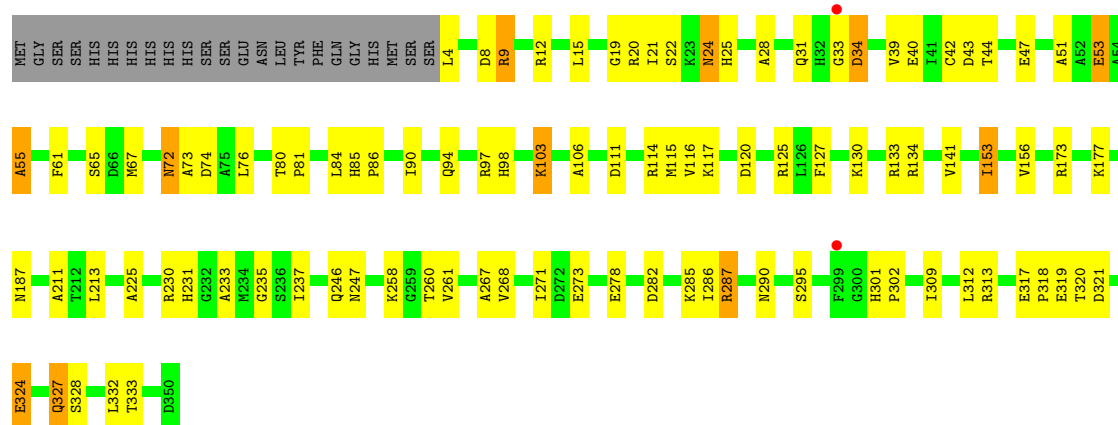
• Molecule 1: oxidoreductase

Chain B: 

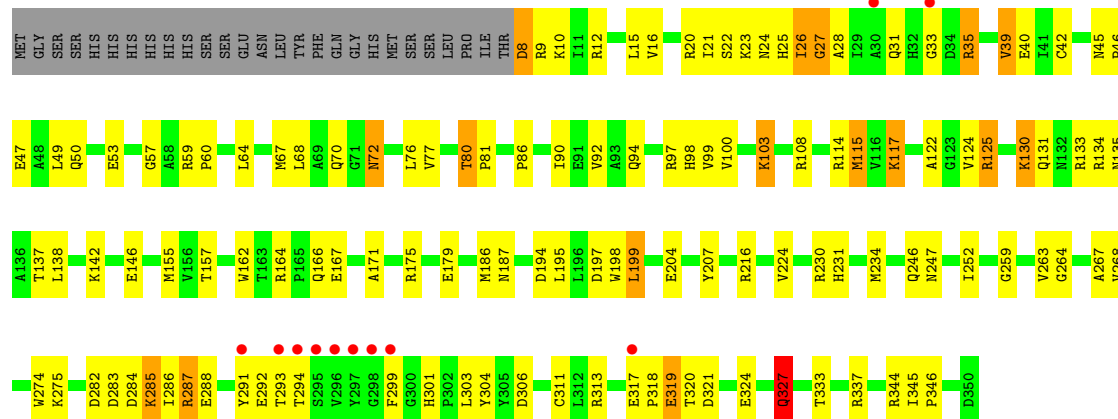


• Molecule 1: oxidoreductase

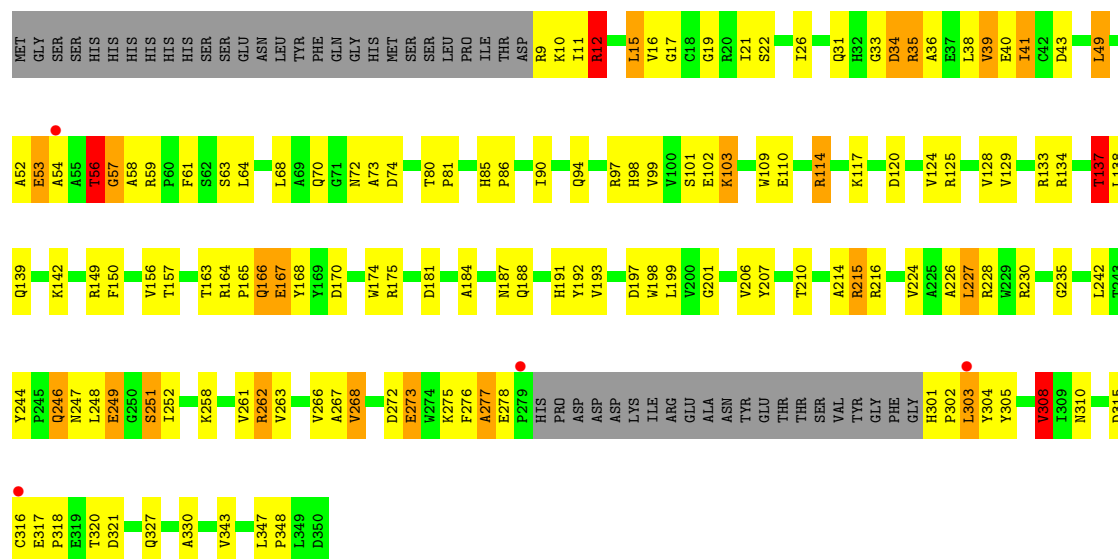
Chain C: 



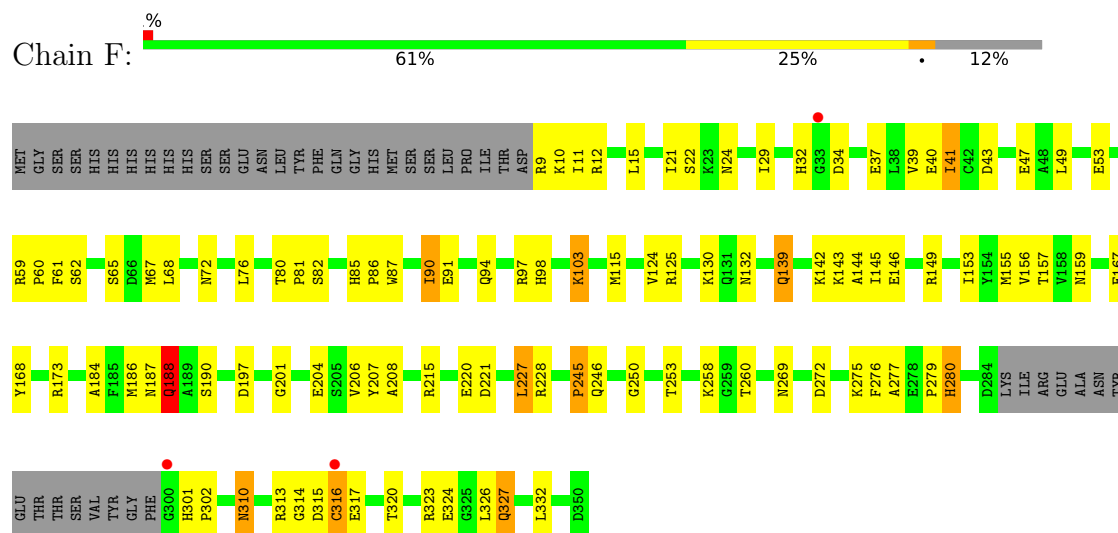
- Molecule 1: oxidoreductase



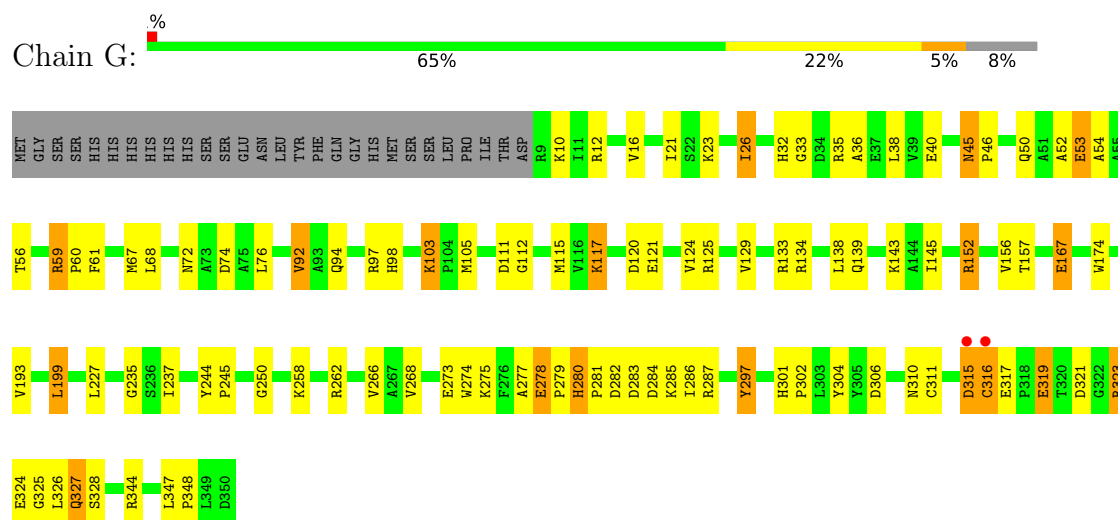
- Molecule 1: oxidoreductase



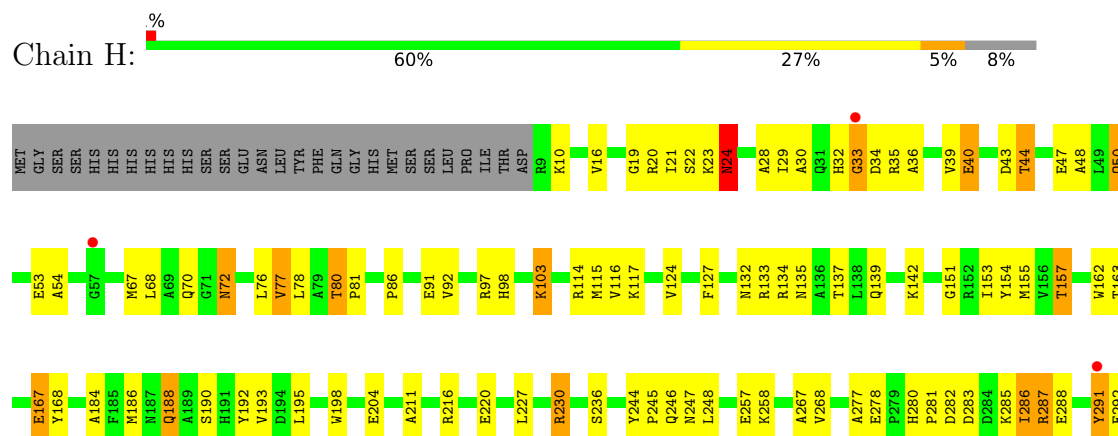
- Molecule 1: oxidoreductase

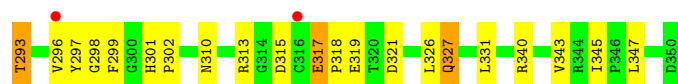


- Molecule 1: oxidoreductase

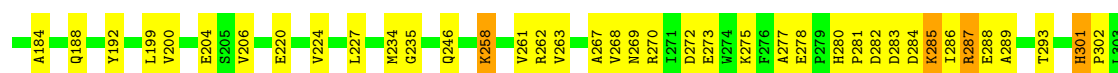
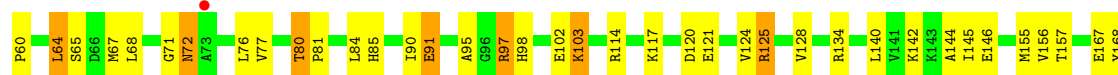


- Molecule 1: oxidoreductase

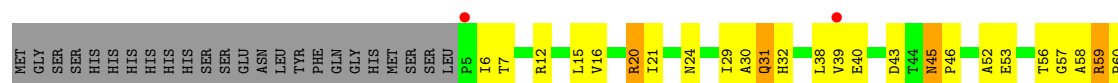




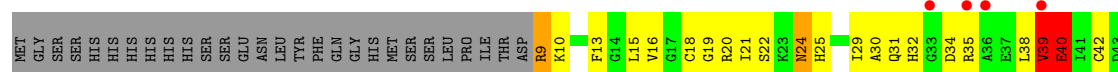
• Molecule 1: oxidoreductase

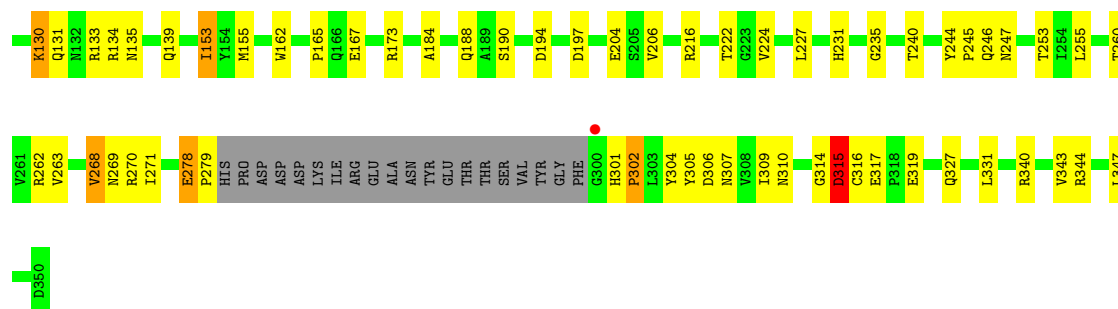


• Molecule 1: oxidoreductase

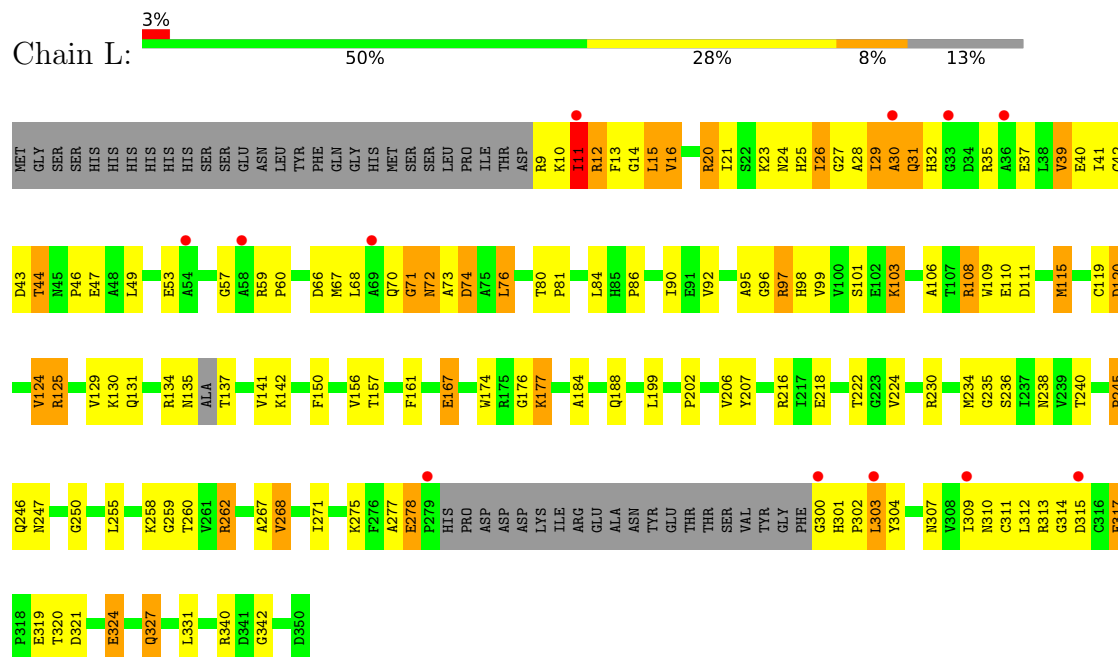


• Molecule 1: oxidoreductase

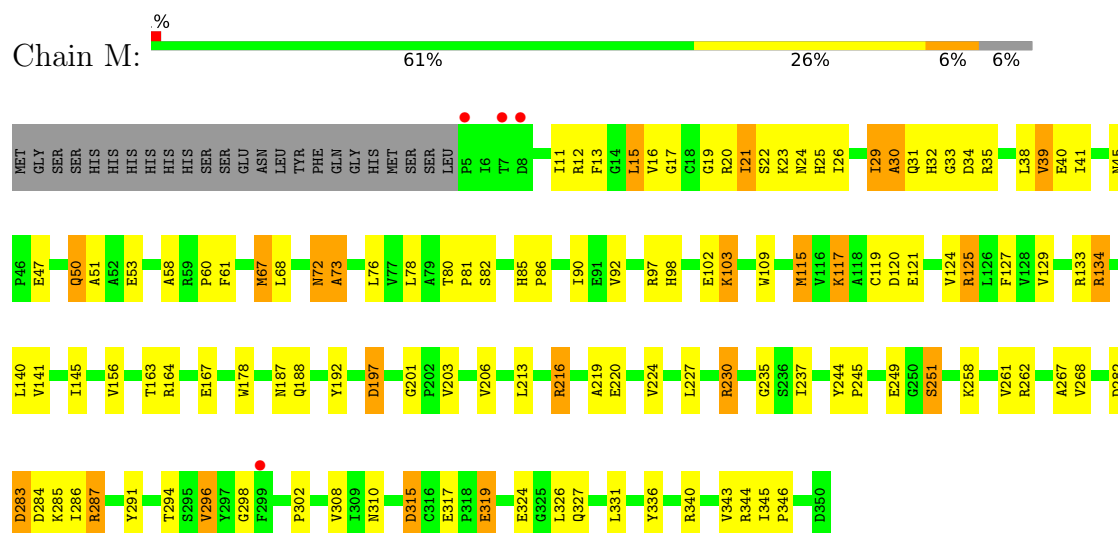




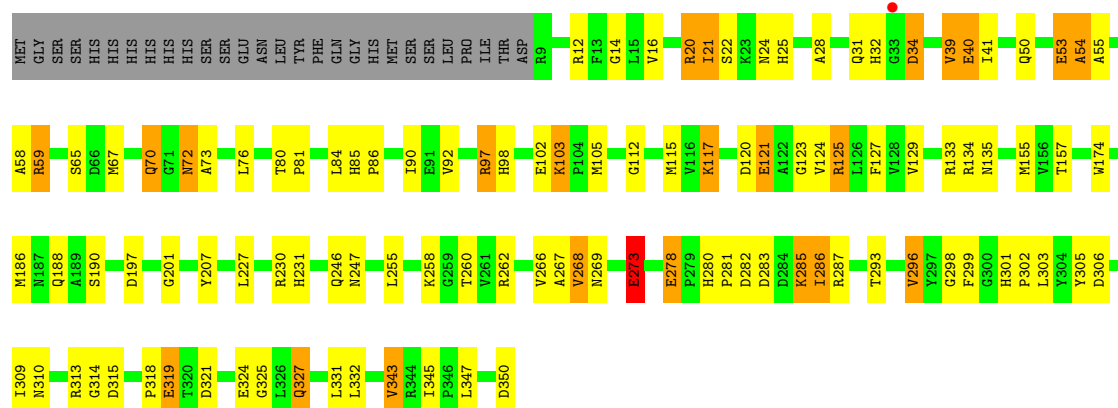
- Molecule 1: oxidoreductase



- Molecule 1: oxidoreductase

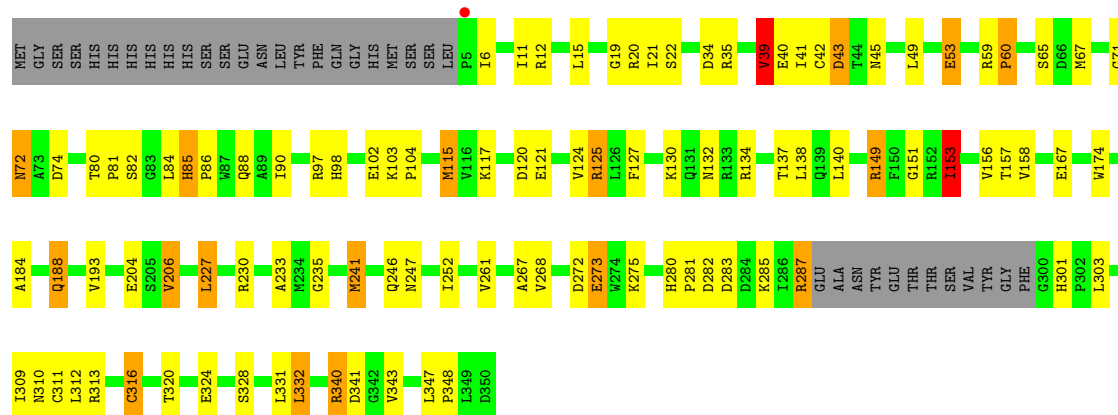


- Molecule 1: oxidoreductase



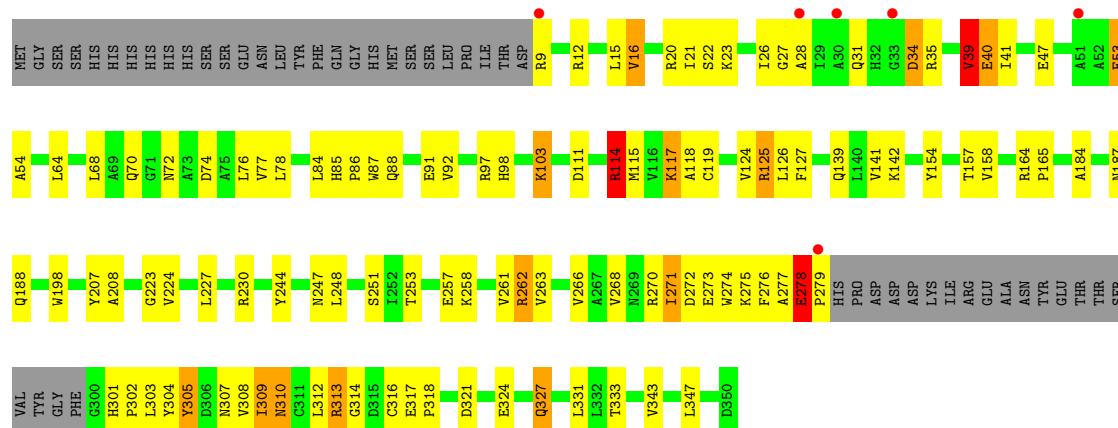
• Molecule 1: oxidoreductase

Chain O: 63% 22% 5% • 10%



• Molecule 1: oxidoreductase

Chain P: 2% 57% 25% • • 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.26Å 319.98Å 103.80Å 90.00° 119.07° 90.00°	Depositor
Resolution (Å)	30.00 – 2.13 30.00 – 2.13	Depositor EDS
% Data completeness (in resolution range)	92.6 (30.00-2.13) 92.6 (30.00-2.13)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.54 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.183 , 0.269 0.184 , 0.265	Depositor DCC
R_{free} test set	15038 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.007 for -h-l,k,h 0.007 for l,k,-h-l 0.026 for h,-k,-h-l 0.024 for -h-l,-k,l 0.024 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	43985	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAI, HP7

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.40	0/2767	1.44	18/3755 (0.5%)
1	B	0.37	0/2650	1.34	13/3593 (0.4%)
1	C	0.37	0/2772	1.40	19/3763 (0.5%)
1	D	0.36	0/2755	1.35	17/3737 (0.5%)
1	E	0.35	0/2554	1.37	20/3464 (0.6%)
1	F	0.37	0/2607	1.40	14/3536 (0.4%)
1	G	0.38	0/2736	1.43	20/3712 (0.5%)
1	H	0.36	0/2743	1.37	14/3722 (0.4%)
1	I	0.35	0/2736	1.37	17/3712 (0.5%)
1	J	0.35	0/2767	1.39	21/3755 (0.6%)
1	K	0.35	0/2564	1.38	16/3476 (0.5%)
1	L	0.34	0/2569	1.29	16/3480 (0.5%)
1	M	0.40	0/2767	1.42	26/3755 (0.7%)
1	N	0.39	0/2736	1.39	15/3712 (0.4%)
1	O	0.36	0/2666	1.44	22/3615 (0.6%)
1	P	0.35	0/2564	1.38	14/3476 (0.4%)
All	All	0.37	0/42953	1.39	282/58263 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	K	0	1

There are no bond length outliers.

All (282) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	230	ARG	NE-CZ-NH2	-10.07	110.14	119.20
1	J	59	ARG	CA-C-N	9.54	129.49	119.85
1	J	59	ARG	C-N-CA	9.54	129.49	119.85
1	J	278	GLU	CA-C-N	9.19	130.40	120.11
1	J	278	GLU	C-N-CA	9.19	130.40	120.11
1	O	230	ARG	NE-CZ-NH1	8.70	130.20	121.50
1	K	32	HIS	N-CA-C	-8.68	98.44	111.81
1	I	59	ARG	N-CA-C	-8.66	98.64	109.64
1	P	164	ARG	CA-C-N	-8.55	111.83	120.98
1	P	164	ARG	C-N-CA	-8.55	111.83	120.98
1	M	230	ARG	CG-CD-NE	-8.54	93.22	112.00
1	B	188	GLN	N-CA-C	8.29	119.94	111.07
1	F	310	ASN	N-CA-C	-8.07	102.49	111.28
1	N	24	ASN	N-CA-C	-8.06	102.07	112.23
1	N	129	VAL	N-CA-C	8.06	118.92	108.12
1	G	52	ALA	N-CA-C	-8.05	102.91	112.89
1	J	188	GLN	N-CA-C	8.02	119.65	111.07
1	M	145	ILE	N-CA-C	-7.90	103.16	110.82
1	P	39	VAL	N-CA-C	7.83	119.53	111.00
1	B	129	VAL	CB-CA-C	-7.77	102.88	111.35
1	O	115	MET	CB-CA-C	-7.77	98.68	110.88
1	C	20	ARG	N-CA-C	7.61	119.57	111.28
1	P	47	GLU	N-CA-C	7.60	119.20	111.07
1	M	129	VAL	CB-CA-C	-7.52	103.15	111.35
1	F	317	GLU	CA-C-N	-7.52	111.71	119.83
1	F	317	GLU	C-N-CA	-7.52	111.71	119.83
1	M	345	ILE	CA-C-N	-7.48	112.77	120.85
1	M	345	ILE	C-N-CA	-7.48	112.77	120.85
1	F	332	LEU	N-CA-C	-7.41	103.23	111.82
1	G	193	VAL	N-CA-C	-7.37	103.10	110.62
1	K	56	THR	N-CA-C	-7.34	105.50	114.75
1	B	164	ARG	CA-C-N	-7.23	113.36	120.52
1	B	164	ARG	C-N-CA	-7.23	113.36	120.52
1	G	199	LEU	N-CA-C	7.22	118.93	111.14
1	O	340	ARG	N-CA-C	7.19	118.76	111.07
1	N	188	GLN	N-CA-C	7.16	119.08	111.28
1	G	26	ILE	N-CA-C	-7.15	103.36	110.30
1	H	44	THR	N-CA-C	-7.11	104.21	113.17
1	E	230	ARG	CG-CD-NE	-7.11	96.36	112.00
1	A	153	ILE	CB-CA-C	-7.11	102.09	110.91
1	M	26	ILE	N-CA-C	-7.08	103.87	110.53
1	F	280	HIS	CA-C-N	-7.07	112.52	119.87
1	F	280	HIS	C-N-CA	-7.07	112.52	119.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	120	ASP	N-CA-C	-7.07	102.63	111.11
1	J	328	SER	N-CA-C	-7.05	103.35	112.23
1	H	151	GLY	N-CA-C	-7.04	98.93	112.02
1	N	327	GLN	N-CA-C	-6.93	103.66	111.14
1	O	85	HIS	CA-C-N	-6.89	111.34	118.85
1	O	85	HIS	C-N-CA	-6.89	111.34	118.85
1	H	48	ALA	N-CA-C	-6.84	103.61	112.23
1	D	252	ILE	CB-CA-C	6.83	119.42	110.12
1	K	153	ILE	CB-CA-C	-6.80	102.48	110.91
1	I	95	ALA	N-CA-C	-6.78	103.38	112.94
1	M	115	MET	CB-CA-C	-6.75	100.18	110.92
1	I	44	THR	N-CA-C	-6.73	105.06	113.20
1	L	115	MET	CB-CA-C	-6.71	100.35	110.88
1	G	344	ARG	CA-C-N	-6.63	117.56	123.33
1	G	344	ARG	C-N-CA	-6.63	117.56	123.33
1	J	160	VAL	N-CA-C	-6.62	95.56	109.34
1	J	32	HIS	N-CA-C	-6.59	105.13	112.57
1	J	258	LYS	CB-CA-C	-6.58	100.36	111.02
1	L	327	GLN	N-CA-C	-6.47	104.14	111.07
1	L	150	PHE	N-CA-C	-6.43	105.25	113.23
1	E	56	THR	N-CA-C	-6.42	106.02	114.31
1	C	8	ASP	N-CA-C	6.41	121.68	111.81
1	N	296	VAL	CB-CA-C	-6.41	104.82	112.19
1	G	111	ASP	N-CA-C	-6.40	104.38	111.36
1	D	263	VAL	CB-CA-C	-6.38	102.39	111.31
1	I	59	ARG	CA-C-N	6.37	127.81	119.84
1	I	59	ARG	C-N-CA	6.37	127.81	119.84
1	C	286	ILE	N-CA-C	6.37	116.52	110.53
1	P	70	GLN	N-CA-C	6.37	118.30	111.36
1	F	29	ILE	N-CA-C	-6.36	104.30	110.72
1	E	207	TYR	N-CA-C	-6.36	97.44	108.69
1	P	313	ARG	N-CA-C	-6.35	105.59	113.15
1	K	40	GLU	N-CA-C	6.34	118.78	108.76
1	M	29	ILE	N-CA-C	6.34	117.02	110.36
1	M	287	ARG	N-CA-C	-6.34	104.45	111.36
1	K	340	ARG	NE-CZ-NH1	-6.33	115.17	121.50
1	I	188	GLN	N-CA-C	6.32	118.25	111.36
1	G	45	ASN	CA-C-N	6.32	127.74	119.84
1	G	45	ASN	C-N-CA	6.32	127.74	119.84
1	P	310	ASN	N-CA-C	-6.27	103.74	111.33
1	G	120	ASP	CB-CA-C	-6.24	101.01	110.92
1	D	164	ARG	CA-C-N	-6.21	114.14	120.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	164	ARG	C-N-CA	-6.21	114.14	120.85
1	P	223	GLY	N-CA-C	6.21	119.57	110.38
1	N	273	GLU	N-CA-C	-6.21	97.30	108.48
1	L	238	ASN	CA-C-N	-6.17	114.41	122.99
1	L	238	ASN	C-N-CA	-6.17	114.41	122.99
1	G	306	ASP	N-CA-C	-6.14	104.50	111.07
1	M	283	ASP	N-CA-C	-6.14	104.89	112.38
1	J	324	GLU	N-CA-C	-6.13	103.93	112.45
1	F	272	ASP	N-CA-C	-6.12	106.13	113.97
1	A	95	ALA	N-CA-C	-6.12	104.98	112.88
1	C	286	ILE	CB-CA-C	-6.11	104.01	112.02
1	P	139	GLN	N-CA-C	-6.11	104.70	111.36
1	A	296	VAL	N-CA-C	6.10	118.03	112.29
1	L	342	GLY	O-C-N	-6.09	116.44	122.41
1	A	44	THR	N-CA-C	-6.08	105.69	113.23
1	O	272	ASP	CA-C-N	-6.07	112.12	122.33
1	O	272	ASP	C-N-CA	-6.07	112.12	122.33
1	D	195	LEU	N-CA-C	6.07	118.69	111.71
1	D	100	VAL	CB-CA-C	-6.01	102.83	111.19
1	I	301	HIS	CA-C-N	-6.01	112.72	118.97
1	I	301	HIS	C-N-CA	-6.01	112.72	118.97
1	I	349	LEU	N-CA-C	6.01	118.97	110.50
1	J	107	THR	N-CA-C	-6.00	106.00	113.38
1	O	273	GLU	CB-CA-C	6.00	120.15	109.65
1	N	345	ILE	CB-CA-C	-5.99	103.97	110.37
1	M	45	ASN	CA-C-N	5.98	125.68	119.05
1	M	45	ASN	C-N-CA	5.98	125.68	119.05
1	O	301	HIS	CA-C-N	-5.97	112.76	118.97
1	O	301	HIS	C-N-CA	-5.97	112.76	118.97
1	E	251	SER	N-CA-C	5.97	117.65	109.18
1	A	327	GLN	CB-CA-C	-5.96	101.52	110.88
1	A	14	GLY	N-CA-C	-5.96	100.76	111.19
1	M	251	SER	N-CA-C	5.96	118.47	109.23
1	M	47	GLU	N-CA-C	5.96	117.44	111.07
1	C	55	ALA	N-CA-C	-5.94	105.11	112.90
1	I	316	CYS	N-CA-C	5.92	117.25	108.60
1	K	173	ARG	N-CA-C	5.91	118.50	111.71
1	A	286	ILE	CB-CA-C	-5.90	104.41	111.97
1	E	210	THR	N-CA-C	-5.90	100.35	109.14
1	A	278	GLU	CA-C-N	5.89	125.86	120.03
1	A	278	GLU	C-N-CA	5.89	125.86	120.03
1	N	54	ALA	N-CA-C	-5.89	105.25	113.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	325	GLY	N-CA-C	-5.88	105.49	113.37
1	I	47	GLU	N-CA-C	5.87	117.35	111.07
1	J	121	GLU	N-CA-C	-5.87	104.23	111.40
1	O	149	ARG	N-CA-C	5.87	119.70	112.54
1	H	292	GLU	N-CA-C	5.87	117.67	111.28
1	F	221	ASP	N-CA-C	-5.86	106.10	113.72
1	C	111	ASP	N-CA-C	-5.84	104.99	111.36
1	D	304	TYR	N-CA-C	-5.83	104.88	112.23
1	O	324	GLU	N-CA-C	-5.83	104.52	111.69
1	K	270	ARG	N-CA-C	5.82	117.88	108.34
1	I	184	ALA	N-CA-C	5.81	118.39	111.71
1	B	271	ILE	CB-CA-C	-5.80	104.96	111.23
1	C	116	VAL	N-CA-C	5.80	116.45	110.36
1	I	144	ALA	CA-C-N	-5.79	112.52	120.46
1	I	144	ALA	C-N-CA	-5.79	112.52	120.46
1	H	248	LEU	N-CA-C	-5.79	106.26	113.55
1	H	286	ILE	N-CA-C	5.77	115.96	110.53
1	M	67	MET	N-CA-C	-5.77	105.13	111.82
1	C	287	ARG	N-CA-C	-5.76	105.00	111.28
1	E	174	TRP	N-CA-C	5.76	118.33	111.71
1	L	109	TRP	N-CA-C	5.75	117.23	111.07
1	K	231	HIS	N-CA-C	-5.74	106.25	113.20
1	A	250	GLY	N-CA-C	-5.73	99.60	113.18
1	G	280	HIS	CA-C-N	5.73	127.00	119.84
1	G	280	HIS	C-N-CA	5.73	127.00	119.84
1	L	12	ARG	N-CA-C	5.73	117.75	108.41
1	O	332	LEU	N-CA-C	-5.72	105.13	111.36
1	E	164	ARG	CA-C-N	5.70	125.68	120.03
1	E	164	ARG	C-N-CA	5.70	125.68	120.03
1	E	224	VAL	CB-CA-C	-5.70	100.93	111.18
1	L	321	ASP	CA-C-N	5.69	126.30	119.98
1	L	321	ASP	C-N-CA	5.69	126.30	119.98
1	H	77	VAL	CB-CA-C	-5.69	103.18	110.98
1	E	215	ARG	N-CA-C	5.69	118.08	110.35
1	F	188	GLN	N-CA-C	5.68	118.24	111.71
1	L	250	GLY	N-CA-C	-5.68	99.73	113.18
1	J	135	ASN	N-CA-C	5.66	118.69	110.42
1	I	200	VAL	N-CA-C	5.64	119.00	111.44
1	J	340	ARG	NE-CZ-NH1	-5.63	115.87	121.50
1	N	20	ARG	N-CA-C	5.63	117.41	111.28
1	B	92	VAL	N-CA-C	5.62	116.27	110.36
1	L	73	ALA	N-CA-C	-5.62	103.06	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	96	GLY	N-CA-C	5.62	122.99	114.61
1	E	64	LEU	N-CA-C	-5.57	105.36	111.82
1	I	339	ALA	N-CA-C	-5.57	105.29	111.36
1	M	141	VAL	CB-CA-C	-5.57	104.63	112.14
1	B	271	ILE	N-CA-C	5.56	116.38	107.98
1	G	250	GLY	N-CA-C	-5.56	100.00	113.18
1	A	327	GLN	CB-CG-CD	-5.55	103.17	112.60
1	G	328	SER	N-CA-C	-5.55	105.39	111.82
1	G	297	TYR	N-CA-C	5.54	118.61	110.30
1	O	241	MET	N-CA-C	-5.54	105.83	112.59
1	N	266	VAL	N-CA-C	-5.53	106.42	113.22
1	D	264	GLY	N-CA-C	5.52	120.50	112.55
1	L	13	PHE	N-CA-C	5.51	118.23	109.24
1	A	112	GLY	N-CA-C	-5.51	106.12	112.73
1	O	151	GLY	N-CA-C	-5.50	101.79	111.80
1	K	340	ARG	NE-CZ-NH2	5.50	124.15	119.20
1	P	114	ARG	N-CA-C	5.49	117.27	111.28
1	A	298	GLY	N-CA-C	-5.49	108.08	115.21
1	M	296	VAL	CB-CA-C	-5.47	105.89	112.19
1	F	316	CYS	N-CA-C	5.46	118.48	109.85
1	K	59	ARG	CA-C-N	5.45	126.66	119.84
1	K	59	ARG	C-N-CA	5.45	126.66	119.84
1	B	333	THR	N-CA-C	-5.45	105.42	111.36
1	D	199	LEU	N-CA-C	5.45	117.03	111.14
1	C	28	ALA	N-CA-C	-5.45	104.99	111.69
1	J	215	ARG	N-CA-C	5.45	118.54	110.48
1	E	308	VAL	CB-CA-C	-5.44	104.91	112.04
1	D	231	HIS	N-CA-C	-5.43	106.42	113.16
1	J	20	ARG	N-CA-C	5.41	117.60	111.11
1	D	345	ILE	CB-CA-C	-5.40	104.53	110.52
1	F	90	ILE	N-CA-C	-5.40	105.27	110.72
1	O	102	GLU	N-CA-C	-5.40	103.77	110.41
1	L	44	THR	N-CA-C	-5.39	106.68	113.20
1	A	136	ALA	N-CA-C	-5.39	105.97	112.54
1	M	230	ARG	NE-CZ-NH2	-5.38	114.35	119.20
1	G	92	VAL	CB-CA-C	-5.38	104.99	111.88
1	D	122	ALA	N-CA-C	-5.38	106.72	113.28
1	F	215	ARG	N-CA-C	5.37	118.07	110.50
1	H	340	ARG	N-CA-C	-5.36	105.51	111.36
1	B	320	THR	CB-CA-C	-5.36	103.62	111.77
1	C	332	LEU	N-CA-C	-5.36	105.44	111.28
1	O	120	ASP	N-CA-C	-5.36	104.68	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	309	ILE	N-CA-C	5.36	115.56	110.53
1	G	152	ARG	NE-CZ-NH2	5.35	124.02	119.20
1	D	327	GLN	N-CA-C	-5.34	104.89	111.40
1	M	192	TYR	CA-CB-CG	-5.33	104.30	113.90
1	B	132	ASN	N-CA-C	5.33	119.05	112.54
1	D	99	VAL	CB-CA-C	-5.33	102.55	110.33
1	J	270	ARG	N-CA-C	5.33	117.43	107.99
1	C	231	HIS	CA-C-N	-5.33	115.89	123.08
1	C	231	HIS	C-N-CA	-5.33	115.89	123.08
1	O	188	GLN	N-CA-C	5.31	117.07	111.28
1	E	35	ARG	N-CA-C	5.31	120.41	113.30
1	E	114	ARG	N-CA-C	5.30	117.05	111.28
1	F	32	HIS	N-CA-C	-5.29	104.41	111.87
1	M	340	ARG	NE-CZ-NH1	-5.29	116.22	121.50
1	M	308	VAL	N-CA-CB	5.28	116.73	110.55
1	B	182	GLY	N-CA-C	-5.27	104.28	112.45
1	H	70	GLN	N-CA-C	5.26	119.83	113.41
1	H	345	ILE	CB-CA-C	-5.25	104.69	110.52
1	H	230	ARG	CG-CD-NE	-5.24	100.47	112.00
1	H	24	ASN	N-CA-C	-5.23	106.74	113.23
1	D	171	ALA	N-CA-C	5.23	118.44	111.75
1	O	206	VAL	CB-CA-C	-5.22	102.62	110.55
1	N	343	VAL	N-CA-CB	-5.21	102.18	111.92
1	C	19	GLY	N-CA-C	-5.20	105.06	112.55
1	G	325	GLY	N-CA-C	-5.20	106.49	112.73
1	E	12	ARG	N-CA-C	5.20	116.78	108.41
1	E	316	CYS	N-CA-C	5.19	115.40	108.23
1	K	19	GLY	CA-C-N	5.19	127.96	120.38
1	K	19	GLY	C-N-CA	5.19	127.96	120.38
1	C	25	HIS	N-CA-C	-5.18	105.28	111.03
1	M	92	VAL	CB-CA-C	-5.17	105.15	112.14
1	A	44	THR	N-CA-CB	-5.17	102.38	110.44
1	M	115	MET	CB-CG-SD	-5.17	97.19	112.70
1	D	157	THR	CB-CA-C	-5.16	100.36	109.70
1	N	201	GLY	CA-C-N	5.16	125.40	119.83
1	N	201	GLY	C-N-CA	5.16	125.40	119.83
1	M	188	GLN	N-CA-C	5.15	116.89	111.28
1	E	99	VAL	N-CA-C	5.14	115.31	108.11
1	K	260	THR	CA-C-N	-5.14	115.31	122.71
1	K	260	THR	C-N-CA	-5.14	115.31	122.71
1	M	78	LEU	N-CA-C	5.14	117.03	107.99
1	B	157	THR	CB-CA-C	5.13	119.00	109.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	305	TYR	N-CA-C	-5.13	106.53	112.89
1	N	39	VAL	CB-CA-C	-5.13	105.40	111.81
1	G	174	TRP	N-CA-C	-5.13	106.28	112.54
1	I	304	TYR	N-CA-C	5.12	116.55	111.07
1	H	188	GLN	N-CA-C	5.12	116.55	111.07
1	P	208	ALA	N-CA-C	5.12	117.59	109.50
1	C	4	LEU	CA-C-N	-5.11	114.52	119.78
1	C	4	LEU	C-N-CA	-5.11	114.52	119.78
1	H	92	VAL	CB-CA-C	-5.10	105.26	112.14
1	J	327	GLN	N-CA-C	-5.09	105.81	111.36
1	C	39	VAL	N-CA-C	-5.09	108.54	113.53
1	J	279	PRO	N-CA-C	5.08	118.59	111.33
1	P	333	THR	N-CA-C	-5.08	105.82	111.36
1	O	39	VAL	CB-CA-C	-5.07	105.55	111.94
1	C	120	ASP	N-CA-C	-5.07	105.44	110.97
1	A	201	GLY	CA-C-N	5.06	125.85	119.98
1	A	201	GLY	C-N-CA	5.06	125.85	119.98
1	E	193	VAL	N-CA-C	-5.06	105.46	110.62
1	K	39	VAL	N-CA-C	5.05	119.84	109.34
1	C	120	ASP	CB-CA-C	-5.04	103.20	110.96
1	O	153	ILE	N-CA-C	5.04	115.54	108.89
1	E	262	ARG	CB-CA-C	-5.04	103.26	110.62
1	J	45	ASN	CA-C-N	5.04	126.14	119.84
1	J	45	ASN	C-N-CA	5.04	126.14	119.84
1	D	115	MET	CB-CA-C	-5.03	102.98	110.88
1	A	55	ALA	N-CA-C	5.03	118.19	111.75
1	B	25	HIS	N-CA-C	5.03	116.57	111.14
1	M	315	ASP	N-CA-C	5.01	116.75	111.28
1	E	277	ALA	N-CA-C	-5.00	107.45	113.21

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	K	315	ASP	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2707	0	2654	71	0
1	B	2587	0	2547	129	0
1	C	2712	0	2655	77	0
1	D	2693	0	2641	139	0
1	E	2501	0	2465	139	0
1	F	2552	0	2505	87	0
1	G	2677	0	2624	74	0
1	H	2681	0	2633	114	2
1	I	2677	0	2624	121	1
1	J	2707	0	2654	92	1
1	K	2511	0	2479	112	0
1	L	2514	0	2486	136	0
1	M	2707	0	2654	95	0
1	N	2677	0	2624	108	0
1	O	2610	0	2572	91	0
1	P	2511	0	2479	100	0
2	A	44	0	27	1	0
2	B	44	0	27	6	0
2	C	44	0	27	6	0
2	D	44	0	27	7	0
2	E	44	0	27	7	0
2	F	44	0	27	4	0
2	G	44	0	27	4	0
2	H	44	0	27	8	0
2	I	44	0	27	12	0
2	J	44	0	27	7	0
2	K	44	0	27	4	0
2	L	44	0	27	6	0
2	M	44	0	27	4	0
2	N	44	0	27	4	0
2	O	44	0	27	3	0
2	P	44	0	27	5	0
3	A	40	0	22	2	0
3	B	40	0	22	1	0
3	C	40	0	22	1	0
3	D	40	0	22	1	0
3	E	40	0	22	5	0
3	F	40	0	22	2	0
3	G	40	0	22	2	0
3	H	40	0	22	3	0
3	I	40	0	22	3	0
3	J	40	0	22	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	40	0	22	6	0
3	L	40	0	22	0	0
3	M	40	0	22	4	0
3	N	40	0	22	1	0
3	O	40	0	22	2	0
3	P	40	0	22	1	0
4	A	85	0	0	8	0
4	B	54	0	0	6	0
4	C	58	0	0	3	0
4	D	51	0	0	3	0
4	E	21	0	0	2	0
4	F	24	0	0	0	0
4	G	49	0	0	4	0
4	H	35	0	0	2	0
4	I	36	0	0	2	0
4	J	30	0	0	1	0
4	K	26	0	0	2	0
4	L	37	0	0	3	0
4	M	36	0	0	1	0
4	N	34	0	0	4	0
4	O	17	0	0	1	0
4	P	24	0	0	0	0
All	All	43985	0	42080	1679	2

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 20.

All (1679) 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:K:39:VAL:HG12	1:K:40:GLU:CG	1.49	1.43
1:I:64:LEU:HD23	1:I:67:MET:CE	1.59	1.31
1:B:12:ARG:HG2	1:B:39:VAL:CG2	1.61	1.28
1:B:12:ARG:CG	1:B:39:VAL:HG21	1.64	1.27
1:N:12:ARG:NH1	1:N:72:ASN:OD1	1.70	1.25
1:E:317:GLU:OE1	1:E:318:PRO:CD	1.84	1.23
1:E:98:HIS:HA	1:E:124:VAL:CG1	1.71	1.20
1:B:98:HIS:HA	1:B:124:VAL:CG1	1.73	1.19
1:O:98:HIS:HA	1:O:124:VAL:CG1	1.74	1.16
2:J:500:NAI:H6N	2:J:500:NAI:H51N	1.20	1.12
1:K:39:VAL:HG12	1:K:40:GLU:HG2	1.28	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:39:VAL:CG1	1:D:40:GLU:HG3	1.78	1.11
1:O:39:VAL:HG12	1:O:40:GLU:HG3	1.20	1.11
1:P:39:VAL:HG12	1:P:40:GLU:CG	1.79	1.11
1:B:166:GLN:HB2	4:B:366:HOH:O	1.47	1.11
2:J:500:NAI:H51N	2:J:500:NAI:C6N	1.81	1.11
1:O:125:ARG:NH1	1:O:311:CYS:SG	2.25	1.10
1:K:39:VAL:HG12	1:K:40:GLU:HG3	1.21	1.10
1:M:216:ARG:HH11	1:M:216:ARG:CG	1.65	1.09
1:E:103:LYS:O	1:E:103:LYS:HD3	1.50	1.09
1:N:98:HIS:HA	1:N:124:VAL:CG1	1.82	1.08
1:K:278:GLU:O	1:K:278:GLU:HG2	1.46	1.08
1:P:277:ALA:C	1:P:278:GLU:HG2	1.76	1.08
1:E:317:GLU:OE1	1:E:318:PRO:HD2	1.51	1.07
1:M:216:ARG:NH1	1:M:216:ARG:HG3	1.51	1.07
1:E:97:ARG:O	1:E:124:VAL:HG11	1.52	1.06
1:K:9:ARG:HG2	1:K:9:ARG:HH11	0.93	1.06
1:L:324:GLU:OE2	1:L:324:GLU:HA	1.56	1.06
1:E:98:HIS:HA	1:E:124:VAL:HG13	1.34	1.05
1:E:317:GLU:OE1	1:E:318:PRO:HD3	1.48	1.05
1:D:98:HIS:HA	1:D:124:VAL:CG1	1.86	1.05
1:B:127:PHE:HE1	1:B:318:PRO:HB3	1.17	1.04
1:P:97:ARG:O	1:P:124:VAL:HG11	1.57	1.04
1:I:39:VAL:HG12	1:I:40:GLU:HG3	1.36	1.04
1:D:39:VAL:HG12	1:D:40:GLU:CG	1.86	1.04
1:E:12:ARG:HG2	1:E:74:ASP:OD2	1.58	1.03
1:E:137:THR:HG22	1:E:138:LEU:N	1.71	1.03
1:G:16:VAL:HG22	1:G:67:MET:HE1	1.41	1.03
1:B:307:ASN:HD21	1:B:318:PRO:HA	1.20	1.03
1:E:305:TYR:HA	1:E:308:VAL:CG2	1.88	1.03
1:H:327:GLN:HA	1:H:327:GLN:NE2	1.74	1.03
1:K:103:LYS:O	1:K:103:LYS:HD3	1.59	1.03
1:F:67:MET:HE2	1:F:76:LEU:HD21	1.36	1.02
1:B:124:VAL:HG12	1:B:125:ARG:H	1.18	1.02
1:E:12:ARG:NH2	1:E:72:ASN:OD1	1.91	1.02
1:P:270:ARG:HG2	1:P:272:ASP:OD1	1.59	1.02
1:K:278:GLU:O	1:K:278:GLU:CG	2.05	1.01
1:P:103:LYS:C	1:P:103:LYS:HD3	1.85	1.01
1:O:53:GLU:HG3	1:O:60:PRO:HG3	1.40	1.01
1:O:97:ARG:O	1:O:124:VAL:HG11	1.59	1.01
1:B:98:HIS:HA	1:B:124:VAL:HG11	1.36	1.00
1:B:166:GLN:CB	4:B:366:HOH:O	1.99	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:313:ARG:HG2	1:B:313:ARG:HH11	1.25	1.00
1:J:75:ALA:C	1:J:76:LEU:HD23	1.87	1.00
1:D:287:ARG:NH1	1:M:24:ASN:OD1	1.94	0.99
1:I:64:LEU:HD23	1:I:67:MET:HE1	1.41	0.99
1:C:327:GLN:HE21	1:C:327:GLN:HA	1.23	0.99
1:D:39:VAL:HG12	1:D:40:GLU:HG3	0.99	0.99
1:B:313:ARG:HH11	1:B:313:ARG:CG	1.76	0.99
1:P:39:VAL:CG1	1:P:40:GLU:HG3	1.92	0.99
1:B:12:ARG:HG2	1:B:39:VAL:HG21	0.99	0.98
1:L:40:GLU:HB2	1:L:67:MET:HE3	1.43	0.97
1:N:97:ARG:O	1:N:124:VAL:HG11	1.65	0.97
2:D:500:NAI:H42N	3:D:550:HP7:H3'	1.46	0.97
1:D:103:LYS:C	1:D:103:LYS:HD3	1.87	0.97
1:I:98:HIS:HA	1:I:124:VAL:CG1	1.93	0.97
1:D:103:LYS:HD3	1:D:103:LYS:O	1.64	0.97
2:D:500:NAI:H51N	2:D:500:NAI:H6N	1.47	0.97
1:K:39:VAL:CG1	1:K:40:GLU:CG	2.41	0.96
1:B:124:VAL:HG12	1:B:125:ARG:N	1.74	0.96
1:O:340:ARG:HD3	1:O:341:ASP:OD1	1.66	0.96
1:K:103:LYS:HD3	1:K:103:LYS:C	1.89	0.96
1:H:43:ASP:OD2	2:H:500:NAI:O3B	1.84	0.96
1:P:39:VAL:HG12	1:P:40:GLU:HG3	0.97	0.96
4:A:390:HOH:O	1:D:230:ARG:HD3	1.65	0.95
1:A:16:VAL:HG22	1:A:67:MET:HE1	1.44	0.95
1:L:262:ARG:HG2	1:L:262:ARG:HH11	1.28	0.95
1:M:98:HIS:HA	1:M:124:VAL:CG1	1.95	0.95
1:M:97:ARG:O	1:M:124:VAL:HG11	1.66	0.95
1:I:39:VAL:HG12	1:I:40:GLU:CG	1.97	0.95
1:G:53:GLU:OE1	1:G:60:PRO:HG3	1.66	0.95
1:P:98:HIS:HA	1:P:124:VAL:CG1	1.95	0.95
1:L:32:HIS:CE1	1:L:35:ARG:HH11	1.85	0.94
1:J:76:LEU:HD23	1:J:76:LEU:N	1.83	0.94
1:K:39:VAL:CG1	1:K:40:GLU:HG2	1.95	0.94
1:J:173:ARG:O	1:J:177:LYS:HE2	1.66	0.94
1:G:98:HIS:HA	1:G:124:VAL:HG13	1.49	0.94
2:B:500:NAI:H6N	2:B:500:NAI:H51N	1.45	0.94
1:E:305:TYR:HA	1:E:308:VAL:HG23	1.49	0.94
1:K:9:ARG:HG2	1:K:9:ARG:NH1	1.74	0.94
1:A:67:MET:HE3	1:A:76:LEU:HD22	1.48	0.94
1:J:58:ALA:O	1:J:60:PRO:HD3	1.68	0.94
1:K:9:ARG:HH11	1:K:9:ARG:CG	1.81	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ARG:HB2	1:A:114:ARG:HH11	1.32	0.93
1:K:206:VAL:HG12	1:K:227:LEU:HD23	1.49	0.93
1:P:277:ALA:O	1:P:278:GLU:HG2	1.66	0.92
1:H:327:GLN:HA	1:H:327:GLN:HE21	1.29	0.92
1:L:11:ILE:HD13	1:L:11:ILE:H	1.31	0.92
1:H:97:ARG:O	1:H:124:VAL:HG11	1.69	0.92
1:O:281:PRO:O	1:O:282:ASP:HB2	1.66	0.92
1:C:40:GLU:HB3	1:C:67:MET:HE3	1.52	0.91
1:B:127:PHE:CE1	1:B:318:PRO:HB3	2.05	0.91
1:D:133:ARG:HH12	1:D:324:GLU:HG2	1.35	0.91
1:F:206:VAL:HG12	1:F:227:LEU:HD23	1.51	0.91
1:K:103:LYS:NZ	3:K:550:HP7:O3'	2.02	0.90
1:B:310:ASN:HB3	1:B:316:CYS:SG	2.11	0.90
1:I:10:LYS:HG2	1:I:34:ASP:O	1.70	0.90
1:L:29:ILE:O	1:L:32:HIS:N	2.04	0.90
1:E:103:LYS:HD3	1:E:103:LYS:C	1.96	0.90
1:I:10:LYS:CG	1:I:34:ASP:O	2.20	0.90
1:L:9:ARG:HG3	1:L:10:LYS:N	1.84	0.90
1:I:284:ASP:C	1:I:285:LYS:HD3	1.97	0.90
1:H:39:VAL:HG12	1:H:40:GLU:HG3	1.52	0.89
1:C:86:PRO:HA	1:C:115:MET:HG2	1.52	0.89
1:O:340:ARG:CD	1:O:341:ASP:OD1	2.21	0.89
1:I:103:LYS:HD3	1:I:103:LYS:O	1.73	0.89
1:O:98:HIS:HA	1:O:124:VAL:HG13	1.53	0.89
1:L:108:ARG:HG2	1:L:108:ARG:HH11	1.36	0.88
1:F:142:LYS:HE3	1:F:146:GLU:OE2	1.72	0.88
1:L:184:ALA:HA	1:L:188:GLN:NE2	1.90	0.87
1:H:288:GLU:HA	1:H:291:TYR:HB2	1.56	0.87
2:K:500:NAI:H42N	3:K:550:HP7:H3'	1.57	0.87
1:P:98:HIS:HA	1:P:124:VAL:HG12	1.55	0.86
1:D:16:VAL:HG22	1:D:67:MET:HE1	1.57	0.86
1:I:97:ARG:O	1:I:124:VAL:HG11	1.76	0.85
1:D:344:ARG:NH1	4:D:571:HOH:O	2.09	0.85
1:B:124:VAL:CG1	1:B:125:ARG:H	1.89	0.85
2:M:500:NAI:H42N	3:M:550:HP7:H3'	1.57	0.85
1:B:313:ARG:HG2	1:B:313:ARG:NH1	1.90	0.85
1:D:15:LEU:HD21	1:D:22:SER:HB2	1.59	0.85
1:L:108:ARG:HH11	1:L:108:ARG:CG	1.87	0.84
1:C:103:LYS:HD3	1:C:103:LYS:C	2.00	0.84
1:F:67:MET:HE2	1:F:76:LEU:CD2	2.07	0.84
1:K:16:VAL:HG22	1:K:67:MET:HE1	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ARG:HG2	1:C:117:LYS:HE2	1.59	0.84
2:N:500:NAI:H42N	3:N:550:HP7:H3'	1.58	0.84
1:I:64:LEU:CD2	1:I:67:MET:CE	2.51	0.84
1:B:280[B]:HIS:CD2	1:B:281:PRO:HD2	2.12	0.84
2:N:500:NAI:H6N	2:N:500:NAI:H51N	1.58	0.84
1:H:103:LYS:O	1:H:103:LYS:HD3	1.78	0.84
1:B:80:THR:HB	1:B:81:PRO:HD2	1.58	0.83
1:P:86:PRO:HA	1:P:115:MET:HG2	1.59	0.83
1:F:98:HIS:HA	1:F:124:VAL:CG1	2.08	0.83
1:B:317:GLU:HG3	1:C:173:ARG:HH12	1.43	0.83
1:K:216:ARG:HG3	1:K:216:ARG:O	1.78	0.83
1:K:97:ARG:O	1:K:124:VAL:HG21	1.79	0.83
1:L:277:ALA:C	1:L:278:GLU:HG2	2.04	0.83
1:M:39:VAL:CG1	1:M:40:GLU:HG3	2.08	0.83
1:E:305:TYR:HA	1:E:308:VAL:HG21	1.59	0.82
1:C:34:ASP:OD2	1:C:34:ASP:N	2.06	0.82
1:H:35:ARG:HG2	1:H:313:ARG:NH1	1.94	0.82
1:L:32:HIS:CE1	1:L:35:ARG:NH1	2.46	0.82
1:N:282:ASP:OD1	1:N:285:LYS:HE2	1.77	0.82
1:O:98:HIS:HA	1:O:124:VAL:HG12	1.61	0.82
2:D:500:NAI:H51N	2:D:500:NAI:C6N	2.09	0.82
1:H:98:HIS:HA	1:H:124:VAL:CG1	2.08	0.82
1:N:76:LEU:HD12	1:N:92:VAL:HG13	1.61	0.82
1:N:280:HIS:CG	1:N:281:PRO:HD2	2.13	0.82
2:N:500:NAI:H51N	2:N:500:NAI:C6N	2.10	0.82
1:I:310:ASN:N	1:I:310:ASN:HD22	1.75	0.82
1:E:59:ARG:NH2	1:E:70:GLN:HB3	1.95	0.82
2:H:500:NAI:H42N	3:H:550:HP7:H3'	1.61	0.82
1:L:174:TRP:O	1:L:177:LYS:HB2	1.79	0.82
1:N:310:ASN:O	1:N:315:ASP:HB2	1.80	0.82
1:B:311:CYS:SG	1:B:318:PRO:HD3	2.20	0.82
1:C:21:ILE:HD13	2:C:500:NAI:H4N	1.62	0.82
1:D:86:PRO:HA	1:D:115:MET:HG2	1.60	0.82
1:L:324:GLU:OE2	1:L:324:GLU:CA	2.28	0.82
1:N:39:VAL:O	1:N:58:ALA:HB1	1.79	0.82
1:F:98:HIS:HA	1:F:124:VAL:HG13	1.60	0.81
1:E:59:ARG:HH22	1:E:70:GLN:HB3	1.45	0.81
1:D:9:ARG:NH2	1:D:12:ARG:HH21	1.78	0.81
1:I:21:ILE:HD13	2:I:500:NAI:H4N	1.60	0.81
1:G:310:ASN:O	1:G:315:ASP:HB2	1.80	0.81
1:O:206:VAL:HG12	1:O:227:LEU:HD23	1.61	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:500:NAI:H51N	2:B:500:NAI:C6N	2.10	0.80
1:L:11:ILE:HD13	1:L:11:ILE:N	1.91	0.80
1:O:42:CYS:HB2	1:O:67:MET:HE1	1.64	0.80
1:E:165:PRO:HB2	1:E:167:GLU:HG2	1.64	0.80
1:J:53:GLU:OE2	1:J:60:PRO:HG3	1.82	0.80
1:H:33:GLY:HA2	1:H:36:ALA:O	1.80	0.80
1:F:15:LEU:HD21	1:F:22:SER:HB2	1.62	0.79
1:H:280:HIS:ND1	1:H:281:PRO:HD2	1.98	0.79
1:D:197:ASP:OD1	1:D:327:GLN:HG2	1.82	0.79
1:M:15:LEU:HD21	1:M:17:GLY:O	1.81	0.79
1:B:135:ASN:N	1:B:135:ASN:HD22	1.78	0.79
1:E:305:TYR:CA	1:E:308:VAL:HG23	2.13	0.79
1:E:310:ASN:O	1:E:315:ASP:HB2	1.83	0.79
1:F:90:ILE:O	1:F:94:GLN:HG3	1.83	0.79
1:M:216:ARG:HH11	1:M:216:ARG:HG3	0.72	0.79
1:P:9:ARG:HH22	1:P:12:ARG:NH2	1.79	0.79
1:C:9:ARG:HG3	1:C:9:ARG:HH11	1.48	0.79
1:C:103:LYS:HD3	1:C:103:LYS:O	1.83	0.79
1:C:327:GLN:HE21	1:C:327:GLN:CA	1.95	0.79
1:F:41:ILE:HD12	1:F:49:LEU:HD11	1.64	0.79
1:D:26:ILE:HG22	1:D:27:GLY:N	1.97	0.78
1:E:327:GLN:OE1	1:E:327:GLN:HA	1.83	0.78
1:K:86:PRO:HA	1:K:115:MET:HG2	1.64	0.78
1:E:12:ARG:HD3	1:E:72:ASN:OD1	1.83	0.78
1:I:34:ASP:OD2	1:I:34:ASP:N	2.13	0.78
1:N:98:HIS:HA	1:N:124:VAL:HG12	1.63	0.78
1:K:10:LYS:HD3	1:K:34:ASP:O	1.83	0.78
1:I:157:THR:HG21	4:I:362:HOH:O	1.84	0.78
1:A:67:MET:HE3	1:A:76:LEU:CD2	2.13	0.78
1:I:64:LEU:HD23	1:I:67:MET:HE2	1.63	0.78
1:L:76:LEU:N	1:L:76:LEU:HD23	1.98	0.78
1:B:124:VAL:CG1	1:B:125:ARG:N	2.47	0.78
1:J:29:ILE:O	1:J:31:GLN:N	2.16	0.78
1:O:42:CYS:HB2	1:O:67:MET:CE	2.14	0.77
1:N:14:GLY:HA3	1:N:76:LEU:HD23	1.63	0.77
1:B:12:ARG:CG	1:B:39:VAL:CG2	2.42	0.77
1:I:103:LYS:HD3	1:I:103:LYS:C	2.09	0.77
1:L:21:ILE:HD13	2:L:500:NAI:H4N	1.64	0.77
1:M:72:ASN:HD22	1:M:72:ASN:H	1.32	0.77
1:C:24:ASN:HD22	1:C:24:ASN:H	1.32	0.77
1:I:64:LEU:HD23	1:I:67:MET:HE3	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:184:ALA:HA	1:B:188:GLN:NE2	2.00	0.77
1:L:307:ASN:CG	1:L:319:GLU:HG3	2.10	0.76
1:N:16:VAL:HG22	1:N:67:MET:HE1	1.67	0.76
1:O:310:ASN:HB2	1:O:316:CYS:SG	2.26	0.76
1:P:21:ILE:HG22	2:P:500:NAI:H52N	1.66	0.76
1:J:109:TRP:NE1	1:J:113:LYS:HE2	2.01	0.76
1:A:20:ARG:O	1:A:23:LYS:HE3	1.86	0.76
1:D:86:PRO:HA	1:D:115:MET:CG	2.15	0.76
1:A:114:ARG:HH11	1:A:114:ARG:CB	1.99	0.76
1:D:133:ARG:HH12	1:D:324:GLU:CG	1.98	0.76
1:N:53:GLU:HG2	1:N:54:ALA:N	2.01	0.76
1:M:39:VAL:HG13	1:M:40:GLU:HG3	1.68	0.76
1:E:12:ARG:HH21	1:E:72:ASN:CG	1.94	0.75
1:H:43:ASP:CG	2:H:500:NAI:O3B	2.29	0.75
1:E:39:VAL:O	1:E:58:ALA:HB1	1.85	0.75
1:I:269:ASN:HA	1:I:293:THR:HG21	1.68	0.75
1:M:16:VAL:HG22	1:M:67:MET:HE1	1.68	0.75
1:I:21:ILE:HG22	2:I:500:NAI:O2N	1.87	0.75
1:O:98:HIS:CA	1:O:124:VAL:CG1	2.63	0.75
1:B:307:ASN:ND2	1:B:318:PRO:HA	2.01	0.75
2:J:500:NAI:H42N	3:J:550:HP7:H3'	1.67	0.75
2:G:500:NAI:H42N	3:G:550:HP7:H3'	1.68	0.75
1:J:29:ILE:C	1:J:31:GLN:H	1.92	0.75
1:N:76:LEU:HD12	1:N:92:VAL:CG1	2.16	0.75
1:D:98:HIS:HA	1:D:124:VAL:HG11	1.67	0.74
1:F:41:ILE:HD12	1:F:49:LEU:CD1	2.17	0.74
1:G:21:ILE:HD13	2:G:500:NAI:H4N	1.68	0.74
1:N:12:ARG:NH1	1:N:72:ASN:CG	2.45	0.74
1:L:108:ARG:CG	1:L:108:ARG:NH1	2.49	0.74
1:A:114:ARG:HB2	1:A:114:ARG:NH1	2.00	0.74
1:D:125:ARG:HG2	1:D:125:ARG:HH11	1.52	0.74
1:E:98:HIS:CA	1:E:124:VAL:HG13	2.16	0.74
1:D:35:ARG:HD2	1:D:313:ARG:HH12	1.52	0.74
1:H:103:LYS:C	1:H:103:LYS:HE2	2.12	0.74
1:K:25:HIS:ND1	1:K:305:TYR:OH	2.20	0.74
1:D:291:TYR:OH	1:M:302:PRO:HD3	1.88	0.74
1:E:137:THR:HG21	1:E:263:VAL:HG11	1.70	0.74
1:H:257:GLU:OE2	1:H:258:LYS:HE2	1.87	0.74
1:J:80:THR:HB	1:J:81:PRO:HD2	1.68	0.74
1:K:246:GLN:O	1:K:247:ASN:C	2.30	0.74
1:D:9:ARG:CZ	1:D:12:ARG:NH2	2.50	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:25:HIS:O	1:L:29:ILE:HG13	1.88	0.73
1:L:98:HIS:HA	1:L:124:VAL:CG1	2.17	0.73
2:C:500:NAI:H42N	3:C:550:HP7:H3'	1.68	0.73
1:O:6:ILE:HG21	1:O:11:ILE:HD13	1.69	0.73
1:D:142:LYS:NZ	1:D:146:GLU:OE2	2.20	0.73
1:O:39:VAL:CG1	1:O:40:GLU:HG3	2.11	0.73
1:F:173:ARG:NH2	1:G:317:GLU:OE1	2.20	0.73
1:N:98:HIS:CA	1:N:124:VAL:CG1	2.64	0.73
2:I:500:NAI:H42N	3:I:550:HP7:H3'	1.68	0.73
1:L:98:HIS:HA	1:L:124:VAL:HG13	1.70	0.73
1:D:53:GLU:OE1	1:D:60:PRO:HG3	1.89	0.72
1:P:9:ARG:HH12	1:P:12:ARG:CZ	2.02	0.72
1:I:128:VAL:O	1:I:320:THR:HG22	1.89	0.72
1:H:19:GLY:O	1:H:22:SER:OG	2.08	0.72
1:G:76:LEU:HD12	1:G:92:VAL:HG22	1.69	0.72
1:N:40:GLU:C	1:N:41:ILE:HG23	2.14	0.72
1:P:103:LYS:HD3	1:P:103:LYS:O	1.88	0.72
1:I:285:LYS:HD3	1:I:285:LYS:N	2.02	0.72
1:M:30:ALA:O	1:M:32:HIS:N	2.22	0.72
1:N:103:LYS:HD3	1:N:103:LYS:O	1.90	0.72
1:D:133:ARG:NH1	1:D:324:GLU:HG2	2.04	0.71
1:D:59:ARG:HG2	1:D:60:PRO:HD2	1.72	0.71
1:D:274:TRP:CD1	1:D:286:ILE:HD11	2.24	0.71
1:K:253:THR:OG1	1:K:262:ARG:HG3	1.90	0.71
2:I:500:NAI:H6N	2:I:500:NAI:H51N	1.71	0.71
1:M:15:LEU:HD23	1:M:15:LEU:C	2.14	0.71
1:I:310:ASN:HD22	1:I:310:ASN:H	1.37	0.71
1:L:23:LYS:HA	1:L:26:ILE:HD12	1.72	0.71
1:F:86:PRO:HA	1:F:115:MET:HG2	1.73	0.71
1:H:16:VAL:HG11	1:H:78:LEU:HD23	1.72	0.71
1:L:262:ARG:HH11	1:L:262:ARG:CG	2.02	0.71
1:A:67:MET:CE	1:A:76:LEU:HD22	2.20	0.71
1:J:12:ARG:HG2	1:J:39:VAL:HG21	1.73	0.71
1:L:80:THR:HB	1:L:81:PRO:HD2	1.74	0.70
1:E:39:VAL:C	1:E:58:ALA:HB1	2.16	0.70
1:G:98:HIS:HA	1:G:124:VAL:CG1	2.19	0.70
1:H:21:ILE:HD13	2:H:500:NAI:H4N	1.73	0.70
1:P:39:VAL:CG1	1:P:40:GLU:CG	2.62	0.70
1:D:97:ARG:O	1:D:124:VAL:HG11	1.91	0.70
1:B:23:LYS:H	1:B:23:LYS:HD2	1.57	0.70
1:M:86:PRO:O	1:M:90:ILE:HG13	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:327:GLN:HA	1:C:327:GLN:NE2	2.00	0.70
1:D:90:ILE:HD11	1:D:114:ARG:HG2	1.72	0.70
1:B:64:LEU:HD11	1:B:68:LEU:HD11	1.71	0.70
1:D:9:ARG:CZ	1:D:12:ARG:HH21	2.03	0.70
1:G:68:LEU:HD21	1:G:76:LEU:HD11	1.73	0.70
1:C:80:THR:HB	1:C:81:PRO:HD2	1.74	0.70
1:E:61:PHE:HE1	1:E:70:GLN:OE1	1.74	0.70
1:H:280:HIS:CE1	1:H:281:PRO:HD2	2.26	0.70
1:C:86:PRO:HA	1:C:115:MET:CG	2.22	0.70
4:D:368:HOH:O	1:H:230:ARG:HD3	1.92	0.70
1:E:168:TYR:OH	3:E:550:HP7:O'Q	2.09	0.70
1:B:98:HIS:CA	1:B:124:VAL:CG1	2.62	0.70
1:O:103:LYS:HD2	1:O:103:LYS:C	2.16	0.69
1:M:310:ASN:O	1:M:315:ASP:HB2	1.92	0.69
1:P:117:LYS:CD	1:P:117:LYS:C	2.66	0.69
1:K:98:HIS:ND1	1:K:125:ARG:HB2	2.07	0.69
1:B:80:THR:HB	1:B:81:PRO:CD	2.22	0.69
1:C:51:ALA:O	1:C:55:ALA:HB2	1.93	0.69
1:N:98:HIS:ND1	1:N:124:VAL:HG13	2.08	0.69
2:A:500:NAI:H42N	3:A:550:HP7:H3'	1.74	0.69
1:I:64:LEU:HD13	1:I:91:GLU:OE2	1.92	0.69
1:I:310:ASN:O	1:I:313:ARG:N	2.21	0.69
1:N:31:GLN:O	1:N:31:GLN:HG2	1.93	0.69
1:P:9:ARG:NH2	1:P:12:ARG:NH2	2.39	0.69
1:A:16:VAL:CG2	1:A:67:MET:HE1	2.22	0.69
1:B:130:LYS:CG	1:B:320:THR:HG21	2.23	0.69
1:D:35:ARG:HD2	1:D:313:ARG:NH1	2.06	0.69
1:D:318:PRO:HB2	1:D:321:ASP:HB3	1.74	0.69
1:L:262:ARG:HG2	1:L:262:ARG:NH1	2.07	0.69
1:I:90:ILE:HD11	1:I:114:ARG:HG2	1.75	0.68
1:B:12:ARG:HG2	1:B:39:VAL:HG23	1.71	0.68
1:B:127:PHE:HE1	1:B:318:PRO:CB	2.01	0.68
1:I:41:ILE:HD13	1:I:58:ALA:HB3	1.75	0.68
1:K:45:ASN:OD1	1:K:48:ALA:N	2.23	0.68
1:O:49:LEU:HD12	1:O:49:LEU:O	1.93	0.68
1:O:267:ALA:O	1:O:268:VAL:C	2.37	0.68
3:O:550:HP7:O2A	3:O:550:HP7:O2B	2.10	0.68
1:D:76:LEU:HD12	1:D:92:VAL:HG13	1.73	0.68
2:I:500:NAI:H51N	2:I:500:NAI:C6N	2.24	0.68
1:P:270:ARG:CG	1:P:272:ASP:OD1	2.40	0.68
1:J:76:LEU:N	1:J:76:LEU:CD2	2.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:LYS:HG3	1:B:320:THR:HG21	1.76	0.68
1:A:68:LEU:HD21	1:A:76:LEU:HD11	1.75	0.68
1:D:274:TRP:CG	1:D:286:ILE:HD11	2.29	0.68
1:G:310:ASN:HB3	1:G:316:CYS:SG	2.33	0.68
1:I:98:HIS:HA	1:I:124:VAL:HG13	1.76	0.68
1:E:103:LYS:NZ	3:E:550:HP7:O3'	2.26	0.67
1:F:97:ARG:O	1:F:124:VAL:HG11	1.94	0.67
1:F:206:VAL:CG1	1:F:227:LEU:HD23	2.25	0.67
1:L:246:GLN:O	1:L:247:ASN:C	2.36	0.67
1:A:80:THR:HB	1:A:81:PRO:HD2	1.75	0.67
1:L:32:HIS:ND1	1:L:35:ARG:NH1	2.37	0.67
1:M:39:VAL:HG12	1:M:40:GLU:HG3	1.76	0.67
1:H:86:PRO:HA	1:H:115:MET:HG2	1.75	0.67
1:H:127:PHE:CE1	1:H:318:PRO:HB3	2.29	0.67
1:M:291:TYR:CD1	1:M:291:TYR:C	2.72	0.67
1:C:125:ARG:NH2	1:C:317:GLU:OE1	2.27	0.67
1:E:12:ARG:NH2	1:E:72:ASN:CG	2.53	0.67
1:F:184:ALA:HA	1:F:188:GLN:NE2	2.10	0.67
1:H:327:GLN:HE21	1:H:327:GLN:CA	1.99	0.67
1:F:10:LYS:HE2	1:F:34:ASP:O	1.94	0.67
1:N:280:HIS:CE1	1:N:281:PRO:HG2	2.28	0.67
1:P:21:ILE:HD13	2:P:500:NAI:H4N	1.75	0.67
1:H:16:VAL:CG1	1:H:78:LEU:HD23	2.25	0.67
1:E:103:LYS:C	1:E:103:LYS:CD	2.67	0.66
1:H:32:HIS:O	1:H:34:ASP:N	2.27	0.66
1:A:110:GLU:HB2	4:A:362:HOH:O	1.94	0.66
1:E:35:ARG:O	1:E:36:ALA:HB2	1.96	0.66
1:L:14:GLY:HA3	1:L:67:MET:CE	2.25	0.66
1:O:15:LEU:HD21	1:O:22:SER:HB2	1.77	0.66
1:A:46:PRO:O	1:A:50:GLN:HG3	1.94	0.66
1:B:86:PRO:HA	1:B:115:MET:HG2	1.78	0.66
1:E:11:ILE:O	1:E:36:ALA:HB1	1.95	0.66
2:F:500:NAI:H42N	3:F:550:HP7:H3'	1.78	0.66
1:K:59:ARG:HG2	1:K:60:PRO:CD	2.26	0.66
1:M:117:LYS:HD3	1:M:121:GLU:OE2	1.96	0.66
1:A:197:ASP:OD1	1:A:327:GLN:HG2	1.95	0.66
1:I:128:VAL:O	1:I:320:THR:CG2	2.44	0.66
1:H:154:TYR:OH	1:H:257:GLU:HB2	1.96	0.66
1:K:59:ARG:HG2	1:K:60:PRO:HD2	1.78	0.66
1:O:98:HIS:CA	1:O:124:VAL:HG13	2.26	0.66
1:B:41:ILE:HG13	1:B:49:LEU:CD1	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:103:LYS:HD3	1:H:103:LYS:C	2.21	0.65
2:H:500:NAI:H6N	2:H:500:NAI:H51N	1.77	0.65
1:L:310:ASN:O	1:L:315:ASP:HB2	1.96	0.65
1:P:86:PRO:CA	1:P:115:MET:HG2	2.26	0.65
1:H:16:VAL:HG11	1:H:78:LEU:CD2	2.26	0.65
1:D:287:ARG:NH1	1:M:24:ASN:CG	2.54	0.65
1:L:103:LYS:O	1:L:103:LYS:HD3	1.97	0.65
1:P:261:VAL:HA	1:P:273:GLU:O	1.96	0.65
1:H:16:VAL:CG1	1:H:78:LEU:HA	2.27	0.65
1:E:15:LEU:HD11	1:E:17:GLY:O	1.97	0.65
1:E:98:HIS:HA	1:E:124:VAL:HG11	1.76	0.65
1:F:139:GLN:O	1:F:143:LYS:HG2	1.97	0.65
1:O:310:ASN:CB	1:O:316:CYS:SG	2.85	0.65
1:P:21:ILE:CG2	2:P:500:NAI:H52N	2.27	0.65
1:P:142:LYS:HE2	1:P:198:TRP:NE1	2.12	0.65
1:C:40:GLU:CB	1:C:67:MET:HE3	2.25	0.65
1:E:166:GLN:NE2	1:E:216:ARG:H	1.94	0.65
1:E:267:ALA:O	1:E:268:VAL:C	2.39	0.65
1:H:317:GLU:OE2	1:H:317:GLU:HA	1.97	0.65
1:K:39:VAL:C	1:K:40:GLU:CG	2.69	0.65
1:E:301:HIS:N	1:E:302:PRO:HD2	2.11	0.64
1:J:206:VAL:HG12	1:J:227:LEU:HD23	1.79	0.64
1:L:15:LEU:N	1:L:67:MET:HE1	2.13	0.64
1:B:166:GLN:N	4:B:366:HOH:O	1.77	0.64
1:L:259:GLY:HA2	1:L:275:LYS:O	1.98	0.64
1:P:97:ARG:O	1:P:124:VAL:CG1	2.42	0.64
1:B:12:ARG:CD	1:B:39:VAL:HG21	2.28	0.64
1:I:64:LEU:CD2	1:I:67:MET:HE1	2.22	0.64
1:K:86:PRO:HA	1:K:115:MET:CG	2.26	0.64
1:O:97:ARG:O	1:O:124:VAL:CG1	2.42	0.64
1:P:97:ARG:C	1:P:124:VAL:HG11	2.21	0.64
1:E:327:GLN:OE1	1:E:327:GLN:CA	2.45	0.64
1:F:43:ASP:OD2	2:F:500:NAI:O3B	2.14	0.64
1:G:32:HIS:ND1	1:G:35:ARG:NH1	2.46	0.64
1:M:13:PHE:O	1:M:38:LEU:HD12	1.98	0.64
1:O:86:PRO:HA	1:O:115:MET:HG2	1.79	0.64
1:A:110:GLU:HG3	4:A:363:HOH:O	1.98	0.64
1:A:80:THR:HB	1:A:81:PRO:CD	2.28	0.64
1:E:38:LEU:HD21	1:E:41:ILE:CG2	2.28	0.64
1:L:20:ARG:HG2	1:L:20:ARG:HH11	1.61	0.64
1:L:176:GLY:O	1:L:218:GLU:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:PHE:CE1	1:B:318:PRO:CB	2.80	0.63
1:E:304:TYR:O	1:E:308:VAL:HG23	1.98	0.63
1:O:340:ARG:HD2	1:O:341:ASP:OD1	1.96	0.63
1:K:25:HIS:O	1:K:29:ILE:HG13	1.97	0.63
1:L:20:ARG:HG2	1:L:20:ARG:NH1	2.13	0.63
1:D:35:ARG:NH1	1:D:306:ASP:OD1	2.32	0.63
1:E:246:GLN:O	1:E:247:ASN:C	2.41	0.63
1:L:92:VAL:O	1:L:92:VAL:CG1	2.46	0.63
1:E:12:ARG:HG2	1:E:74:ASP:CG	2.24	0.63
1:H:28:ALA:O	1:H:32:HIS:HD2	1.81	0.63
1:I:224:VAL:HG21	1:J:235:GLY:HA2	1.80	0.63
1:N:86:PRO:O	1:N:90:ILE:HG13	1.98	0.63
1:P:253:THR:OG1	1:P:262:ARG:HG3	1.98	0.63
1:L:11:ILE:N	1:L:11:ILE:CD1	2.62	0.63
1:N:12:ARG:HH12	1:N:72:ASN:CG	2.06	0.63
2:C:500:NAI:H6N	2:C:500:NAI:H51N	1.80	0.63
1:F:67:MET:CE	1:F:76:LEU:CD2	2.77	0.63
1:J:80:THR:HB	1:J:81:PRO:CD	2.28	0.63
1:L:92:VAL:O	1:L:92:VAL:HG12	1.98	0.63
1:O:184:ALA:HA	1:O:188:GLN:HE21	1.64	0.63
1:B:97:ARG:O	1:B:124:VAL:HG11	1.99	0.63
1:D:86:PRO:O	1:D:90:ILE:HG13	1.99	0.63
1:I:142:LYS:HE3	1:I:146:GLU:OE2	1.99	0.63
1:E:90:ILE:O	1:E:94:GLN:HG3	1.99	0.63
1:H:98:HIS:HA	1:H:124:VAL:HG13	1.80	0.63
1:O:39:VAL:HG11	1:O:72:ASN:HD21	1.64	0.63
1:C:24:ASN:HD22	1:C:24:ASN:N	1.97	0.62
1:E:43:ASP:OD2	2:E:500:NAI:O3B	2.16	0.62
1:L:29:ILE:O	1:L:30:ALA:C	2.42	0.62
1:B:301:HIS:N	1:B:302:PRO:HD2	2.14	0.62
1:F:40:GLU:OE2	1:F:72:ASN:N	2.32	0.62
1:E:38:LEU:HD11	1:E:40:GLU:O	1.99	0.62
1:F:21:ILE:HD13	2:F:500:NAI:H4N	1.80	0.62
1:J:134:ARG:NH2	1:J:319:GLU:OE2	2.28	0.62
1:B:184:ALA:HA	1:B:188:GLN:HE21	1.63	0.62
1:L:29:ILE:O	1:L:31:GLN:N	2.33	0.62
1:M:98:HIS:ND1	1:M:124:VAL:HG13	2.14	0.62
1:G:16:VAL:HG22	1:G:67:MET:CE	2.25	0.62
1:H:133:ARG:O	1:H:139:GLN:OE1	2.16	0.62
1:N:97:ARG:C	1:N:124:VAL:HG11	2.24	0.62
1:K:18:CYS:HA	1:K:22:SER:OG	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:80:THR:HB	1:O:81:PRO:HD2	1.82	0.62
1:J:298:GLY:C	1:J:299:PHE:CD2	2.77	0.62
1:L:317:GLU:HA	1:L:317:GLU:OE2	1.95	0.62
1:B:101:SER:O	1:B:129:VAL:HG23	1.99	0.62
1:B:135:ASN:HD22	1:B:135:ASN:H	1.47	0.62
1:M:30:ALA:O	1:M:33:GLY:N	2.33	0.62
1:E:181:ASP:OD1	1:E:187:ASN:ND2	2.28	0.61
1:I:30:ALA:O	1:I:33:GLY:N	2.32	0.61
1:I:41:ILE:HD11	1:I:53:GLU:HA	1.81	0.61
1:J:310:ASN:O	1:J:315:ASP:HB2	2.00	0.61
1:M:86:PRO:HA	1:M:115:MET:CG	2.30	0.61
1:P:277:ALA:C	1:P:278:GLU:CG	2.60	0.61
1:K:82:SER:HB3	1:K:104:PRO:HD2	1.81	0.61
1:L:97:ARG:O	1:L:124:VAL:HG11	2.00	0.61
1:E:305:TYR:C	1:E:308:VAL:HG23	2.26	0.61
1:H:103:LYS:C	1:H:103:LYS:CD	2.73	0.61
1:L:37:GLU:O	1:L:37:GLU:HG3	2.00	0.61
1:J:262:ARG:HG2	1:J:262:ARG:HH11	1.66	0.61
1:M:216:ARG:CG	1:M:216:ARG:NH1	2.36	0.61
1:C:301:HIS:N	1:C:302:PRO:HD2	2.16	0.61
1:D:333:THR:O	1:D:337:ARG:HG3	2.00	0.61
1:G:76:LEU:CD1	1:G:92:VAL:HG22	2.31	0.61
1:P:184:ALA:HA	1:P:188:GLN:OE1	1.99	0.61
1:G:280:HIS:CG	1:G:281:PRO:HD2	2.36	0.61
1:H:72:ASN:HD22	1:H:72:ASN:H	1.48	0.61
1:N:59:ARG:NH1	1:N:59:ARG:HG3	2.15	0.61
1:C:81:PRO:HD2	1:C:84:LEU:HD12	1.83	0.61
1:M:80:THR:HB	1:M:81:PRO:HD2	1.82	0.61
1:E:90:ILE:HD13	1:E:114:ARG:HD3	1.83	0.61
1:L:40:GLU:OE1	1:L:71:GLY:HA3	2.00	0.61
1:B:307:ASN:ND2	1:B:307:ASN:C	2.59	0.60
1:D:287:ARG:NH2	3:M:550:HP7:O1B	2.34	0.60
1:I:310:ASN:O	1:I:311:CYS:C	2.42	0.60
1:I:77:VAL:HG21	1:I:305:TYR:OH	2.01	0.60
1:C:156:VAL:O	1:C:235:GLY:HA3	2.02	0.60
1:E:98:HIS:CA	1:E:124:VAL:CG1	2.64	0.60
1:H:297:TYR:C	1:H:297:TYR:CD2	2.79	0.60
1:L:137:THR:O	1:L:141:VAL:HG23	2.01	0.60
1:A:98:HIS:HA	1:A:124:VAL:HG13	1.82	0.60
1:D:134:ARG:O	1:D:135:ASN:C	2.42	0.60
1:E:117:LYS:O	1:E:120:ASP:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:175:ARG:HG2	1:E:175:ARG:HH21	1.67	0.60
1:L:110:GLU:HG3	4:L:437:HOH:O	2.02	0.60
1:N:230:ARG:NE	4:N:452:HOH:O	2.30	0.60
1:B:98:HIS:CA	1:B:124:VAL:HG11	2.22	0.60
1:D:53:GLU:O	1:D:57:GLY:N	2.34	0.60
1:D:287:ARG:NE	1:M:298:GLY:O	2.34	0.60
1:I:21:ILE:CD1	2:I:500:NAI:H4N	2.31	0.60
1:K:34:ASP:OD1	1:K:35:ARG:HG3	2.01	0.60
1:D:39:VAL:CG1	1:D:40:GLU:CG	2.59	0.60
1:L:14:GLY:HA3	1:L:67:MET:HE2	1.83	0.60
1:A:249:GLU:OE2	1:B:262:ARG:NH2	2.30	0.60
1:G:103:LYS:O	1:G:103:LYS:HD3	2.02	0.60
1:P:98:HIS:CA	1:P:124:VAL:CG1	2.74	0.60
1:A:16:VAL:HG22	1:A:67:MET:CE	2.28	0.60
1:L:184:ALA:HA	1:L:188:GLN:HE21	1.62	0.60
1:M:53:GLU:HG3	1:M:60:PRO:HG3	1.83	0.60
1:B:265:GLY:N	4:B:380:HOH:O	2.06	0.59
1:F:86:PRO:HA	1:F:115:MET:CG	2.32	0.59
1:I:80:THR:HB	1:I:81:PRO:HD2	1.84	0.59
1:L:86:PRO:HA	1:L:115:MET:CG	2.32	0.59
1:O:184:ALA:HA	1:O:188:GLN:NE2	2.17	0.59
1:I:306:ASP:O	1:I:310:ASN:ND2	2.34	0.59
1:L:40:GLU:CB	1:L:67:MET:HE3	2.26	0.59
1:L:80:THR:HB	1:L:81:PRO:CD	2.32	0.59
1:N:12:ARG:HB3	1:N:39:VAL:HG21	1.83	0.59
1:H:29:ILE:O	1:H:32:HIS:N	2.26	0.59
1:I:39:VAL:HG12	1:I:40:GLU:HG2	1.84	0.59
1:K:206:VAL:CG1	1:K:227:LEU:HD23	2.27	0.59
1:P:87:TRP:HH2	1:P:114:ARG:HH21	1.50	0.59
1:E:98:HIS:ND1	1:E:125:ARG:HB2	2.17	0.59
1:M:58:ALA:O	1:M:60:PRO:HD3	2.02	0.59
1:I:35:ARG:HB3	1:I:313:ARG:NH1	2.17	0.59
1:A:76:LEU:HD12	1:A:92:VAL:HG22	1.85	0.59
1:D:9:ARG:NH2	1:D:12:ARG:NH2	2.51	0.59
1:D:39:VAL:C	1:D:40:GLU:HG3	2.23	0.59
1:E:248:LEU:HD22	1:F:260:THR:HG21	1.84	0.59
2:E:500:NAI:H42N	3:E:550:HP7:H3'	1.85	0.59
2:H:500:NAI:H51N	2:H:500:NAI:C6N	2.33	0.59
1:J:58:ALA:O	1:J:60:PRO:CD	2.47	0.59
1:G:10:LYS:HB3	1:G:36:ALA:HA	1.85	0.59
1:M:25:HIS:O	1:M:29:ILE:HD12	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:LEU:HD21	1:D:76:LEU:CD1	2.33	0.59
1:D:125:ARG:HH11	1:D:125:ARG:CG	2.15	0.59
3:K:550:HP7:H6	3:K:550:HP7:O5C	2.03	0.59
1:L:310:ASN:C	1:L:315:ASP:HB2	2.27	0.59
1:A:81:PRO:HB3	1:A:174:TRP:CD2	2.38	0.59
1:B:23:LYS:HD2	1:B:23:LYS:N	2.17	0.59
1:J:296:VAL:O	1:J:297:TYR:C	2.44	0.59
1:K:39:VAL:O	1:K:40:GLU:HG2	2.03	0.59
1:E:15:LEU:HD12	1:E:16:VAL:O	2.02	0.58
1:F:67:MET:CE	1:F:76:LEU:HD21	2.22	0.58
1:H:28:ALA:HB2	1:H:302:PRO:HD3	1.85	0.58
1:D:47:GLU:HG3	1:D:50:GLN:NE2	2.18	0.58
1:F:11:ILE:HD13	1:F:11:ILE:N	2.17	0.58
1:I:64:LEU:O	1:I:64:LEU:HD22	2.03	0.58
1:J:29:ILE:C	1:J:31:GLN:N	2.59	0.58
1:B:43:ASP:OD1	2:B:500:NAI:O2B	2.16	0.58
1:E:97:ARG:C	1:E:124:VAL:HG11	2.27	0.58
1:J:173:ARG:O	1:J:177:LYS:CE	2.48	0.58
1:C:328:SER:HB3	4:C:373:HOH:O	2.02	0.58
1:G:124:VAL:CG1	1:G:125:ARG:N	2.66	0.58
1:I:310:ASN:N	1:I:310:ASN:ND2	2.48	0.58
1:L:98:HIS:ND1	1:L:125:ARG:HB2	2.19	0.58
1:P:248:LEU:HD12	1:P:248:LEU:O	2.04	0.58
1:D:24:ASN:O	1:D:28:ALA:HB2	2.04	0.58
1:E:137:THR:CG2	1:E:263:VAL:HG11	2.32	0.58
1:F:61:PHE:CD2	1:F:67:MET:HG3	2.38	0.58
1:H:39:VAL:C	1:H:40:GLU:HG3	2.27	0.58
1:L:310:ASN:HB3	1:L:315:ASP:HB3	1.86	0.58
1:H:43:ASP:OD1	2:H:500:NAI:O3B	2.22	0.58
1:H:193:VAL:HG13	1:H:331:LEU:HD13	1.86	0.58
1:K:278:GLU:O	1:K:278:GLU:HG3	2.01	0.58
1:O:130:LYS:HB2	1:O:320:THR:HG21	1.85	0.58
1:E:166:GLN:HE22	1:E:216:ARG:H	1.51	0.58
1:P:9:ARG:HH22	1:P:12:ARG:HH21	1.48	0.58
1:D:98:HIS:HA	1:D:124:VAL:HG12	1.83	0.57
1:I:140:LEU:HD11	1:I:289:ALA:HB2	1.84	0.57
1:K:301:HIS:N	1:K:302:PRO:HD2	2.19	0.57
1:N:40:GLU:C	1:N:41:ILE:CG2	2.77	0.57
1:N:278:GLU:HG2	4:N:503:HOH:O	2.02	0.57
1:C:21:ILE:CD1	2:C:500:NAI:H4N	2.33	0.57
1:H:103:LYS:O	1:H:103:LYS:CD	2.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:188:GLN:HG2	1:O:241:MET:SD	2.44	0.57
1:O:261:VAL:HA	1:O:273:GLU:O	2.04	0.57
1:C:24:ASN:N	1:C:24:ASN:ND2	2.53	0.57
1:H:245:PRO:HD2	1:H:246:GLN:HG2	1.85	0.57
1:J:103:LYS:HD3	1:J:103:LYS:C	2.29	0.57
1:L:340:ARG:HH22	1:N:350:ASP:CG	2.12	0.57
1:N:53:GLU:C	1:N:55:ALA:H	2.10	0.57
1:D:68:LEU:HD21	1:D:76:LEU:HD13	1.86	0.57
1:H:283:ASP:O	1:H:286:ILE:HD12	2.05	0.57
1:J:167:GLU:H	1:J:167:GLU:CD	2.12	0.57
1:K:10:LYS:CD	1:K:34:ASP:O	2.51	0.57
1:L:157:THR:HG22	1:L:236:SER:OG	2.03	0.57
1:O:21:ILE:HD13	2:O:500:NAI:H4N	1.86	0.57
1:B:72:ASN:H	1:B:72:ASN:HD22	1.52	0.57
1:B:98:HIS:HA	1:B:124:VAL:HG12	1.81	0.57
1:B:309:ILE:O	1:B:310:ASN:C	2.48	0.57
1:D:288:GLU:O	1:D:291:TYR:HB2	2.05	0.57
1:H:32:HIS:C	1:H:34:ASP:H	2.10	0.57
1:N:72:ASN:H	1:N:72:ASN:HD22	1.52	0.57
1:C:127:PHE:CE1	1:C:318:PRO:HB3	2.40	0.57
1:K:20:ARG:NH2	3:K:550:HP7:H5C	2.20	0.57
1:D:175:ARG:HG2	1:D:175:ARG:HH21	1.70	0.57
1:H:67:MET:HE3	1:H:76:LEU:HD13	1.86	0.57
1:H:72:ASN:HD22	1:H:72:ASN:N	2.03	0.57
1:H:80:THR:HB	1:H:81:PRO:HD2	1.86	0.57
1:M:206:VAL:HG12	1:M:227:LEU:HD23	1.87	0.57
1:D:108:ARG:NH2	1:D:179:GLU:HG3	2.20	0.57
1:I:10:LYS:CD	1:I:34:ASP:O	2.53	0.57
1:L:267:ALA:O	1:L:268:VAL:HG23	2.04	0.57
1:E:80:THR:HB	1:E:81:PRO:HD2	1.87	0.56
1:H:157:THR:HG22	1:H:236:SER:OG	2.05	0.56
1:N:282:ASP:HA	1:N:285:LYS:HE2	1.87	0.56
1:B:9:ARG:HG3	1:B:9:ARG:HH11	1.70	0.56
1:K:51:ALA:O	1:K:55:ALA:HB2	2.04	0.56
1:M:61:PHE:CD1	1:M:67:MET:HA	2.40	0.56
1:P:68:LEU:HD21	1:P:76:LEU:CD1	2.34	0.56
1:G:26:ILE:HD13	1:G:56:THR:CG2	2.35	0.56
2:K:500:NAI:H51N	2:K:500:NAI:H6N	1.86	0.56
1:L:14:GLY:CA	1:L:67:MET:CE	2.83	0.56
1:M:98:HIS:HA	1:M:124:VAL:HG11	1.85	0.56
1:N:98:HIS:HA	1:N:124:VAL:HG11	1.80	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:133:ARG:HH12	1:N:324:GLU:HG2	1.70	0.56
1:N:157:THR:HG21	4:N:473:HOH:O	2.04	0.56
1:E:15:LEU:HD12	1:E:16:VAL:C	2.31	0.56
1:F:103:LYS:HD3	1:F:103:LYS:C	2.31	0.56
1:G:12:ARG:HB2	1:G:74:ASP:OD2	2.05	0.56
1:J:194:ASP:OD2	4:J:386:HOH:O	2.18	0.56
1:A:297:TYR:HA	4:A:401:HOH:O	2.05	0.56
1:B:72:ASN:HD22	1:B:72:ASN:N	2.04	0.56
1:E:53:GLU:HG3	1:E:54:ALA:N	2.18	0.56
1:G:139:GLN:O	1:G:143:LYS:HG3	2.05	0.56
1:G:134:ARG:HH21	1:G:319:GLU:HG2	1.69	0.56
1:K:184:ALA:HA	1:K:188:GLN:NE2	2.21	0.56
1:P:103:LYS:C	1:P:103:LYS:CD	2.70	0.56
1:L:15:LEU:HD23	1:L:16:VAL:H	1.69	0.56
1:E:15:LEU:HD12	1:E:16:VAL:N	2.21	0.56
1:J:197:ASP:OD1	1:J:327:GLN:HG2	2.06	0.56
1:L:301:HIS:HB2	1:L:302:PRO:HD3	1.87	0.56
1:P:273:GLU:OE2	1:P:275:LYS:HE3	2.06	0.56
1:E:303:LEU:H	1:E:303:LEU:HD12	1.71	0.56
1:G:21:ILE:CD1	2:G:500:NAI:H4N	2.36	0.56
1:N:309:ILE:O	1:N:313:ARG:HG3	2.06	0.56
1:A:109:TRP:NE1	1:A:113:LYS:HE2	2.21	0.55
1:B:244:TYR:CE1	1:B:245:PRO:HB3	2.41	0.55
1:K:39:VAL:CG1	1:K:39:VAL:O	2.54	0.55
1:P:76:LEU:HD12	1:P:92:VAL:HG13	1.89	0.55
1:P:97:ARG:C	1:P:124:VAL:CG1	2.79	0.55
1:C:80:THR:HB	1:C:81:PRO:CD	2.36	0.55
1:G:266:VAL:HG22	4:G:389:HOH:O	2.05	0.55
1:H:288:GLU:CA	1:H:291:TYR:HB2	2.33	0.55
1:N:34:ASP:OD2	1:N:34:ASP:N	2.32	0.55
1:O:40:GLU:OE2	1:O:71:GLY:CA	2.55	0.55
1:A:68:LEU:HD21	1:A:76:LEU:CD1	2.37	0.55
1:B:10:LYS:HE2	1:B:33:GLY:O	2.06	0.55
1:D:166:GLN:HG3	1:D:166:GLN:O	2.06	0.55
1:N:67:MET:HE3	1:N:76:LEU:HD22	1.89	0.55
1:P:154:TYR:OH	1:P:257:GLU:HB2	2.06	0.55
1:H:24:ASN:N	1:H:24:ASN:HD22	2.04	0.55
1:K:39:VAL:C	1:K:40:GLU:HG3	2.31	0.55
1:N:103:LYS:HD3	1:N:103:LYS:C	2.31	0.55
1:O:53:GLU:CG	1:O:60:PRO:HG3	2.27	0.55
1:B:84:LEU:O	1:B:85:HIS:C	2.49	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:SER:CB	4:C:373:HOH:O	2.53	0.55
1:I:31:GLN:CG	1:I:31:GLN:O	2.55	0.55
1:N:39:VAL:O	1:N:58:ALA:CB	2.52	0.55
1:H:103:LYS:C	1:H:103:LYS:CE	2.80	0.55
1:J:40:GLU:OE2	1:J:72:ASN:N	2.35	0.55
1:P:317:GLU:HB3	1:P:318:PRO:HD2	1.89	0.55
1:F:68:LEU:CD1	1:F:91:GLU:HG2	2.36	0.55
1:I:71:GLY:C	1:I:72:ASN:HD22	2.15	0.55
1:P:277:ALA:O	1:P:278:GLU:CG	2.49	0.55
1:B:28:ALA:HB2	1:B:302:PRO:HD3	1.88	0.55
1:B:313:ARG:CG	1:B:313:ARG:NH1	2.46	0.55
2:C:500:NAI:H51N	2:C:500:NAI:C6N	2.37	0.55
1:F:245:PRO:HD2	1:F:246:GLN:H	1.72	0.55
1:H:135:ASN:O	1:H:139:GLN:HG2	2.06	0.55
1:M:15:LEU:HD11	1:M:22:SER:HB2	1.88	0.55
1:N:282:ASP:HA	1:N:285:LYS:CE	2.35	0.55
1:O:42:CYS:O	1:O:43:ASP:HB2	2.07	0.55
1:O:42:CYS:CB	1:O:67:MET:HE1	2.35	0.55
1:P:88:GLN:O	1:P:92:VAL:HG23	2.06	0.55
1:D:318:PRO:O	1:D:319:GLU:C	2.50	0.55
1:E:12:ARG:HG3	1:E:73:ALA:HA	1.89	0.55
1:L:222:THR:HG23	1:L:240:THR:HB	1.88	0.55
1:B:206:VAL:HG12	1:B:227:LEU:HD23	1.89	0.55
1:J:285:LYS:NZ	1:J:288:GLU:OE1	2.30	0.55
1:L:86:PRO:HA	1:L:115:MET:HG2	1.87	0.55
1:L:246:GLN:O	1:L:247:ASN:O	2.25	0.55
1:L:267:ALA:O	1:L:268:VAL:C	2.50	0.55
1:M:98:HIS:HA	1:M:124:VAL:HG13	1.84	0.55
1:A:157:THR:HG22	1:A:253:THR:HB	1.89	0.54
1:H:280:HIS:ND1	1:H:281:PRO:CD	2.69	0.54
1:K:97:ARG:C	1:K:124:VAL:HG21	2.32	0.54
1:K:301:HIS:N	1:K:302:PRO:CD	2.70	0.54
1:C:15:LEU:HD21	1:C:22:SER:HB2	1.89	0.54
1:E:80:THR:HB	1:E:81:PRO:CD	2.36	0.54
1:E:101:SER:O	1:E:129:VAL:HG23	2.07	0.54
1:E:133:ARG:O	1:E:139:GLN:NE2	2.37	0.54
1:J:156:VAL:O	1:J:235:GLY:HA3	2.07	0.54
1:B:94:GLN:C	1:B:96:GLY:H	2.15	0.54
1:E:10:LYS:HE2	1:E:33:GLY:O	2.06	0.54
1:I:310:ASN:H	1:I:310:ASN:ND2	2.02	0.54
1:P:35:ARG:NH2	1:P:310:ASN:OD1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:38:LEU:HD21	1:E:41:ILE:HG23	1.89	0.54
1:F:149:ARG:O	1:F:258:LYS:HG3	2.07	0.54
1:L:46:PRO:O	1:L:49:LEU:HB3	2.07	0.54
1:L:76:LEU:N	1:L:76:LEU:CD2	2.69	0.54
1:M:82:SER:HA	1:M:85:HIS:CE1	2.43	0.54
1:N:59:ARG:HH11	1:N:59:ARG:CG	2.19	0.54
1:N:331:LEU:HD23	1:N:347:LEU:HD11	1.90	0.54
1:C:318:PRO:HG2	1:C:321:ASP:HB3	1.89	0.54
1:G:124:VAL:HG12	1:G:125:ARG:N	2.23	0.54
4:I:362:HOH:O	1:J:157:THR:HG21	2.06	0.54
1:E:214:ALA:HB3	1:E:242:LEU:HD22	1.89	0.54
1:P:271:ILE:O	1:P:271:ILE:HG22	2.08	0.54
1:P:271:ILE:HD13	1:P:274:TRP:CE3	2.43	0.54
1:D:46:PRO:O	1:D:50:GLN:HG3	2.08	0.54
1:D:90:ILE:CD1	1:D:114:ARG:HG2	2.38	0.54
1:F:310:ASN:HB3	1:F:316:CYS:SG	2.48	0.54
1:M:203:VAL:HG21	1:M:331:LEU:HD11	1.89	0.54
1:I:224:VAL:HG21	1:J:235:GLY:CA	2.37	0.54
1:K:24:ASN:HD22	1:K:24:ASN:H	1.56	0.54
1:L:300:GLY:O	1:L:303:LEU:HB2	2.07	0.54
1:F:98:HIS:ND1	1:F:125:ARG:HB2	2.23	0.53
1:G:68:LEU:HD21	1:G:76:LEU:CD1	2.36	0.53
1:G:68:LEU:CD2	1:G:76:LEU:HD11	2.39	0.53
1:I:155:MET:HE1	1:J:224:VAL:CG2	2.39	0.53
1:I:346:PRO:HB2	1:O:340:ARG:HG2	1.90	0.53
1:L:262:ARG:CG	1:L:262:ARG:NH1	2.66	0.53
1:C:173:ARG:O	1:C:177:LYS:HE3	2.08	0.53
1:E:12:ARG:NH2	1:E:72:ASN:HD21	2.06	0.53
1:L:9:ARG:HG3	1:L:10:LYS:H	1.67	0.53
1:E:12:ARG:NH2	1:E:72:ASN:ND2	2.56	0.53
1:H:16:VAL:HG12	1:H:77:VAL:O	2.07	0.53
1:J:94:GLN:C	1:J:96:GLY:H	2.17	0.53
1:C:141:VAL:HG22	1:C:261:VAL:HG11	1.91	0.53
1:D:35:ARG:HB3	1:D:313:ARG:NH1	2.24	0.53
1:N:124:VAL:HG12	1:N:125:ARG:N	2.21	0.53
1:N:301:HIS:N	1:N:302:PRO:CD	2.72	0.53
1:P:53:GLU:HG3	1:P:54:ALA:N	2.23	0.53
1:E:12:ARG:HH22	1:E:72:ASN:HD21	1.55	0.53
1:E:175:ARG:HG2	1:E:175:ARG:NH2	2.23	0.53
1:B:167:GLU:H	1:B:167:GLU:CD	2.13	0.53
1:L:43:ASP:OD2	2:L:500:NAI:O3B	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:117:LYS:C	1:P:117:LYS:HD2	2.33	0.53
1:E:272:ASP:O	1:E:273:GLU:HB2	2.09	0.53
1:I:313:ARG:C	1:I:315:ASP:H	2.16	0.53
1:K:307:ASN:ND2	1:K:307:ASN:O	2.42	0.53
1:M:102:GLU:HG3	2:M:500:NAI:O4D	2.09	0.53
1:P:317:GLU:HB3	1:P:318:PRO:CD	2.39	0.53
1:B:11:ILE:HB	1:B:36:ALA:HB2	1.91	0.53
1:B:66:ASP:O	1:B:70:GLN:HG3	2.09	0.53
1:E:228:ARG:HD3	4:E:358:HOH:O	2.08	0.53
1:K:344:ARG:HD3	1:L:207:TYR:OH	2.08	0.53
1:M:125:ARG:HG2	1:M:127:PHE:CE2	2.44	0.53
1:G:157:THR:HG21	4:H:375:HOH:O	2.07	0.53
4:L:454:HOH:O	1:N:231:HIS:HB3	2.08	0.53
1:M:103:LYS:C	1:M:103:LYS:HE2	2.34	0.53
1:O:39:VAL:HG12	1:O:40:GLU:CG	2.14	0.53
1:B:313:ARG:HH11	1:B:313:ARG:HG3	1.69	0.52
1:J:20:ARG:NH2	3:J:550:HP7:O2A	2.40	0.52
1:N:98:HIS:CA	1:N:124:VAL:HG13	2.39	0.52
1:G:97:ARG:O	1:G:124:VAL:HG11	2.09	0.52
1:K:29:ILE:C	1:K:31:GLN:H	2.17	0.52
1:N:98:HIS:HA	1:N:124:VAL:HG13	1.82	0.52
1:O:81:PRO:HD2	1:O:84:LEU:HD12	1.90	0.52
1:O:156:VAL:O	1:O:235:GLY:HA3	2.07	0.52
1:A:235:GLY:HA2	1:B:224:VAL:HG21	1.91	0.52
1:B:130:LYS:HG2	1:B:320:THR:HG21	1.90	0.52
1:F:39:VAL:HG12	1:F:40:GLU:HG3	1.90	0.52
1:H:133:ARG:HD3	1:H:198:TRP:CE2	2.43	0.52
1:I:21:ILE:CG2	2:I:500:NAI:H52N	2.39	0.52
1:I:204:GLU:O	1:I:204:GLU:HG2	2.07	0.52
1:L:134:ARG:O	1:L:135:ASN:C	2.51	0.52
1:O:45:ASN:C	1:O:45:ASN:OD1	2.52	0.52
1:D:197:ASP:OD1	1:D:327:GLN:CG	2.56	0.52
1:G:129:VAL:HG22	1:G:304:TYR:CE1	2.45	0.52
1:O:80:THR:HB	1:O:81:PRO:CD	2.38	0.52
1:D:98:HIS:ND1	1:D:124:VAL:HG13	2.24	0.52
1:H:68:LEU:CD1	1:H:91:GLU:HG2	2.40	0.52
1:L:108:ARG:NH1	1:L:108:ARG:HG3	2.24	0.52
1:D:130:LYS:HB2	1:D:320:THR:HG21	1.91	0.52
1:L:10:LYS:O	1:L:12:ARG:HG3	2.10	0.52
1:O:98:HIS:CD2	1:O:312:LEU:HD22	2.45	0.52
1:A:15:LEU:HD21	1:A:22:SER:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:ARG:HB3	1:B:303:LEU:HD13	1.92	0.52
1:L:20:ARG:HH11	1:L:20:ARG:CG	2.21	0.52
1:M:34:ASP:OD1	1:M:35:ARG:HG3	2.09	0.52
1:N:301:HIS:N	1:N:302:PRO:HD2	2.25	0.52
1:E:187:ASN:OD1	3:E:550:HP7:O4'	2.22	0.52
1:G:53:GLU:HG3	1:G:60:PRO:HB3	1.91	0.52
1:G:277:ALA:HA	1:H:244:TYR:OH	2.10	0.52
1:H:35:ARG:HG2	1:H:313:ARG:HH12	1.71	0.52
1:H:127:PHE:HE1	1:H:318:PRO:HB3	1.72	0.52
1:J:75:ALA:C	1:J:76:LEU:CD2	2.75	0.52
1:K:103:LYS:O	1:K:103:LYS:CD	2.46	0.52
1:O:72:ASN:HD22	1:O:72:ASN:C	2.16	0.52
1:A:110:GLU:CG	4:A:363:HOH:O	2.55	0.52
1:E:40:GLU:OE1	1:E:73:ALA:HB2	2.09	0.52
1:G:59:ARG:HG2	1:G:60:PRO:HD2	1.91	0.52
1:J:73:ALA:HB3	1:J:76:LEU:HD21	1.91	0.52
1:J:127:PHE:CE1	1:J:318:PRO:HB3	2.45	0.52
1:K:9:ARG:NH1	1:K:9:ARG:CG	2.51	0.52
1:A:72:ASN:HD22	1:A:72:ASN:H	1.57	0.52
1:I:220:GLU:O	1:I:220:GLU:HG2	2.09	0.52
1:J:21:ILE:HD13	2:J:500:NAI:H4N	1.92	0.52
1:O:6:ILE:HG21	1:O:11:ILE:CD1	2.37	0.52
1:B:53:GLU:O	1:B:57:GLY:N	2.31	0.51
1:B:246:GLN:O	1:B:247:ASN:C	2.51	0.51
1:K:20:ARG:HH22	3:K:550:HP7:H5C	1.73	0.51
1:A:76:LEU:CD1	1:A:92:VAL:HG22	2.40	0.51
1:B:39:VAL:O	1:B:58:ALA:HB1	2.10	0.51
1:G:50:GLN:O	1:G:53:GLU:HB2	2.10	0.51
1:H:16:VAL:HG12	1:H:78:LEU:HA	1.92	0.51
1:H:280:HIS:CG	1:H:281:PRO:HD2	2.45	0.51
1:N:59:ARG:NH1	1:N:59:ARG:CG	2.72	0.51
1:P:312:LEU:C	1:P:314:GLY:H	2.17	0.51
1:A:134:ARG:O	1:A:135:ASN:C	2.53	0.51
1:E:184:ALA:HA	1:E:188:GLN:OE1	2.10	0.51
1:I:64:LEU:HA	1:I:67:MET:HE2	1.92	0.51
1:K:46:PRO:O	1:K:47:GLU:C	2.49	0.51
1:L:267:ALA:C	1:L:268:VAL:CG2	2.83	0.51
1:B:109:TRP:NE1	1:B:113:LYS:HE2	2.26	0.51
1:D:318:PRO:O	1:D:320:THR:N	2.44	0.51
2:G:500:NAI:C4N	3:G:550:HP7:H3'	2.40	0.51
1:H:86:PRO:HA	1:H:115:MET:CG	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:10:LYS:HD3	1:I:34:ASP:O	2.11	0.51
1:J:127:PHE:CD1	1:J:318:PRO:HB3	2.45	0.51
1:J:145:ILE:HG22	1:J:146:GLU:N	2.24	0.51
1:M:85:HIS:N	1:M:86:PRO:CD	2.74	0.51
1:N:72:ASN:HD22	1:N:72:ASN:N	2.08	0.51
1:N:282:ASP:OD1	1:N:285:LYS:CE	2.53	0.51
1:P:117:LYS:HD2	1:P:118:ALA:N	2.26	0.51
1:D:59:ARG:HG2	1:D:60:PRO:CD	2.41	0.51
1:F:10:LYS:CE	1:F:34:ASP:O	2.59	0.51
1:F:86:PRO:HB3	1:F:115:MET:HG3	1.92	0.51
1:H:20:ARG:NH2	3:H:550:HP7:O2A	2.43	0.51
1:F:80:THR:HB	1:F:81:PRO:HD2	1.91	0.51
1:O:137:THR:OG1	1:O:138:LEU:N	2.44	0.51
1:A:112:GLY:O	1:A:115:MET:HG2	2.11	0.51
1:B:307:ASN:ND2	1:B:307:ASN:O	2.43	0.51
1:I:64:LEU:CD2	1:I:67:MET:HE3	2.34	0.51
1:J:154:TYR:OH	1:J:257:GLU:HB2	2.11	0.51
1:M:261:VAL:HG12	1:M:262:ARG:N	2.26	0.51
1:O:117:LYS:HG2	1:O:121:GLU:OE2	2.11	0.51
1:O:282:ASP:OD1	1:O:285:LYS:NZ	2.40	0.51
1:A:197:ASP:HB3	4:A:385:HOH:O	2.10	0.51
1:C:42:CYS:HA	1:C:61:PHE:O	2.11	0.51
1:C:127:PHE:CD1	1:C:318:PRO:HB3	2.46	0.51
1:D:103:LYS:HD2	2:D:500:NAI:H2N	1.92	0.51
1:E:9:ARG:HH12	1:E:12:ARG:HD2	1.75	0.51
1:F:103:LYS:C	1:F:103:LYS:CD	2.84	0.51
1:N:255:LEU:CD2	1:N:260:THR:HG23	2.41	0.51
1:O:6:ILE:HB	1:O:11:ILE:HD11	1.91	0.51
1:D:98:HIS:CA	1:D:124:VAL:CG1	2.76	0.51
1:F:245:PRO:CD	1:F:246:GLN:H	2.24	0.51
1:K:13:PHE:O	1:K:38:LEU:HD12	2.11	0.51
1:L:15:LEU:CD2	1:L:16:VAL:N	2.74	0.51
1:L:124:VAL:CG1	1:L:125:ARG:N	2.73	0.51
1:M:72:ASN:HD22	1:M:72:ASN:N	1.99	0.51
1:N:80:THR:HB	1:N:81:PRO:HD2	1.93	0.51
1:N:102:GLU:OE2	2:N:500:NAI:H2N	2.10	0.51
1:D:103:LYS:HB2	1:D:130:LYS:HZ1	1.75	0.51
1:F:144:ALA:O	1:F:145:ILE:C	2.53	0.51
1:H:116:VAL:HG21	1:H:326:LEU:HD11	1.93	0.51
1:I:97:ARG:C	1:I:124:VAL:HG11	2.35	0.51
1:M:41:ILE:HD11	1:M:53:GLU:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:305:TYR:O	1:N:309:ILE:HG13	2.11	0.51
1:P:64:LEU:HD23	1:P:91:GLU:OE2	2.11	0.51
1:P:324:GLU:OE2	1:P:324:GLU:HA	2.10	0.51
1:E:197:ASP:HA	1:E:201:GLY:O	2.11	0.50
1:K:9:ARG:CG	1:K:10:LYS:N	2.73	0.50
1:N:16:VAL:CG2	1:N:67:MET:HE1	2.38	0.50
1:N:186:MET:O	1:N:190:SER:HB3	2.11	0.50
1:P:21:ILE:CG2	2:P:500:NAI:C5D	2.89	0.50
1:I:12:ARG:HH21	1:I:39:VAL:HG21	1.76	0.50
1:I:64:LEU:HD22	1:I:68:LEU:HG	1.93	0.50
1:I:98:HIS:CA	1:I:124:VAL:CG1	2.79	0.50
1:J:85:HIS:N	1:J:86:PRO:CD	2.75	0.50
1:C:86:PRO:O	1:C:90:ILE:HG13	2.11	0.50
1:K:184:ALA:HA	1:K:188:GLN:HE21	1.75	0.50
1:L:15:LEU:HD23	1:L:16:VAL:N	2.27	0.50
1:N:20:ARG:HG2	1:N:20:ARG:HH11	1.76	0.50
1:A:24:ASN:N	1:A:24:ASN:HD22	2.09	0.50
1:L:277:ALA:O	1:L:278:GLU:HG2	2.11	0.50
1:L:313:ARG:O	1:L:315:ASP:N	2.45	0.50
1:M:11:ILE:N	1:M:35:ARG:O	2.34	0.50
1:O:281:PRO:O	1:O:282:ASP:CB	2.46	0.50
1:F:323:ARG:O	1:F:326:LEU:HB2	2.12	0.50
1:K:103:LYS:HE2	1:K:190:SER:OG	2.11	0.50
1:L:92:VAL:HG11	1:L:99:VAL:HG22	1.94	0.50
1:M:294:THR:HG22	1:M:294:THR:O	2.10	0.50
1:M:310:ASN:HB3	1:M:315:ASP:HB2	1.94	0.50
1:A:98:HIS:ND1	1:A:125:ARG:HB2	2.26	0.50
1:B:99:VAL:O	1:B:126:LEU:HA	2.12	0.50
1:B:197:ASP:OD1	1:B:327:GLN:HG2	2.12	0.50
1:F:9:ARG:NH1	1:F:12:ARG:HE	2.09	0.50
1:H:53:GLU:HG3	1:H:54:ALA:H	1.76	0.50
1:I:280:HIS:O	1:I:281:PRO:C	2.55	0.50
1:K:98:HIS:HA	1:K:124:VAL:HG22	1.94	0.50
1:K:306:ASP:OD1	1:K:306:ASP:C	2.55	0.50
1:N:40:GLU:O	1:N:41:ILE:CG2	2.60	0.50
1:N:73:ALA:O	1:N:97:ARG:NE	2.37	0.50
1:N:262:ARG:HB3	1:N:273:GLU:HB2	1.93	0.50
1:B:41:ILE:HG13	1:B:49:LEU:HD12	1.92	0.50
1:H:310:ASN:O	1:H:315:ASP:HB2	2.12	0.50
1:I:103:LYS:HD2	2:I:500:NAI:H2N	1.94	0.50
1:J:52:ALA:O	1:J:56:THR:OG1	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:14:GLY:HA3	1:N:76:LEU:CD2	2.40	0.50
1:O:40:GLU:OE2	1:O:72:ASN:N	2.44	0.50
1:E:318:PRO:HG2	1:E:321:ASP:HB3	1.94	0.50
1:F:245:PRO:CD	1:F:246:GLN:N	2.73	0.50
1:G:61:PHE:CE2	1:G:67:MET:HG3	2.46	0.50
1:N:12:ARG:HB3	1:N:39:VAL:CG2	2.42	0.50
1:D:72:ASN:C	1:D:72:ASN:HD22	2.20	0.50
1:D:125:ARG:NH1	1:D:311:CYS:SG	2.84	0.50
1:G:282:ASP:C	1:G:284:ASP:N	2.69	0.50
1:N:321:ASP:C	1:N:321:ASP:OD2	2.54	0.50
1:B:85:HIS:CE1	2:B:500:NAI:O3D	2.64	0.49
1:B:167:GLU:OE2	1:B:167:GLU:N	2.33	0.49
1:G:273:GLU:HG3	1:G:275:LYS:HE3	1.94	0.49
1:M:197:ASP:HA	1:M:201:GLY:O	2.12	0.49
1:H:135:ASN:CB	1:H:293:THR:HG23	2.42	0.49
1:B:64:LEU:HD12	1:B:64:LEU:O	2.13	0.49
1:M:156:VAL:O	1:M:235:GLY:HA2	2.12	0.49
1:A:72:ASN:HD22	1:A:72:ASN:N	2.10	0.49
1:D:26:ILE:HG22	1:D:27:GLY:H	1.75	0.49
1:P:307:ASN:O	1:P:308:VAL:C	2.54	0.49
1:J:263:VAL:HG12	1:J:268:VAL:HA	1.93	0.49
1:L:40:GLU:CD	1:L:71:GLY:HA3	2.38	0.49
1:B:32:HIS:HE1	1:B:306:ASP:HB2	1.77	0.49
1:G:323:ARG:CG	1:G:323:ARG:HH11	2.25	0.49
1:H:163:THR:OG1	1:H:246:GLN:HA	2.12	0.49
1:J:43:ASP:OD2	2:J:500:NAI:O3B	2.20	0.49
1:F:49:LEU:HD21	1:F:60:PRO:HB2	1.94	0.49
1:F:130:LYS:HG2	1:F:320:THR:HG21	1.94	0.49
1:H:10:LYS:HE2	1:H:34:ASP:HA	1.93	0.49
1:L:313:ARG:C	1:L:315:ASP:N	2.70	0.49
1:N:331:LEU:CD2	1:N:347:LEU:HD11	2.42	0.49
1:B:262:ARG:HD3	4:B:379:HOH:O	2.13	0.49
1:C:85:HIS:N	1:C:86:PRO:CD	2.75	0.49
1:L:53:GLU:OE2	1:L:60:PRO:HG3	2.13	0.49
1:N:280:HIS:CD2	1:N:281:PRO:HD2	2.48	0.49
1:P:12:ARG:N	1:P:74:ASP:OD2	2.39	0.49
1:P:74:ASP:O	1:P:97:ARG:HB3	2.12	0.49
1:B:10:LYS:HB3	1:B:36:ALA:HA	1.95	0.49
1:B:215:ARG:HG2	1:B:242:LEU:HD21	1.95	0.49
1:I:98:HIS:HA	1:I:124:VAL:HG12	1.88	0.49
1:L:103:LYS:HD3	1:L:103:LYS:C	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:184:ALA:HA	1:H:188:GLN:NE2	2.28	0.49
1:I:102:GLU:OE2	2:I:500:NAI:H2N	2.13	0.49
1:J:7:THR:HG22	1:J:313:ARG:O	2.12	0.49
1:P:125:ARG:HG2	1:P:127:PHE:CZ	2.48	0.49
1:B:322:GLY:O	1:B:325:GLY:N	2.46	0.48
1:G:167:GLU:H	1:G:167:GLU:CD	2.21	0.48
1:P:98:HIS:ND1	1:P:125:ARG:HB2	2.28	0.48
1:E:137:THR:CG2	1:E:138:LEU:N	2.42	0.48
1:E:252:ILE:HG22	1:E:263:VAL:HB	1.95	0.48
1:H:287:ARG:HH11	1:H:287:ARG:HB3	1.78	0.48
1:L:26:ILE:O	1:L:27:GLY:C	2.56	0.48
1:P:310:ASN:HB3	1:P:316:CYS:SG	2.52	0.48
1:D:9:ARG:NE	1:D:12:ARG:NH2	2.61	0.48
1:D:10:LYS:HE2	1:D:33:GLY:O	2.13	0.48
1:E:19:GLY:O	1:E:22:SER:OG	2.31	0.48
1:K:307:ASN:C	1:K:307:ASN:HD22	2.20	0.48
1:M:344:ARG:HD3	1:N:207:TYR:OH	2.12	0.48
1:O:309:ILE:O	1:O:313:ARG:HG3	2.12	0.48
1:P:165:PRO:HD3	3:P:550:HP7:O2	2.13	0.48
1:P:327:GLN:HA	1:P:327:GLN:HE21	1.78	0.48
1:E:35:ARG:O	1:E:36:ALA:CB	2.62	0.48
1:H:103:LYS:O	1:H:103:LYS:HE2	2.13	0.48
1:H:186:MET:O	1:H:190:SER:HB3	2.13	0.48
1:J:222:THR:HG23	1:J:240:THR:HB	1.95	0.48
1:K:76:LEU:HD12	1:K:92:VAL:HG13	1.96	0.48
1:O:86:PRO:HA	1:O:115:MET:CG	2.43	0.48
1:C:153:ILE:O	1:C:233:ALA:HB2	2.14	0.48
1:E:85:HIS:N	1:E:86:PRO:HD2	2.28	0.48
1:E:103:LYS:O	1:E:103:LYS:CD	2.41	0.48
1:I:267:ALA:O	1:I:268:VAL:C	2.56	0.48
2:J:500:NAI:H6N	2:J:500:NAI:C5D	2.14	0.48
1:O:347:LEU:HB3	1:O:348:PRO:HA	1.95	0.48
1:P:34:ASP:OD2	1:P:34:ASP:N	2.46	0.48
1:B:64:LEU:CD1	1:B:68:LEU:HD11	2.43	0.48
1:C:43:ASP:OD1	1:C:44:THR:N	2.47	0.48
1:H:135:ASN:HB3	1:H:293:THR:CG2	2.44	0.48
1:H:192:TYR:HA	1:H:195:LEU:HG	1.95	0.48
1:I:98:HIS:CA	1:I:124:VAL:HG13	2.44	0.48
1:K:331:LEU:HD23	1:K:347:LEU:HD11	1.96	0.48
1:N:117:LYS:O	1:N:120:ASP:HB2	2.13	0.48
1:C:86:PRO:HG3	1:C:106:ALA:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:226:ALA:C	1:E:227:LEU:HG	2.39	0.48
2:E:500:NAI:H6N	2:E:500:NAI:H51N	1.95	0.48
1:F:87:TRP:CD1	1:F:87:TRP:H	2.32	0.48
1:G:138:LEU:HD11	1:G:268:VAL:HG21	1.96	0.48
1:H:21:ILE:CD1	2:H:500:NAI:H4N	2.44	0.48
1:A:282:ASP:C	1:A:284:ASP:H	2.21	0.48
1:B:125:ARG:NH2	1:B:317:GLU:OE1	2.46	0.48
1:E:150:PHE:CZ	1:E:261:VAL:HG23	2.49	0.48
1:E:277:ALA:O	1:E:278:GLU:CG	2.61	0.48
1:I:140:LEU:HD11	1:I:289:ALA:CB	2.44	0.48
1:I:263:VAL:HG12	1:I:268:VAL:HA	1.96	0.48
1:J:39:VAL:C	1:J:40:GLU:HG3	2.38	0.48
1:L:14:GLY:CA	1:L:67:MET:HE1	2.43	0.48
1:L:66:ASP:C	1:L:68:LEU:N	2.70	0.48
1:M:178:TRP:CZ2	1:M:219:ALA:HA	2.49	0.48
1:M:249:GLU:OE1	1:M:251:SER:OG	2.20	0.48
1:P:98:HIS:HA	1:P:124:VAL:HG11	1.90	0.48
1:C:134:ARG:NH2	1:C:319:GLU:OE2	2.47	0.48
1:C:333:THR:HG23	4:C:363:HOH:O	2.13	0.48
1:E:33:GLY:O	1:E:34:ASP:C	2.56	0.48
1:F:12:ARG:NH1	1:F:72:ASN:OD1	2.41	0.48
1:G:321:ASP:OD2	1:G:321:ASP:C	2.55	0.48
1:H:86:PRO:HB3	1:H:115:MET:HG3	1.96	0.48
1:J:139:GLN:O	1:J:143:LYS:HG3	2.13	0.48
1:J:338:SER:HB2	1:J:345:ILE:HG12	1.96	0.48
1:L:184:ALA:HA	1:L:188:GLN:HE22	1.73	0.48
1:M:97:ARG:C	1:M:124:VAL:HG11	2.38	0.48
1:N:21:ILE:HD12	1:N:21:ILE:HA	1.67	0.48
1:C:320:THR:HG23	1:C:324:GLU:HB3	1.96	0.48
1:E:41:ILE:HD11	1:E:53:GLU:HA	1.95	0.48
1:E:53:GLU:O	1:E:57:GLY:HA2	2.13	0.48
1:E:347:LEU:HB3	1:E:348:PRO:HA	1.96	0.48
1:F:184:ALA:HA	1:F:188:GLN:HE22	1.79	0.48
1:F:275:LYS:C	1:F:276:PHE:CD2	2.91	0.48
1:P:278:GLU:HA	1:P:279:PRO:HD2	1.55	0.48
1:P:318:PRO:HG2	1:P:321:ASP:HB3	1.96	0.48
1:B:135:ASN:H	1:B:135:ASN:ND2	2.11	0.47
1:D:287:ARG:CZ	1:M:24:ASN:OD1	2.60	0.47
1:E:149:ARG:HB3	1:E:276:PHE:CD1	2.49	0.47
1:H:246:GLN:O	1:H:247:ASN:C	2.56	0.47
1:I:30:ALA:O	1:I:32:HIS:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:117:LYS:O	1:I:120:ASP:HB2	2.13	0.47
1:K:9:ARG:HG3	1:K:10:LYS:H	1.78	0.47
1:O:82:SER:HA	1:O:85:HIS:CE1	2.49	0.47
1:E:21:ILE:CG2	2:E:500:NAI:H52N	2.44	0.47
1:F:124:VAL:CG1	1:F:125:ARG:N	2.77	0.47
1:H:327:GLN:NE2	1:H:327:GLN:CA	2.53	0.47
1:J:136:ALA:HB3	1:J:293:THR:OG1	2.13	0.47
1:J:213:LEU:HA	1:J:213:LEU:HD23	1.66	0.47
1:K:103:LYS:HA	1:K:104:PRO:C	2.39	0.47
1:P:68:LEU:HD21	1:P:76:LEU:HD11	1.96	0.47
1:B:14:GLY:HA3	1:B:67:MET:CE	2.45	0.47
1:H:282:ASP:HA	1:H:285:LYS:HD3	1.96	0.47
1:J:187:ASN:C	1:J:187:ASN:OD1	2.56	0.47
1:L:310:ASN:O	1:L:311:CYS:C	2.56	0.47
1:M:50:GLN:O	1:M:51:ALA:C	2.58	0.47
1:N:53:GLU:C	1:N:55:ALA:N	2.72	0.47
1:O:12:ARG:O	1:O:74:ASP:N	2.42	0.47
1:P:77:VAL:HG21	1:P:305:TYR:OH	2.14	0.47
1:A:75:ALA:HB2	1:A:98:HIS:HB2	1.97	0.47
1:F:156:VAL:HA	1:F:253:THR:O	2.15	0.47
1:L:15:LEU:H	1:L:67:MET:HE1	1.78	0.47
1:L:86:PRO:HG3	1:L:106:ALA:CB	2.44	0.47
1:N:269:ASN:HA	1:N:293:THR:HG21	1.96	0.47
1:E:214:ALA:HB3	1:E:242:LEU:CD2	2.45	0.47
1:I:269:ASN:HA	1:I:293:THR:CG2	2.42	0.47
1:L:59:ARG:HH12	1:L:70:GLN:CG	2.28	0.47
1:O:6:ILE:O	1:O:6:ILE:HG22	2.14	0.47
1:O:86:PRO:O	1:O:90:ILE:HD12	2.15	0.47
1:F:34:ASP:OD2	1:F:34:ASP:N	2.48	0.47
1:H:103:LYS:O	1:H:103:LYS:CE	2.62	0.47
1:J:59:ARG:HA	1:J:60:PRO:HD2	1.64	0.47
1:J:109:TRP:CE2	1:J:113:LYS:HE2	2.48	0.47
1:K:39:VAL:O	1:K:39:VAL:HG13	2.13	0.47
1:N:70:GLN:HE21	1:N:70:GLN:HB3	1.43	0.47
2:O:500:NAI:H42N	3:O:550:HP7:H3'	1.96	0.47
1:A:20:ARG:NH2	3:A:550:HP7:O2A	2.43	0.47
1:A:347:LEU:HB3	1:A:348:PRO:HA	1.96	0.47
1:E:12:ARG:HB2	1:E:39:VAL:HG21	1.96	0.47
1:E:109:TRP:CZ3	1:E:330:ALA:HB2	2.50	0.47
1:E:167:GLU:HA	1:E:170:ASP:HB2	1.96	0.47
1:E:304:TYR:O	1:E:308:VAL:CG2	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:103:LYS:HD3	1:G:103:LYS:C	2.40	0.47
1:G:244:TYR:CE1	1:G:245:PRO:HB3	2.50	0.47
1:P:117:LYS:C	1:P:117:LYS:HD3	2.39	0.47
1:B:310:ASN:CB	1:B:316:CYS:SG	2.96	0.47
1:H:347:LEU:HD23	1:H:347:LEU:HA	1.68	0.47
1:L:72:ASN:HA	1:L:97:ARG:NH1	2.29	0.47
1:M:237:ILE:HG23	1:M:237:ILE:O	2.13	0.47
1:A:139:GLN:O	1:A:143:LYS:HG3	2.15	0.47
1:D:21:ILE:HG22	2:D:500:NAI:H52N	1.97	0.47
1:D:125:ARG:CG	1:D:125:ARG:NH1	2.75	0.47
1:D:246:GLN:O	1:D:247:ASN:C	2.58	0.47
1:H:267:ALA:O	1:H:268:VAL:C	2.58	0.47
1:I:346:PRO:HG2	1:O:340:ARG:HD3	1.95	0.47
1:J:67:MET:HE3	1:J:76:LEU:CD1	2.45	0.47
1:M:109:TRP:CZ3	1:M:326:LEU:HD22	2.50	0.47
1:M:117:LYS:NZ	1:P:87:TRP:CZ2	2.76	0.47
1:B:280[B]:HIS:CD2	1:B:281:PRO:CD	2.93	0.47
1:D:117:LYS:HE2	1:D:117:LYS:HB3	1.35	0.47
1:D:327:GLN:HE21	1:D:327:GLN:HA	1.80	0.47
1:G:145:ILE:HD13	1:G:199:LEU:O	2.14	0.47
1:I:273:GLU:OE2	1:I:275:LYS:HE3	2.14	0.47
1:L:41:ILE:HD11	1:L:53:GLU:HA	1.97	0.47
1:N:28:ALA:O	1:N:32:HIS:HD2	1.98	0.47
1:C:72:ASN:HD22	1:C:72:ASN:H	1.63	0.46
1:D:12:ARG:HG2	1:D:39:VAL:HG21	1.97	0.46
1:H:298:GLY:C	1:H:299:PHE:CD2	2.93	0.46
1:J:130:LYS:HG2	1:J:320:THR:HG21	1.96	0.46
1:K:278:GLU:HA	1:K:279:PRO:HD3	1.63	0.46
1:N:124:VAL:CG1	1:N:125:ARG:N	2.77	0.46
1:N:296:VAL:O	1:N:296:VAL:HG23	2.14	0.46
1:A:273:GLU:HG2	1:B:248:LEU:HD11	1.97	0.46
1:A:280:HIS:CG	1:A:281:PRO:HD2	2.50	0.46
1:E:103:LYS:HD2	2:E:500:NAI:C2N	2.46	0.46
1:F:149:ARG:HB3	1:F:276:PHE:CD1	2.50	0.46
1:G:274:TRP:CG	1:G:286:ILE:HD11	2.50	0.46
1:H:133:ARG:NH1	1:H:198:TRP:CD1	2.83	0.46
1:J:155:MET:HE2	1:J:155:MET:HB2	1.70	0.46
1:K:39:VAL:HG12	1:K:40:GLU:CD	2.31	0.46
1:O:137:THR:O	1:O:140:LEU:HB2	2.14	0.46
1:B:12:ARG:HE	1:B:12:ARG:HB2	1.47	0.46
1:E:15:LEU:CD1	1:E:17:GLY:O	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:280:HIS:ND1	1:G:281:PRO:HD2	2.30	0.46
1:I:206:VAL:HG12	1:I:227:LEU:HD23	1.97	0.46
1:N:283:ASP:O	1:N:286:ILE:HD12	2.16	0.46
1:B:134:ARG:CB	1:B:303:LEU:HD13	2.45	0.46
1:B:307:ASN:CG	1:B:319:GLU:H	2.24	0.46
1:C:125:ARG:HG2	1:C:127:PHE:CZ	2.51	0.46
1:C:230:ARG:HD3	4:G:357:HOH:O	2.14	0.46
1:D:137:THR:CG2	1:D:293:THR:HG21	2.46	0.46
1:E:49:LEU:HD21	1:E:61:PHE:C	2.41	0.46
1:G:40:GLU:OE2	1:G:72:ASN:N	2.47	0.46
1:G:347:LEU:HB3	1:G:348:PRO:HA	1.98	0.46
1:H:29:ILE:HG22	1:H:30:ALA:N	2.30	0.46
1:H:220:GLU:OE1	1:H:220:GLU:N	2.42	0.46
1:L:309:ILE:O	1:L:312:LEU:N	2.48	0.46
1:M:283:ASP:O	1:M:286:ILE:HD12	2.16	0.46
1:N:28:ALA:HB1	1:N:302:PRO:HA	1.97	0.46
1:C:133:ARG:HH12	1:C:324:GLU:HG3	1.80	0.46
1:F:258:LYS:HB2	1:F:277:ALA:HB2	1.98	0.46
1:H:80:THR:HB	1:H:81:PRO:CD	2.45	0.46
1:I:21:ILE:HG21	2:I:500:NAI:H52N	1.97	0.46
1:M:15:LEU:C	1:M:15:LEU:CD2	2.86	0.46
1:D:267:ALA:C	1:D:268:VAL:HG22	2.41	0.46
1:H:142:LYS:HE2	1:H:198:TRP:CE2	2.50	0.46
1:K:67:MET:HE3	1:K:76:LEU:HD22	1.98	0.46
1:L:39:VAL:HG12	1:L:40:GLU:HG3	1.97	0.46
1:L:74:ASP:OD2	1:L:74:ASP:N	2.48	0.46
1:N:197:ASP:OD1	1:N:327:GLN:HG2	2.16	0.46
1:B:192:TYR:O	1:B:193:VAL:C	2.56	0.46
1:E:137:THR:O	1:E:138:LEU:C	2.58	0.46
1:F:76:LEU:N	1:F:76:LEU:HD12	2.31	0.46
1:I:145:ILE:HD13	1:I:199:LEU:O	2.16	0.46
1:J:61:PHE:CD1	1:J:67:MET:HA	2.51	0.46
1:K:53:GLU:C	1:K:55:ALA:H	2.23	0.46
1:B:9:ARG:HG3	1:B:9:ARG:NH1	2.31	0.46
1:C:271:ILE:H	1:C:290:ASN:ND2	2.14	0.46
1:D:287:ARG:HE	1:M:298:GLY:HA2	1.81	0.46
1:E:192:TYR:CD2	1:E:192:TYR:N	2.84	0.46
1:J:38:LEU:HD23	1:J:56:THR:HG21	1.98	0.46
1:J:309:ILE:O	1:J:310:ASN:C	2.55	0.46
1:K:86:PRO:O	1:K:90:ILE:HG13	2.16	0.46
1:M:72:ASN:O	1:M:73:ALA:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:134:ARG:O	1:N:135:ASN:C	2.58	0.46
1:O:267:ALA:C	1:O:268:VAL:CG2	2.87	0.46
1:A:20:ARG:O	1:A:23:LYS:CE	2.61	0.46
1:D:285:LYS:NZ	1:D:285:LYS:HB3	2.30	0.46
1:E:262:ARG:HB3	1:E:273:GLU:HB3	1.98	0.46
1:H:168:TYR:C	1:H:168:TYR:CD2	2.93	0.46
1:H:297:TYR:CD2	1:H:297:TYR:O	2.69	0.46
1:H:301:HIS:O	1:H:302:PRO:C	2.57	0.46
1:O:206:VAL:CG1	1:O:227:LEU:HD23	2.39	0.46
1:B:197:ASP:CG	1:B:327:GLN:HG2	2.41	0.46
1:E:90:ILE:CD1	1:E:114:ARG:HD3	2.46	0.46
1:H:132:ASN:HB2	4:H:380:HOH:O	2.15	0.46
1:J:267:ALA:O	1:J:268:VAL:C	2.58	0.46
1:K:52:ALA:O	1:K:56:THR:HG23	2.16	0.46
1:K:67:MET:HE3	1:K:76:LEU:CD2	2.46	0.46
1:C:246:GLN:O	1:C:247:ASN:C	2.59	0.45
1:F:103:LYS:HD3	1:F:103:LYS:O	2.16	0.45
1:F:188:GLN:HE21	1:F:188:GLN:HB2	1.38	0.45
1:F:279:PRO:O	1:F:280:HIS:HD2	1.99	0.45
1:H:32:HIS:C	1:H:34:ASP:N	2.72	0.45
1:K:130:LYS:HG2	1:K:194:ASP:OD2	2.16	0.45
1:K:165:PRO:HD3	3:K:550:HP7:O2	2.16	0.45
1:M:76:LEU:HD23	1:M:76:LEU:HA	1.60	0.45
1:P:187:ASN:OD1	1:P:187:ASN:C	2.59	0.45
1:B:185:PHE:HE2	1:B:223:GLY:HA3	1.82	0.45
1:B:279:PRO:C	1:B:280[A]:HIS:HD1	2.24	0.45
1:D:138:LEU:HD23	1:D:138:LEU:HA	1.67	0.45
1:D:282:ASP:C	1:D:284:ASP:H	2.24	0.45
1:E:15:LEU:CD1	1:E:16:VAL:O	2.65	0.45
1:F:82:SER:HA	1:F:85:HIS:CE1	2.51	0.45
1:F:245:PRO:HD2	1:F:246:GLN:N	2.31	0.45
1:G:133:ARG:HH22	1:G:324:GLU:HG3	1.81	0.45
1:K:307:ASN:ND2	1:K:307:ASN:C	2.72	0.45
1:N:298:GLY:C	1:N:299:PHE:CD2	2.94	0.45
1:O:82:SER:OG	1:O:104:PRO:HD2	2.16	0.45
1:B:305:TYR:O	1:B:309:ILE:HG13	2.16	0.45
1:D:72:ASN:ND2	1:D:72:ASN:H	2.14	0.45
1:E:102:GLU:HA	1:E:129:VAL:CG2	2.46	0.45
1:E:133:ARG:HD3	1:E:198:TRP:CE2	2.51	0.45
1:E:142:LYS:HD2	1:E:199:LEU:HD23	1.99	0.45
1:I:285:LYS:O	1:I:286:ILE:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:105:MET:HG2	4:K:406:HOH:O	2.16	0.45
1:L:92:VAL:CG1	1:L:99:VAL:HG22	2.46	0.45
1:O:246:GLN:O	1:O:247:ASN:C	2.59	0.45
1:P:158:VAL:HA	1:P:251:SER:O	2.16	0.45
1:P:301:HIS:O	1:P:304:TYR:N	2.50	0.45
1:C:98:HIS:ND1	1:C:125:ARG:HB2	2.31	0.45
1:D:287:ARG:HH11	1:M:24:ASN:HD21	1.63	0.45
1:G:45:ASN:HA	1:G:46:PRO:HD2	1.67	0.45
1:I:46:PRO:O	1:I:49:LEU:HB3	2.16	0.45
1:K:263:VAL:HG22	1:K:271:ILE:HG12	1.98	0.45
1:C:327:GLN:CA	1:C:327:GLN:NE2	2.67	0.45
1:D:25:HIS:ND1	1:D:77:VAL:HG11	2.32	0.45
1:E:68:LEU:O	1:E:97:ARG:NH2	2.48	0.45
1:G:97:ARG:O	1:G:124:VAL:HG21	2.17	0.45
1:H:142:LYS:HE2	1:H:198:TRP:NE1	2.32	0.45
1:L:59:ARG:HH12	1:L:70:GLN:HG3	1.81	0.45
1:L:320:THR:HG23	1:L:324:GLU:HG3	1.97	0.45
1:O:117:LYS:HE2	1:O:117:LYS:HB3	1.64	0.45
1:P:119:CYS:SG	1:P:126:LEU:HB2	2.57	0.45
1:D:39:VAL:HG12	1:D:40:GLU:CD	2.41	0.45
1:D:291:TYR:OH	1:M:302:PRO:CD	2.63	0.45
1:E:277:ALA:O	1:E:278:GLU:HG2	2.17	0.45
1:G:53:GLU:O	1:G:54:ALA:C	2.59	0.45
1:I:273:GLU:OE2	1:I:275:LYS:CE	2.65	0.45
1:M:30:ALA:C	1:M:32:HIS:N	2.75	0.45
1:P:309:ILE:O	1:P:310:ASN:C	2.59	0.45
1:C:9:ARG:HH11	1:C:9:ARG:CG	2.24	0.45
1:E:261:VAL:HG12	1:E:262:ARG:N	2.31	0.45
2:E:500:NAI:H51N	2:E:500:NAI:C6N	2.46	0.45
1:H:162:TRP:HA	1:H:247:ASN:HA	1.99	0.45
1:I:347:LEU:HB3	1:I:348:PRO:HA	1.98	0.45
1:J:305:TYR:O	1:J:306:ASP:C	2.56	0.45
1:N:20:ARG:HG2	1:N:20:ARG:NH1	2.32	0.45
1:O:103:LYS:HD2	1:O:103:LYS:O	2.17	0.45
1:A:103:LYS:C	1:A:103:LYS:HE2	2.42	0.45
1:F:10:LYS:HG2	1:F:34:ASP:O	2.17	0.45
1:F:204:GLU:OE2	1:F:228:ARG:NE	2.47	0.45
1:G:310:ASN:CB	1:G:316:CYS:SG	3.03	0.45
1:H:10:LYS:HB3	1:H:36:ALA:HA	1.99	0.45
3:H:550:HP7:O5C	3:H:550:HP7:H6	2.17	0.45
1:I:124:VAL:HG12	1:I:125:ARG:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:269:ASN:OD1	1:K:269:ASN:N	2.33	0.45
1:L:103:LYS:HD2	2:L:500:NAI:H2N	1.99	0.45
1:N:21:ILE:O	1:N:25:HIS:HD2	1.99	0.45
1:P:244:TYR:CD1	1:P:244:TYR:C	2.95	0.45
1:I:68:LEU:HD21	1:I:76:LEU:CD1	2.47	0.45
1:I:80:THR:HB	1:I:81:PRO:CD	2.46	0.45
1:L:301:HIS:O	1:L:304:TYR:N	2.50	0.45
1:N:97:ARG:C	1:N:124:VAL:CG1	2.90	0.45
1:O:125:ARG:HB3	1:O:127:PHE:CE2	2.52	0.45
1:P:85:HIS:N	1:P:86:PRO:HD2	2.32	0.45
1:B:58:ALA:O	1:B:60:PRO:HD3	2.17	0.45
1:E:301:HIS:N	1:E:302:PRO:CD	2.78	0.45
1:G:282:ASP:OD1	1:G:285:LYS:HE2	2.17	0.45
1:I:58:ALA:O	1:I:60:PRO:HD3	2.17	0.45
1:M:16:VAL:HG22	1:M:67:MET:CE	2.42	0.45
1:M:282:ASP:C	1:M:284:ASP:N	2.74	0.45
1:P:327:GLN:HA	1:P:327:GLN:NE2	2.31	0.45
1:A:20:ARG:HD3	4:A:353:HOH:O	2.17	0.44
4:A:391:HOH:O	1:D:230:ARG:HD2	2.17	0.44
1:D:39:VAL:C	1:D:40:GLU:CG	2.88	0.44
1:D:98:HIS:HA	1:D:124:VAL:HG13	1.87	0.44
1:E:262:ARG:HB3	1:E:273:GLU:CB	2.47	0.44
1:F:186:MET:O	1:F:190:SER:HB3	2.17	0.44
1:F:187:ASN:OD1	1:F:187:ASN:C	2.61	0.44
1:I:20:ARG:NH1	3:I:550:HP7:O2B	2.42	0.44
1:B:117:LYS:HD2	1:B:121:GLU:OE2	2.17	0.44
1:C:73:ALA:O	1:C:97:ARG:HD2	2.17	0.44
1:J:53:GLU:O	1:J:57:GLY:N	2.47	0.44
1:K:235:GLY:CA	1:L:224:VAL:HG21	2.47	0.44
1:L:167:GLU:H	1:L:167:GLU:CD	2.24	0.44
1:L:310:ASN:HB3	1:L:315:ASP:CB	2.47	0.44
1:O:81:PRO:HB3	1:O:174:TRP:CE3	2.52	0.44
1:C:320:THR:HA	1:C:324:GLU:HG2	2.00	0.44
1:D:42:CYS:HB2	1:D:67:MET:SD	2.57	0.44
1:H:97:ARG:C	1:H:124:VAL:HG11	2.38	0.44
1:H:195:LEU:N	1:H:195:LEU:HD23	2.32	0.44
1:K:9:ARG:CG	1:K:10:LYS:H	2.31	0.44
1:L:81:PRO:HD2	1:L:84:LEU:HD12	2.00	0.44
1:N:32:HIS:HE1	1:N:306:ASP:HB2	1.83	0.44
1:N:133:ARG:HH22	1:N:324:GLU:HG3	1.82	0.44
1:D:287:ARG:HE	1:M:298:GLY:CA	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:282:ASP:HA	1:I:285:LYS:HG2	1.98	0.44
1:K:72:ASN:O	1:K:72:ASN:CG	2.60	0.44
1:K:307:ASN:OD1	1:K:319:GLU:HG3	2.18	0.44
1:P:230:ARG:NH1	1:P:347:LEU:O	2.48	0.44
1:E:156:VAL:O	1:E:235:GLY:HA3	2.18	0.44
1:G:105:MET:HG2	4:G:377:HOH:O	2.16	0.44
1:G:282:ASP:C	1:G:284:ASP:H	2.25	0.44
1:J:103:LYS:HD3	1:J:103:LYS:O	2.16	0.44
2:J:500:NAI:C4N	3:J:550:HP7:H3'	2.44	0.44
1:K:222:THR:HG23	1:K:240:THR:HB	1.99	0.44
1:L:74:ASP:O	1:L:97:ARG:HB3	2.17	0.44
1:M:21:ILE:HD13	2:M:500:NAI:H4N	1.99	0.44
1:N:267:ALA:O	1:N:268:VAL:C	2.61	0.44
1:A:278:GLU:HA	1:A:279:PRO:HD3	1.71	0.44
1:D:64:LEU:CD1	1:D:67:MET:CE	2.96	0.44
1:D:137:THR:HG23	1:D:293:THR:CB	2.47	0.44
1:E:206:VAL:HG12	1:E:227:LEU:HD23	1.99	0.44
1:H:116:VAL:HG21	1:H:326:LEU:CD1	2.46	0.44
1:L:119:CYS:O	1:L:120:ASP:C	2.59	0.44
1:M:53:GLU:HG3	1:M:60:PRO:HD3	2.00	0.44
1:O:310:ASN:HB3	1:O:316:CYS:SG	2.58	0.44
1:B:86:PRO:CA	1:B:115:MET:HG2	2.46	0.44
1:E:138:LEU:H	1:E:138:LEU:HG	1.62	0.44
1:G:301:HIS:O	1:G:302:PRO:C	2.60	0.44
1:J:102:GLU:OE1	1:J:129:VAL:HG11	2.18	0.44
1:K:73:ALA:O	1:K:97:ARG:HD2	2.16	0.44
1:N:85:HIS:N	1:N:86:PRO:CD	2.80	0.44
1:A:64:LEU:HD12	1:A:67:MET:HE2	1.99	0.44
1:A:82:SER:HA	1:A:85:HIS:CE1	2.53	0.44
1:A:282:ASP:C	1:A:284:ASP:N	2.76	0.44
1:B:284:ASP:O	1:B:285:LYS:C	2.59	0.44
1:C:309:ILE:HG22	1:C:313:ARG:HD3	2.00	0.44
1:D:282:ASP:C	1:D:284:ASP:N	2.74	0.44
1:H:16:VAL:HG13	1:H:16:VAL:O	2.18	0.44
1:J:155:MET:HA	1:J:234:MET:O	2.18	0.44
1:K:310:ASN:O	1:K:315:ASP:HB2	2.18	0.44
1:L:255:LEU:CD2	1:L:260:THR:HG23	2.47	0.44
2:M:500:NAI:C4N	3:M:550:HP7:H3'	2.37	0.44
1:A:109:TRP:CE2	1:A:113:LYS:HE2	2.52	0.44
1:C:235:GLY:HA2	1:D:224:VAL:HG21	1.98	0.44
1:D:76:LEU:HD23	1:D:76:LEU:HA	1.59	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:38:LEU:O	1:E:58:ALA:HB2	2.18	0.44
1:F:21:ILE:CD1	2:F:500:NAI:H4N	2.47	0.44
1:I:155:MET:HE1	1:J:224:VAL:HG23	2.00	0.44
1:I:313:ARG:C	1:I:315:ASP:N	2.75	0.44
1:J:267:ALA:O	1:J:268:VAL:HG23	2.18	0.44
1:J:278:GLU:O	1:J:278:GLU:HG2	2.18	0.44
1:K:80:THR:O	2:K:500:NAI:H4D	2.18	0.44
1:N:14:GLY:O	1:N:76:LEU:HA	2.18	0.44
1:F:143:LYS:O	1:F:144:ALA:C	2.60	0.43
1:H:318:PRO:HG2	1:H:321:ASP:HB3	1.99	0.43
1:I:326:LEU:HD23	1:I:326:LEU:HA	1.68	0.43
1:M:133:ARG:HH12	1:M:324:GLU:CG	2.31	0.43
1:M:310:ASN:C	1:M:315:ASP:HB2	2.42	0.43
1:A:68:LEU:CD2	1:A:76:LEU:HD11	2.44	0.43
1:C:103:LYS:HD2	2:C:500:NAI:H2N	1.99	0.43
1:D:207:TYR:C	1:D:207:TYR:CD2	2.96	0.43
1:E:277:ALA:C	1:E:278:GLU:HG3	2.43	0.43
4:E:360:HOH:O	1:H:211:ALA:HB1	2.17	0.43
1:F:24:ASN:H	1:F:24:ASN:ND2	2.16	0.43
1:K:131:GLN:HE22	2:K:500:NAI:C7N	2.30	0.43
1:K:155:MET:HE2	1:K:155:MET:HB2	1.94	0.43
1:L:101:SER:O	1:L:129:VAL:HG23	2.18	0.43
1:M:220:GLU:OE2	1:M:336:TYR:OH	2.28	0.43
1:A:97:ARG:O	1:A:124:VAL:HG11	2.18	0.43
1:A:173:ARG:HH22	1:D:317:GLU:HG3	1.82	0.43
1:C:53:GLU:C	1:C:55:ALA:H	2.27	0.43
1:G:156:VAL:O	1:G:235:GLY:CA	2.67	0.43
1:G:297:TYR:HA	4:G:391:HOH:O	2.19	0.43
1:H:155:MET:HB2	1:H:155:MET:HE2	1.67	0.43
1:I:309:ILE:O	1:I:310:ASN:C	2.58	0.43
1:J:103:LYS:HA	1:J:104:PRO:C	2.43	0.43
1:L:142:LYS:HB2	1:L:199:LEU:CD2	2.48	0.43
1:N:127:PHE:CE1	1:N:318:PRO:HB3	2.54	0.43
1:A:21:ILE:O	1:A:21:ILE:HG13	2.18	0.43
1:C:225:ALA:HB3	1:C:237:ILE:CG2	2.48	0.43
1:E:85:HIS:N	1:E:86:PRO:CD	2.81	0.43
1:E:128:VAL:O	1:E:320:THR:HG21	2.19	0.43
1:J:45:ASN:HA	1:J:46:PRO:HD2	1.72	0.43
1:K:15:LEU:HD12	1:K:77:VAL:HB	2.01	0.43
1:L:24:ASN:O	1:L:28:ALA:HB2	2.18	0.43
1:A:30:ALA:O	1:A:33:GLY:N	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:ARG:NE	1:A:319:GLU:OE2	2.51	0.43
1:A:236:SER:OG	1:B:238:ASN:ND2	2.49	0.43
1:B:192:TYR:N	1:B:192:TYR:CD2	2.86	0.43
1:D:267:ALA:C	1:D:268:VAL:CG2	2.92	0.43
1:E:52:ALA:O	1:E:56:THR:OG1	2.36	0.43
1:F:197:ASP:OD1	1:F:197:ASP:C	2.61	0.43
1:H:288:GLU:O	1:H:291:TYR:CB	2.66	0.43
1:I:64:LEU:CD2	1:I:64:LEU:O	2.67	0.43
1:J:82:SER:HB3	1:J:104:PRO:HD2	2.01	0.43
1:P:305:TYR:HA	1:P:308:VAL:HG23	2.01	0.43
1:D:130:LYS:HG2	1:D:194:ASP:OD2	2.19	0.43
1:D:137:THR:HG23	1:D:293:THR:HG21	2.00	0.43
1:F:168:TYR:OH	3:F:550:HP7:O'Q	2.31	0.43
1:G:117:LYS:HE2	1:G:117:LYS:HB3	1.30	0.43
1:H:167:GLU:CD	1:H:167:GLU:H	2.25	0.43
1:J:207:TYR:C	1:J:207:TYR:CD2	2.95	0.43
1:M:15:LEU:HD23	1:M:16:VAL:N	2.34	0.43
1:N:133:ARG:NH1	1:N:324:GLU:HG2	2.32	0.43
1:A:277:ALA:HA	1:B:244:TYR:OH	2.18	0.43
1:B:103:LYS:NZ	3:B:550:HP7:O3'	2.51	0.43
1:B:156:VAL:O	1:B:235:GLY:HA3	2.18	0.43
1:D:46:PRO:O	1:D:49:LEU:HB3	2.19	0.43
1:D:103:LYS:HD2	2:D:500:NAI:C2N	2.49	0.43
1:E:277:ALA:C	1:E:278:GLU:CG	2.92	0.43
1:F:324:GLU:O	1:F:327:GLN:HB2	2.18	0.43
1:I:331:LEU:HD23	1:I:331:LEU:HA	1.81	0.43
1:J:38:LEU:CD2	1:J:56:THR:HG21	2.49	0.43
1:K:82:SER:CB	1:K:104:PRO:HD2	2.48	0.43
1:K:97:ARG:O	1:K:124:VAL:CG2	2.60	0.43
1:L:320:THR:HG23	1:L:324:GLU:HB3	1.99	0.43
1:M:134:ARG:NE	1:M:319:GLU:OE1	2.51	0.43
1:M:224:VAL:HG23	1:N:155:MET:HE1	2.01	0.43
1:P:263:VAL:HG12	1:P:268:VAL:HA	2.00	0.43
1:B:301:HIS:N	1:B:302:PRO:CD	2.82	0.43
1:C:235:GLY:CA	1:D:224:VAL:HG21	2.49	0.43
1:D:45:ASN:O	1:D:46:PRO:C	2.62	0.43
1:D:162:TRP:HA	1:D:247:ASN:HA	2.00	0.43
1:D:187:ASN:OD1	1:D:187:ASN:C	2.61	0.43
1:F:37:GLU:HG3	1:F:39:VAL:HG23	2.00	0.43
1:J:43:ASP:OD1	1:J:43:ASP:C	2.62	0.43
1:J:262:ARG:HH11	1:J:262:ARG:CG	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:134:ARG:HH21	1:N:319:GLU:CD	2.26	0.43
1:D:318:PRO:C	1:D:320:THR:N	2.77	0.43
1:H:53:GLU:HG3	1:H:54:ALA:N	2.34	0.43
1:I:270:ARG:NE	1:I:272:ASP:OD1	2.36	0.43
1:M:187:ASN:C	1:M:187:ASN:OD1	2.61	0.43
1:P:207:TYR:CD2	1:P:207:TYR:C	2.97	0.43
1:B:59:ARG:HA	1:B:60:PRO:HD2	1.87	0.43
1:B:202:PRO:HB2	1:B:230[A]:ARG:HD3	2.00	0.43
1:C:85:HIS:HB2	1:C:86:PRO:HD3	2.01	0.43
1:D:72:ASN:HD22	1:D:72:ASN:H	1.67	0.43
1:J:259:GLY:HA2	1:J:275:LYS:O	2.19	0.43
1:D:259:GLY:HA2	1:D:275:LYS:O	2.19	0.42
1:I:192:TYR:CD2	1:I:192:TYR:N	2.87	0.42
1:N:21:ILE:O	1:N:21:ILE:HG23	2.18	0.42
1:O:6:ILE:CG2	1:O:11:ILE:HD13	2.44	0.42
1:O:153:ILE:O	1:O:233:ALA:HB2	2.18	0.42
1:C:86:PRO:HG3	1:C:106:ALA:CB	2.49	0.42
1:D:133:ARG:NH1	1:D:324:GLU:CG	2.74	0.42
1:I:65:SER:HB3	1:I:91:GLU:OE1	2.20	0.42
1:L:29:ILE:C	1:L:31:GLN:N	2.77	0.42
1:L:86:PRO:CB	1:L:111:ASP:HB3	2.50	0.42
1:M:163:THR:O	1:M:164:ARG:HD3	2.19	0.42
1:O:19:GLY:HA3	2:O:500:NAI:O2A	2.19	0.42
1:A:14:GLY:HA2	1:A:40:GLU:O	2.19	0.42
1:A:246:GLN:O	1:A:247:ASN:C	2.60	0.42
1:D:142:LYS:HG3	1:D:146:GLU:OE2	2.19	0.42
1:E:102:GLU:HA	1:E:129:VAL:HG23	2.01	0.42
1:G:301:HIS:N	1:G:302:PRO:CD	2.82	0.42
1:K:134:ARG:O	1:K:135:ASN:C	2.62	0.42
1:L:245:PRO:HG2	1:L:246:GLN:N	2.34	0.42
1:P:16:VAL:CG1	1:P:78:LEU:HD23	2.48	0.42
1:C:133:ARG:NH1	1:C:324:GLU:HG3	2.35	0.42
1:C:267:ALA:O	1:C:268:VAL:C	2.62	0.42
1:E:117:LYS:HB3	1:E:117:LYS:HE2	1.86	0.42
1:F:142:LYS:CE	1:F:146:GLU:OE2	2.56	0.42
1:M:98:HIS:HA	1:M:124:VAL:HG12	1.91	0.42
1:M:213:LEU:HD23	1:M:213:LEU:HA	1.82	0.42
1:M:283:ASP:O	1:M:286:ILE:CD1	2.67	0.42
1:O:103:LYS:C	1:O:103:LYS:CD	2.87	0.42
1:P:111:ASP:O	1:P:115:MET:HG3	2.19	0.42
1:A:156:VAL:O	1:A:235:GLY:HA3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:237:ILE:HG23	1:G:237:ILE:O	2.19	0.42
1:I:84:LEU:O	1:I:85:HIS:C	2.61	0.42
1:J:82:SER:CB	1:J:104:PRO:HD2	2.48	0.42
1:K:39:VAL:O	1:K:40:GLU:CG	2.65	0.42
1:K:50:GLN:O	1:K:51:ALA:C	2.62	0.42
1:K:86:PRO:HG3	1:K:106:ALA:HB2	2.01	0.42
1:O:132:ASN:C	1:O:134:ARG:N	2.78	0.42
1:A:81:PRO:HB3	1:A:174:TRP:CE3	2.55	0.42
1:C:211:ALA:HB3	1:D:234:MET:HE1	2.01	0.42
1:D:8:ASP:OD1	1:D:8:ASP:N	2.53	0.42
1:E:128:VAL:O	1:E:320:THR:CG2	2.67	0.42
1:F:24:ASN:H	1:F:24:ASN:HD22	1.68	0.42
1:J:197:ASP:OD2	1:J:202:PRO:HA	2.19	0.42
1:K:18:CYS:C	1:K:22:SER:OG	2.63	0.42
1:K:133:ARG:O	1:K:139:GLN:NE2	2.51	0.42
1:L:98:HIS:HA	1:L:124:VAL:HG11	1.99	0.42
1:P:12:ARG:HG2	1:P:39:VAL:HG21	2.01	0.42
1:P:141:VAL:O	1:P:142:LYS:C	2.56	0.42
1:B:103:LYS:HE2	2:B:500:NAI:C2N	2.49	0.42
1:D:124:VAL:HG12	1:D:125:ARG:O	2.19	0.42
1:J:301:HIS:N	1:J:302:PRO:CD	2.82	0.42
1:K:162:TRP:HA	1:K:247:ASN:HA	2.02	0.42
1:P:31:GLN:HE21	1:P:31:GLN:HB2	1.58	0.42
1:P:312:LEU:C	1:P:314:GLY:N	2.78	0.42
1:C:282:ASP:OD1	1:C:285:LYS:HE2	2.20	0.42
1:D:31:GLN:HE21	1:D:31:GLN:HB2	1.53	0.42
1:F:155:MET:HE2	1:F:155:MET:HB2	1.89	0.42
1:I:39:VAL:O	1:I:58:ALA:HB1	2.19	0.42
1:I:261:VAL:HG12	1:I:262:ARG:N	2.34	0.42
1:K:98:HIS:ND1	1:K:125:ARG:CB	2.80	0.42
1:L:131:GLN:HE22	2:L:500:NAI:C7N	2.27	0.42
1:M:331:LEU:HD23	1:M:331:LEU:HA	1.54	0.42
1:O:80:THR:OG1	1:O:88:GLN:NE2	2.51	0.42
1:A:280:HIS:ND1	1:A:281:PRO:HD2	2.35	0.42
1:F:258:LYS:HB2	1:F:277:ALA:CB	2.50	0.42
1:I:313:ARG:O	1:I:315:ASP:N	2.52	0.42
1:J:12:ARG:CG	1:J:39:VAL:HG21	2.46	0.42
1:L:9:ARG:CG	1:L:10:LYS:H	2.30	0.42
1:M:20:ARG:NH1	3:M:550:HP7:H5C	2.35	0.42
1:N:133:ARG:HH12	1:N:324:GLU:CG	2.32	0.42
1:E:21:ILE:HG22	2:E:500:NAI:H52N	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:68:LEU:HD12	1:F:91:GLU:HG2	2.02	0.42
1:I:156:VAL:O	1:I:235:GLY:HA3	2.20	0.42
1:I:258:LYS:HB2	1:I:277:ALA:HB2	2.01	0.42
1:K:59:ARG:HA	1:K:60:PRO:HD3	1.75	0.42
1:K:255:LEU:HD11	1:L:161:PHE:CG	2.55	0.42
1:L:156:VAL:O	1:L:235:GLY:HA3	2.20	0.42
1:O:6:ILE:CG2	1:O:11:ILE:CD1	2.97	0.42
1:O:86:PRO:HB3	1:O:115:MET:HG3	2.02	0.42
1:P:28:ALA:HB1	1:P:302:PRO:HA	2.01	0.42
1:D:125:ARG:HA	1:D:125:ARG:HD2	1.72	0.41
1:E:191:HIS:CD2	3:E:550:HP7:C7'	3.02	0.41
1:E:249:GLU:OE1	1:E:251:SER:OG	2.30	0.41
1:G:16:VAL:CG2	1:G:67:MET:HE1	2.30	0.41
1:I:72:ASN:ND2	1:I:72:ASN:N	2.68	0.41
1:I:140:LEU:CD1	1:I:289:ALA:CB	2.97	0.41
1:J:136:ALA:H	1:J:293:THR:HG1	1.67	0.41
1:M:85:HIS:N	1:M:86:PRO:HD2	2.34	0.41
1:O:97:ARG:C	1:O:124:VAL:CG1	2.93	0.41
1:O:193:VAL:HG21	1:O:332:LEU:HD21	2.00	0.41
1:P:103:LYS:O	1:P:103:LYS:CD	2.65	0.41
1:A:234:MET:HE3	1:B:222:THR:HG22	2.01	0.41
1:C:312:LEU:HA	1:C:312:LEU:HD23	1.80	0.41
1:F:9:ARG:HH12	1:F:12:ARG:HE	1.68	0.41
1:F:188:GLN:NE2	1:F:188:GLN:H	2.18	0.41
1:H:50:GLN:O	1:H:53:GLU:HG3	2.19	0.41
1:I:30:ALA:C	1:I:32:HIS:H	2.29	0.41
1:J:103:LYS:HB2	1:J:104:PRO:HA	2.02	0.41
1:J:298:GLY:O	1:J:299:PHE:CD2	2.73	0.41
1:K:224:VAL:HG23	1:L:234:MET:HB3	2.01	0.41
1:M:80:THR:HB	1:M:81:PRO:CD	2.45	0.41
1:M:244:TYR:HA	1:M:245:PRO:HA	1.89	0.41
1:O:40:GLU:OE2	1:O:71:GLY:HA3	2.20	0.41
1:P:15:LEU:HD21	1:P:22:SER:HB2	2.02	0.41
1:P:84:LEU:HD23	1:P:84:LEU:HA	1.82	0.41
1:A:100:VAL:HG22	1:A:127:PHE:HB2	2.02	0.41
1:B:67:MET:HE2	1:B:76:LEU:CD2	2.49	0.41
1:B:320:THR:HG23	1:B:324:GLU:HG2	2.03	0.41
1:C:90:ILE:O	1:C:94:GLN:HG3	2.20	0.41
1:E:215:ARG:HA	1:E:215:ARG:HD3	1.96	0.41
1:F:159:ASN:O	1:F:250:GLY:HA2	2.19	0.41
1:G:76:LEU:HD12	1:G:92:VAL:CG2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:103:LYS:C	1:I:103:LYS:CD	2.87	0.41
1:I:320:THR:HG22	1:I:320:THR:O	2.20	0.41
1:J:262:ARG:HG2	1:J:262:ARG:NH1	2.34	0.41
1:K:80:THR:OG1	1:K:88:GLN:NE2	2.53	0.41
1:O:158:VAL:HG22	1:O:252:ILE:HG13	2.01	0.41
1:O:283:ASP:O	1:O:287:ARG:HB2	2.20	0.41
1:P:274:TRP:CE2	1:P:276:PHE:HE2	2.38	0.41
1:A:197:ASP:HA	1:A:201:GLY:O	2.20	0.41
1:B:21:ILE:CG2	1:B:79:ALA:HB1	2.50	0.41
1:B:117:LYS:O	1:B:120:ASP:HB2	2.21	0.41
1:D:72:ASN:ND2	1:D:72:ASN:N	2.68	0.41
1:D:142:LYS:HE2	1:D:198:TRP:O	2.20	0.41
1:F:125:ARG:HD2	1:F:125:ARG:HA	1.89	0.41
1:I:282:ASP:C	1:I:284:ASP:N	2.76	0.41
1:K:34:ASP:CG	1:K:35:ARG:H	2.28	0.41
1:K:42:CYS:HB2	1:K:67:MET:SD	2.60	0.41
1:L:202:PRO:HD2	4:L:458:HOH:O	2.20	0.41
1:N:39:VAL:C	1:N:58:ALA:HB1	2.41	0.41
1:N:112:GLY:O	1:N:115:MET:HB3	2.20	0.41
1:C:42:CYS:HB2	1:C:67:MET:SD	2.60	0.41
1:C:301:HIS:N	1:C:302:PRO:CD	2.82	0.41
1:D:282:ASP:HA	1:D:285:LYS:CD	2.51	0.41
1:F:207:TYR:CD2	1:F:208:ALA:N	2.89	0.41
1:H:154:TYR:HE2	1:H:257:GLU:HA	1.85	0.41
1:I:246:GLN:HE21	1:I:246:GLN:HB3	1.74	0.41
1:J:136:ALA:N	1:J:293:THR:OG1	2.54	0.41
1:J:280:HIS:O	1:J:281:PRO:C	2.64	0.41
1:K:117:LYS:HB3	1:K:117:LYS:HE2	1.51	0.41
1:L:21:ILE:CD1	2:L:500:NAI:H4N	2.42	0.41
1:O:59:ARG:HA	1:O:60:PRO:HD3	1.84	0.41
1:P:247:ASN:HB3	1:P:266:VAL:CG1	2.50	0.41
1:B:191:HIS:HE1	2:B:500:NAI:O7N	2.04	0.41
1:C:53:GLU:C	1:C:55:ALA:N	2.74	0.41
1:E:125:ARG:HA	1:E:125:ARG:HD2	1.87	0.41
1:E:248:LEU:HD22	1:F:260:THR:CG2	2.49	0.41
1:I:81:PRO:HD2	1:I:84:LEU:HD12	2.02	0.41
1:N:332:LEU:HD23	1:N:332:LEU:HA	1.95	0.41
1:P:86:PRO:HB3	1:P:115:MET:CG	2.50	0.41
1:B:186:MET:O	1:B:190:SER:HB3	2.20	0.41
1:B:195:LEU:HA	1:B:195:LEU:HD23	1.88	0.41
1:D:21:ILE:CG2	2:D:500:NAI:H52N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:MET:O	1:D:186:MET:HG2	2.21	0.41
1:F:98:HIS:HA	1:F:124:VAL:HG11	1.99	0.41
1:H:244:TYR:HA	1:H:245:PRO:HA	1.89	0.41
1:I:124:VAL:CG1	1:I:125:ARG:N	2.84	0.41
1:I:267:ALA:C	1:I:268:VAL:CG2	2.93	0.41
1:J:6:ILE:O	1:J:6:ILE:HG22	2.21	0.41
1:K:244:TYR:HA	1:K:245:PRO:HA	1.71	0.41
1:L:14:GLY:C	1:L:67:MET:HE1	2.46	0.41
1:L:68:LEU:HD22	1:L:95:ALA:HB3	2.02	0.41
1:M:19:GLY:O	1:M:22:SER:OG	2.34	0.41
1:M:267:ALA:O	1:M:268:VAL:C	2.64	0.41
1:N:331:LEU:HD23	1:N:331:LEU:HA	1.87	0.41
1:D:26:ILE:O	1:D:27:GLY:C	2.63	0.41
1:G:167:GLU:CD	1:G:167:GLU:N	2.79	0.41
1:J:72:ASN:O	1:J:73:ALA:C	2.64	0.41
1:N:12:ARG:HH11	1:N:12:ARG:HD2	1.70	0.41
1:O:72:ASN:C	1:O:72:ASN:ND2	2.78	0.41
1:P:20:ARG:HA	1:P:23:LYS:NZ	2.34	0.41
1:P:35:ARG:HG2	1:P:313:ARG:NH1	2.36	0.41
1:A:66:ASP:O	1:A:67:MET:C	2.61	0.41
1:A:187:ASN:OD1	1:A:187:ASN:C	2.63	0.41
1:B:40:GLU:HB3	1:B:67:MET:HE3	2.02	0.41
1:B:154:TYR:OH	4:B:353:HOH:O	2.04	0.41
1:B:312:LEU:O	1:B:313:ARG:C	2.63	0.41
1:D:47:GLU:HA	1:D:50:GLN:HG3	2.02	0.41
1:D:142:LYS:HD3	1:D:199:LEU:HD23	2.02	0.41
1:E:244:TYR:C	1:E:244:TYR:CD2	2.98	0.41
1:F:220:GLU:O	1:F:220:GLU:HG2	2.17	0.41
1:G:26:ILE:HD13	1:G:26:ILE:HG21	1.78	0.41
1:G:53:GLU:OE1	1:G:60:PRO:CG	2.54	0.41
1:G:278:GLU:HA	1:G:279:PRO:HD3	1.89	0.41
1:G:324:GLU:O	1:G:327:GLN:HB2	2.21	0.41
1:H:135:ASN:HB3	1:H:293:THR:HG23	2.01	0.41
1:I:90:ILE:CD1	1:I:114:ARG:HG2	2.48	0.41
1:I:155:MET:HE1	1:J:224:VAL:HG22	2.03	0.41
1:I:261:VAL:CG1	1:I:262:ARG:N	2.84	0.41
1:I:301:HIS:O	1:I:302:PRO:C	2.63	0.41
1:K:78:LEU:HB2	1:K:101:SER:HA	2.02	0.41
1:K:127:PHE:HB3	1:K:304:TYR:OH	2.21	0.41
1:L:310:ASN:CA	1:L:315:ASP:HB2	2.51	0.41
1:N:81:PRO:HB3	1:N:174:TRP:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:246:GLN:O	1:N:247:ASN:C	2.64	0.41
1:N:273:GLU:HA	4:N:620:HOH:O	2.19	0.41
1:A:340:ARG:HG3	1:D:346:PRO:HB2	2.02	0.41
1:B:31:GLN:HE21	1:B:31:GLN:HB3	1.75	0.41
1:C:67:MET:HE2	1:C:76:LEU:HD21	2.03	0.41
1:C:213:LEU:HA	1:C:213:LEU:HD23	1.75	0.41
1:D:287:ARG:NH1	1:M:24:ASN:ND2	2.68	0.41
1:G:67:MET:HE3	1:G:76:LEU:HD22	2.03	0.41
1:K:80:THR:HB	1:K:81:PRO:HD2	2.03	0.41
1:K:98:HIS:ND1	1:K:125:ARG:N	2.51	0.41
1:L:21:ILE:HD13	2:L:500:NAI:C4N	2.43	0.41
1:N:85:HIS:HB2	1:N:105:MET:O	2.21	0.41
1:P:86:PRO:HA	1:P:115:MET:CG	2.39	0.41
2:P:500:NAI:C6N	2:P:500:NAI:H51N	2.51	0.41
1:C:134:ARG:CD	1:C:319:GLU:OE1	2.68	0.40
1:C:320:THR:HA	1:C:324:GLU:CG	2.52	0.40
1:D:45:ASN:HA	1:D:46:PRO:HD2	1.92	0.40
1:D:124:VAL:HG12	1:D:125:ARG:N	2.36	0.40
1:F:301:HIS:N	1:F:302:PRO:CD	2.83	0.40
1:G:112:GLY:O	1:G:115:MET:HG2	2.21	0.40
1:G:244:TYR:OH	1:H:277:ALA:HA	2.20	0.40
1:H:135:ASN:ND2	1:H:293:THR:CG2	2.84	0.40
1:K:197:ASP:OD2	4:K:420:HOH:O	2.22	0.40
1:M:310:ASN:HB3	1:M:315:ASP:CB	2.51	0.40
1:O:235:GLY:HA2	1:P:224:VAL:HG21	2.04	0.40
1:C:12:ARG:O	1:C:74:ASP:N	2.45	0.40
1:G:12:ARG:NH1	1:G:72:ASN:O	2.54	0.40
1:L:40:GLU:O	1:L:41:ILE:CG2	2.69	0.40
1:L:42:CYS:HB2	1:L:67:MET:SD	2.61	0.40
1:L:81:PRO:HB3	1:L:174:TRP:CD2	2.56	0.40
1:O:40:GLU:O	1:O:41:ILE:HG23	2.20	0.40
1:B:94:GLN:C	1:B:96:GLY:N	2.79	0.40
1:D:64:LEU:HD12	1:D:67:MET:CE	2.52	0.40
1:D:80:THR:HB	1:D:81:PRO:HD2	2.02	0.40
1:D:204:GLU:OE1	4:D:559:HOH:O	2.22	0.40
1:E:134:ARG:HA	1:E:139:GLN:HE21	1.86	0.40
1:F:12:ARG:HH12	1:F:72:ASN:CG	2.29	0.40
1:F:197:ASP:HA	1:F:201:GLY:O	2.22	0.40
1:F:269:ASN:OD1	1:F:269:ASN:N	2.39	0.40
1:G:156:VAL:O	1:G:235:GLY:HA3	2.20	0.40
1:G:323:ARG:O	1:G:326:LEU:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:21:ILE:HG22	2:I:500:NAI:H52N	2.02	0.40
1:I:21:ILE:HG21	2:I:500:NAI:C5D	2.52	0.40
1:I:168:TYR:OH	3:I:550:HP7:O'Q	2.32	0.40
1:I:234:MET:HE2	1:J:213:LEU:HD11	2.03	0.40
1:L:28:ALA:HA	1:L:302:PRO:HG3	2.03	0.40
1:M:197:ASP:HB2	4:M:478:HOH:O	2.20	0.40
1:N:16:VAL:HG22	1:N:67:MET:CE	2.43	0.40
1:N:76:LEU:HD12	1:N:92:VAL:HG11	1.99	0.40
1:N:121:GLU:C	1:N:123:GLY:H	2.30	0.40
1:O:282:ASP:CG	1:O:285:LYS:CE	2.95	0.40
1:P:154:TYR:CZ	1:P:257:GLU:HB2	2.56	0.40
1:B:11:ILE:HD12	1:B:11:ILE:HG23	1.80	0.40
1:C:40:GLU:HG2	1:C:61:PHE:HE2	1.86	0.40
1:H:137:THR:HG23	1:H:293:THR:OG1	2.21	0.40
1:K:309:ILE:O	1:K:310:ASN:C	2.63	0.40
1:L:301:HIS:CB	1:L:302:PRO:HD3	2.52	0.40
1:N:84:LEU:O	1:N:85:HIS:C	2.64	0.40
1:A:76:LEU:HD12	1:A:92:VAL:CG2	2.50	0.40
1:B:187:ASN:OD1	1:B:187:ASN:C	2.64	0.40
1:C:187:ASN:OD1	1:C:187:ASN:C	2.65	0.40
1:D:131:GLN:NE2	1:D:301:HIS:CE1	2.89	0.40
1:D:155:MET:HE2	1:D:155:MET:HB2	1.92	0.40
1:E:149:ARG:NH1	1:E:278:GLU:O	2.35	0.40
1:M:68:LEU:HD23	1:M:68:LEU:HA	1.95	0.40
1:M:119:CYS:O	1:M:120:ASP:C	2.64	0.40
1:O:35:ARG:NH2	1:O:310:ASN:OD1	2.54	0.40
1:O:149:ARG:HD2	4:O:519:HOH:O	2.20	0.40
1:P:310:ASN:CB	1:P:316:CYS:SG	3.10	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:297:TYR:CE2	1:I:287:ARG:CD[2_746]	1.84	0.36
1:H:287:ARG:NH2	1:J:273:GLU:OE2[2_746]	2.12	0.08

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 X-ray entries followed by that with respect to entries of similar resolution.

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	344/370 (93%)	323 (94%)	20 (6%)	1 (0%)	36	33
1	B	327/370 (88%)	306 (94%)	20 (6%)	1 (0%)	36	33
1	C	345/370 (93%)	322 (93%)	21 (6%)	2 (1%)	21	15
1	D	342/370 (92%)	309 (90%)	29 (8%)	4 (1%)	10	5
1	E	317/370 (86%)	278 (88%)	34 (11%)	5 (2%)	7	2
1	F	323/370 (87%)	297 (92%)	25 (8%)	1 (0%)	36	33
1	G	340/370 (92%)	317 (93%)	20 (6%)	3 (1%)	14	8
1	H	341/370 (92%)	317 (93%)	23 (7%)	1 (0%)	36	33
1	I	340/370 (92%)	306 (90%)	28 (8%)	6 (2%)	6	2
1	J	344/370 (93%)	309 (90%)	31 (9%)	4 (1%)	10	5
1	K	318/370 (86%)	287 (90%)	26 (8%)	5 (2%)	7	2
1	L	316/370 (85%)	281 (89%)	27 (8%)	8 (2%)	4	1
1	M	344/370 (93%)	321 (93%)	20 (6%)	3 (1%)	14	8
1	N	340/370 (92%)	313 (92%)	26 (8%)	1 (0%)	36	33
1	O	330/370 (89%)	299 (91%)	29 (9%)	2 (1%)	21	15
1	P	318/370 (86%)	291 (92%)	24 (8%)	3 (1%)	14	8
All	All	5329/5920 (90%)	4876 (92%)	403 (8%)	50 (1%)	14	8

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	30	ALA
1	L	26	ILE
1	L	30	ALA
1	M	30	ALA
1	M	31	GLN
1	G	33	GLY

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Mol	Chain	Res	Type
1	H	33	GLY
1	I	31	GLN
1	I	72	ASN
1	I	310	ASN
1	J	95	ALA
1	K	30	ALA
1	K	39	VAL
1	K	314	GLY
1	L	57	GLY
1	L	72	ASN
1	L	314	GLY
1	M	73	ALA
1	P	27	GLY
1	E	137	THR
1	G	283	ASP
1	G	315	ASP
1	I	283	ASP
1	I	311	CYS
1	I	314	GLY
1	D	283	ASP
1	E	273	GLU
1	P	278	GLU
1	C	9	ARG
1	E	31	GLN
1	F	314	GLY
1	L	71	GLY
1	O	43	ASP
1	O	60	PRO
1	P	26	ILE
1	D	26	ILE
1	D	319	GLU
1	J	281	PRO
1	L	11	ILE
1	E	57	GLY
1	E	268	VAL
1	K	278	GLU
1	N	314	GLY
1	J	129	VAL
1	C	33	GLY
1	D	27	GLY
1	L	29	ILE
1	A	33	GLY

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Mol	Chain	Res	Type
1	K	268	VAL
1	B	300	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	277/299 (93%)	256 (92%)	21 (8%)	12	7
1	B	264/299 (88%)	239 (90%)	25 (10%)	8	4
1	C	277/299 (93%)	259 (94%)	18 (6%)	15	10
1	D	275/299 (92%)	253 (92%)	22 (8%)	11	7
1	E	254/299 (85%)	228 (90%)	26 (10%)	7	3
1	F	260/299 (87%)	242 (93%)	18 (7%)	14	9
1	G	273/299 (91%)	253 (93%)	20 (7%)	13	8
1	H	274/299 (92%)	247 (90%)	27 (10%)	7	3
1	I	273/299 (91%)	252 (92%)	21 (8%)	12	7
1	J	277/299 (93%)	255 (92%)	22 (8%)	11	7
1	K	255/299 (85%)	229 (90%)	26 (10%)	7	3
1	L	256/299 (86%)	223 (87%)	33 (13%)	4	1
1	M	277/299 (93%)	252 (91%)	25 (9%)	9	4
1	N	273/299 (91%)	247 (90%)	26 (10%)	8	4
1	O	267/299 (89%)	247 (92%)	20 (8%)	12	7
1	P	255/299 (85%)	234 (92%)	21 (8%)	10	6
All	All	4287/4784 (90%)	3916 (91%)	371 (9%)	9	5

All (371) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	23	LYS

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Mol	Chain	Res	Type
1	A	24	ASN
1	A	37	GLU
1	A	44	THR
1	A	53	GLU
1	A	59	ARG
1	A	72	ASN
1	A	103	LYS
1	A	114	ARG
1	A	121	GLU
1	A	124	VAL
1	A	125	ARG
1	A	134	ARG
1	A	143	LYS
1	A	153	ILE
1	A	167	GLU
1	A	287	ARG
1	A	288	GLU
1	A	316	CYS
1	A	343	VAL
1	B	12	ARG
1	B	31	GLN
1	B	41	ILE
1	B	47	GLU
1	B	59	ARG
1	B	65	SER
1	B	72	ASN
1	B	94	GLN
1	B	103	LYS
1	B	121	GLU
1	B	125	ARG
1	B	135	ASN
1	B	143	LYS
1	B	167	GLU
1	B	177	LYS
1	B	188	GLN
1	B	204	GLU
1	B	258	LYS
1	B	268	VAL
1	B	271	ILE
1	B	285	LYS
1	B	303	LEU
1	B	307	ASN

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Mol	Chain	Res	Type
1	B	313	ARG
1	B	331	LEU
1	C	24	ASN
1	C	31	GLN
1	C	34	ASP
1	C	47	GLU
1	C	53	GLU
1	C	65	SER
1	C	72	ASN
1	C	103	LYS
1	C	130	LYS
1	C	153	ILE
1	C	258	LYS
1	C	260	THR
1	C	273	GLU
1	C	278	GLU
1	C	287	ARG
1	C	295	SER
1	C	324	GLU
1	C	327	GLN
1	D	8	ASP
1	D	20	ARG
1	D	23	LYS
1	D	35	ARG
1	D	39	VAL
1	D	70	GLN
1	D	72	ASN
1	D	80	THR
1	D	94	GLN
1	D	103	LYS
1	D	117	LYS
1	D	125	ARG
1	D	130	LYS
1	D	167	GLU
1	D	216	ARG
1	D	285	LYS
1	D	287	ARG
1	D	292	GLU
1	D	294	THR
1	D	299	PHE
1	D	303	LEU
1	D	327	GLN

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Mol	Chain	Res	Type
1	E	12	ARG
1	E	15	LEU
1	E	26	ILE
1	E	34	ASP
1	E	39	VAL
1	E	41	ILE
1	E	49	LEU
1	E	53	GLU
1	E	56	THR
1	E	63	SER
1	E	103	LYS
1	E	110	GLU
1	E	137	THR
1	E	157	THR
1	E	163	THR
1	E	166	GLN
1	E	167	GLU
1	E	227	LEU
1	E	246	GLN
1	E	249	GLU
1	E	258	LYS
1	E	266	VAL
1	E	275	LYS
1	E	303	LEU
1	E	308	VAL
1	E	343	VAL
1	F	41	ILE
1	F	47	GLU
1	F	53	GLU
1	F	59	ARG
1	F	62	SER
1	F	65	SER
1	F	103	LYS
1	F	132	ASN
1	F	139	GLN
1	F	153	ILE
1	F	157	THR
1	F	167	GLU
1	F	188	GLN
1	F	227	LEU
1	F	245	PRO
1	F	313	ARG

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Mol	Chain	Res	Type
1	F	315	ASP
1	F	327	GLN
1	G	23	LYS
1	G	38	LEU
1	G	53	GLU
1	G	59	ARG
1	G	94	GLN
1	G	103	LYS
1	G	117	LYS
1	G	121	GLU
1	G	152	ARG
1	G	167	GLU
1	G	227	LEU
1	G	258	LYS
1	G	262	ARG
1	G	278	GLU
1	G	287	ARG
1	G	311	CYS
1	G	316	CYS
1	G	319	GLU
1	G	323	ARG
1	G	327	GLN
1	H	23	LYS
1	H	24	ASN
1	H	40	GLU
1	H	44	THR
1	H	47	GLU
1	H	50	GLN
1	H	72	ASN
1	H	80	THR
1	H	103	LYS
1	H	114	ARG
1	H	117	LYS
1	H	134	ARG
1	H	153	ILE
1	H	157	THR
1	H	167	GLU
1	H	204	GLU
1	H	216	ARG
1	H	227	LEU
1	H	278	GLU
1	H	287	ARG

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Mol	Chain	Res	Type
1	H	291	TYR
1	H	293	THR
1	H	296	VAL
1	H	317	GLU
1	H	319	GLU
1	H	327	GLN
1	H	343	VAL
1	I	34	ASP
1	I	35	ARG
1	I	39	VAL
1	I	41	ILE
1	I	64	LEU
1	I	80	THR
1	I	91	GLU
1	I	97	ARG
1	I	103	LYS
1	I	121	GLU
1	I	125	ARG
1	I	134	ARG
1	I	167	GLU
1	I	258	LYS
1	I	278	GLU
1	I	285	LYS
1	I	287	ARG
1	I	288	GLU
1	I	310	ASN
1	I	319	GLU
1	I	327	GLN
1	J	15	LEU
1	J	16	VAL
1	J	24	ASN
1	J	31	GLN
1	J	65	SER
1	J	72	ASN
1	J	76	LEU
1	J	103	LYS
1	J	117	LYS
1	J	125	ARG
1	J	134	ARG
1	J	153	ILE
1	J	167	GLU
1	J	177	LYS

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Mol	Chain	Res	Type
1	J	216	ARG
1	J	257	GLU
1	J	268	VAL
1	J	278	GLU
1	J	287	ARG
1	J	288	GLU
1	J	319	GLU
1	J	327	GLN
1	K	9	ARG
1	K	21	ILE
1	K	24	ASN
1	K	39	VAL
1	K	40	GLU
1	K	44	THR
1	K	47	GLU
1	K	53	GLU
1	K	59	ARG
1	K	66	ASP
1	K	70	GLN
1	K	72	ASN
1	K	82	SER
1	K	103	LYS
1	K	117	LYS
1	K	130	LYS
1	K	153	ILE
1	K	167	GLU
1	K	204	GLU
1	K	268	VAL
1	K	302	PRO
1	K	315	ASP
1	K	316	CYS
1	K	317	GLU
1	K	327	GLN
1	K	343	VAL
1	L	11	ILE
1	L	15	LEU
1	L	16	VAL
1	L	20	ARG
1	L	31	GLN
1	L	39	VAL
1	L	44	THR
1	L	47	GLU

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Mol	Chain	Res	Type
1	L	74	ASP
1	L	76	LEU
1	L	90	ILE
1	L	97	ARG
1	L	103	LYS
1	L	108	ARG
1	L	124	VAL
1	L	125	ARG
1	L	130	LYS
1	L	167	GLU
1	L	177	LYS
1	L	206	VAL
1	L	216	ARG
1	L	230	ARG
1	L	245	PRO
1	L	258	LYS
1	L	262	ARG
1	L	268	VAL
1	L	271	ILE
1	L	278	GLU
1	L	303	LEU
1	L	317	GLU
1	L	324	GLU
1	L	327	GLN
1	L	331	LEU
1	M	12	ARG
1	M	15	LEU
1	M	21	ILE
1	M	23	LYS
1	M	39	VAL
1	M	50	GLN
1	M	72	ASN
1	M	103	LYS
1	M	117	LYS
1	M	125	ARG
1	M	134	ARG
1	M	140	LEU
1	M	167	GLU
1	M	197	ASP
1	M	216	ARG
1	M	230	ARG
1	M	258	LYS

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Mol	Chain	Res	Type
1	M	285	LYS
1	M	287	ARG
1	M	296	VAL
1	M	317	GLU
1	M	319	GLU
1	M	327	GLN
1	M	343	VAL
1	M	346	PRO
1	N	21	ILE
1	N	22	SER
1	N	34	ASP
1	N	40	GLU
1	N	50	GLN
1	N	53	GLU
1	N	59	ARG
1	N	65	SER
1	N	70	GLN
1	N	72	ASN
1	N	97	ARG
1	N	103	LYS
1	N	117	LYS
1	N	121	GLU
1	N	125	ARG
1	N	227	LEU
1	N	258	LYS
1	N	268	VAL
1	N	273	GLU
1	N	278	GLU
1	N	285	LYS
1	N	286	ILE
1	N	287	ARG
1	N	303	LEU
1	N	319	GLU
1	N	343	VAL
1	O	20	ARG
1	O	34	ASP
1	O	39	VAL
1	O	53	GLU
1	O	65	SER
1	O	72	ASN
1	O	125	ARG
1	O	153	ILE

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Mol	Chain	Res	Type
1	O	157	THR
1	O	167	GLU
1	O	204	GLU
1	O	227	LEU
1	O	275	LYS
1	O	280	HIS
1	O	287	ARG
1	O	303	LEU
1	O	316	CYS
1	O	328	SER
1	O	331	LEU
1	O	343	VAL
1	P	16	VAL
1	P	34	ASP
1	P	39	VAL
1	P	40	GLU
1	P	41	ILE
1	P	53	GLU
1	P	72	ASN
1	P	103	LYS
1	P	114	ARG
1	P	117	LYS
1	P	125	ARG
1	P	157	THR
1	P	227	LEU
1	P	258	LYS
1	P	262	ARG
1	P	271	ILE
1	P	278	GLU
1	P	303	LEU
1	P	327	GLN
1	P	331	LEU
1	P	343	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	88	GLN
1	A	147	GLN
1	A	159	ASN
1	A	238	ASN

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Mol	Chain	Res	Type
1	A	246	GLN
1	B	24	ASN
1	B	50	GLN
1	B	70	GLN
1	B	72	ASN
1	B	88	GLN
1	B	135	ASN
1	B	188	GLN
1	B	191	HIS
1	B	238	ASN
1	C	24	ASN
1	C	31	GLN
1	C	72	ASN
1	C	132	ASN
1	C	246	GLN
1	C	290	ASN
1	C	301	HIS
1	C	327	GLN
1	D	24	ASN
1	D	31	GLN
1	D	32	HIS
1	D	50	GLN
1	D	70	GLN
1	D	72	ASN
1	D	88	GLN
1	D	135	ASN
1	D	147	GLN
1	D	246	GLN
1	D	301	HIS
1	D	327	GLN
1	E	88	GLN
1	E	159	ASN
1	E	166	GLN
1	E	191	HIS
1	E	246	GLN
1	F	24	ASN
1	F	31	GLN
1	F	88	GLN
1	F	139	GLN
1	F	188	GLN
1	F	246	GLN
1	F	280	HIS

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Mol	Chain	Res	Type
1	F	327	GLN
1	G	246	GLN
1	H	24	ASN
1	H	72	ASN
1	H	88	GLN
1	H	188	GLN
1	H	327	GLN
1	I	24	ASN
1	I	31	GLN
1	I	72	ASN
1	I	88	GLN
1	I	159	ASN
1	I	246	GLN
1	I	310	ASN
1	J	24	ASN
1	J	31	GLN
1	K	24	ASN
1	K	31	GLN
1	K	32	HIS
1	K	88	GLN
1	K	139	GLN
1	K	188	GLN
1	K	246	GLN
1	K	327	GLN
1	L	88	GLN
1	L	132	ASN
1	L	147	GLN
1	L	188	GLN
1	L	301	HIS
1	M	31	GLN
1	M	72	ASN
1	M	88	GLN
1	M	159	ASN
1	N	31	GLN
1	N	70	GLN
1	N	88	GLN
1	N	159	ASN
1	N	238	ASN
1	N	246	GLN
1	O	31	GLN
1	O	72	ASN
1	O	88	GLN

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Mol	Chain	Res	Type
1	O	188	GLN
1	P	31	GLN
1	P	88	GLN
1	P	135	ASN
1	P	191	HIS
1	P	246	GLN
1	P	301	HIS
1	P	327	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 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	$\# Z > 2$
3	HP7	B	550	-	41,42,42	1.03	3 (7%)	60,64,64	1.95	16 (26%)
2	NAI	D	500	-	47,48,48	1.28	2 (4%)	64,73,73	2.22	21 (32%)
3	HP7	K	550	-	41,42,42	1.10	5 (12%)	60,64,64	1.91	12 (20%)
3	HP7	P	550	-	41,42,42	1.05	2 (4%)	60,64,64	1.35	8 (13%)
2	NAI	H	500	-	47,48,48	1.27	3 (6%)	64,73,73	2.51	24 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAI	I	500	-	47,48,48	1.24	2 (4%)	64,73,73	2.34	23 (35%)
3	HP7	O	550	-	41,42,42	1.06	2 (4%)	60,64,64	1.60	8 (13%)
2	NAI	L	500	-	47,48,48	1.30	2 (4%)	64,73,73	2.30	28 (43%)
2	NAI	E	500	-	47,48,48	1.31	3 (6%)	64,73,73	2.14	21 (32%)
3	HP7	N	550	-	41,42,42	1.07	3 (7%)	60,64,64	2.22	18 (30%)
3	HP7	J	550	-	41,42,42	1.02	3 (7%)	60,64,64	1.92	15 (25%)
2	NAI	M	500	-	47,48,48	1.31	3 (6%)	64,73,73	2.30	24 (37%)
3	HP7	E	550	-	41,42,42	1.06	3 (7%)	60,64,64	1.76	12 (20%)
2	NAI	K	500	-	47,48,48	1.27	2 (4%)	64,73,73	2.52	25 (39%)
2	NAI	P	500	-	47,48,48	1.30	2 (4%)	64,73,73	2.00	20 (31%)
3	HP7	I	550	-	41,42,42	1.08	4 (9%)	60,64,64	1.73	14 (23%)
2	NAI	O	500	-	47,48,48	1.29	2 (4%)	64,73,73	2.43	22 (34%)
2	NAI	J	500	-	47,48,48	1.29	2 (4%)	64,73,73	2.39	24 (37%)
2	NAI	F	500	-	47,48,48	1.28	3 (6%)	64,73,73	2.46	31 (48%)
3	HP7	A	550	-	41,42,42	1.10	4 (9%)	60,64,64	2.15	21 (35%)
3	HP7	F	550	-	41,42,42	1.05	3 (7%)	60,64,64	1.67	12 (20%)
2	NAI	B	500	-	47,48,48	1.33	2 (4%)	64,73,73	2.22	25 (39%)
3	HP7	M	550	-	41,42,42	1.03	3 (7%)	60,64,64	2.19	21 (35%)
3	HP7	G	550	-	41,42,42	1.05	5 (12%)	60,64,64	2.01	17 (28%)
3	HP7	D	550	-	41,42,42	1.05	3 (7%)	60,64,64	1.74	12 (20%)
2	NAI	C	500	-	47,48,48	1.32	3 (6%)	64,73,73	2.37	25 (39%)
3	HP7	H	550	-	41,42,42	1.04	3 (7%)	60,64,64	2.10	17 (28%)
3	HP7	L	550	-	41,42,42	1.09	4 (9%)	60,64,64	1.82	12 (20%)
2	NAI	A	500	-	47,48,48	1.27	3 (6%)	64,73,73	2.31	25 (39%)
2	NAI	G	500	-	47,48,48	1.27	2 (4%)	64,73,73	2.30	29 (45%)
2	NAI	N	500	-	47,48,48	1.29	2 (4%)	64,73,73	2.38	25 (39%)
3	HP7	C	550	-	41,42,42	1.01	2 (4%)	60,64,64	2.10	24 (40%)

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
3	HP7	B	550	-	-	2/28/65/65	0/3/3/3
2	NAI	D	500	-	-	13/29/72/72	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HP7	K	550	-	-	2/28/65/65	0/3/3/3
3	HP7	P	550	-	-	3/28/65/65	0/3/3/3
2	NAI	H	500	-	-	13/29/72/72	0/5/5/5
2	NAI	I	500	-	-	13/29/72/72	0/5/5/5
3	HP7	O	550	-	-	7/28/65/65	0/3/3/3
2	NAI	L	500	-	-	15/29/72/72	0/5/5/5
2	NAI	E	500	-	-	12/29/72/72	0/5/5/5
3	HP7	N	550	-	-	4/28/65/65	0/3/3/3
3	HP7	J	550	-	-	1/28/65/65	0/3/3/3
2	NAI	M	500	-	-	18/29/72/72	0/5/5/5
3	HP7	E	550	-	-	4/28/65/65	0/3/3/3
2	NAI	K	500	-	-	12/29/72/72	0/5/5/5
2	NAI	P	500	-	-	13/29/72/72	0/5/5/5
3	HP7	I	550	-	-	3/28/65/65	0/3/3/3
2	NAI	O	500	-	-	16/29/72/72	0/5/5/5
2	NAI	J	500	-	-	12/29/72/72	0/5/5/5
2	NAI	F	500	-	-	13/29/72/72	0/5/5/5
3	HP7	A	550	-	-	1/28/65/65	0/3/3/3
3	HP7	F	550	-	-	2/28/65/65	0/3/3/3
2	NAI	B	500	-	-	14/29/72/72	0/5/5/5
3	HP7	M	550	-	-	6/28/65/65	0/3/3/3
3	HP7	G	550	-	-	7/28/65/65	0/3/3/3
3	HP7	D	550	-	-	6/28/65/65	0/3/3/3
2	NAI	C	500	-	-	15/29/72/72	0/5/5/5
3	HP7	H	550	-	-	0/28/65/65	0/3/3/3
3	HP7	L	550	-	-	4/28/65/65	0/3/3/3
2	NAI	A	500	-	-	11/29/72/72	0/5/5/5
2	NAI	G	500	-	-	12/29/72/72	0/5/5/5
2	NAI	N	500	-	-	15/29/72/72	0/5/5/5
3	HP7	C	550	-	-	2/28/65/65	0/3/3/3

All (90) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	NAI	C4N-C3N	-5.37	1.39	1.50
2	F	500	NAI	C4N-C3N	-5.13	1.40	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	NAI	C4N-C3N	-5.04	1.40	1.50
2	E	500	NAI	C4N-C3N	-5.04	1.40	1.50
2	O	500	NAI	C4N-C3N	-4.96	1.40	1.50
2	L	500	NAI	C4N-C3N	-4.96	1.40	1.50
2	P	500	NAI	C4N-C3N	-4.95	1.40	1.50
2	D	500	NAI	C4N-C3N	-4.94	1.40	1.50
2	N	500	NAI	C4N-C3N	-4.93	1.40	1.50
2	H	500	NAI	C4N-C3N	-4.87	1.40	1.50
2	I	500	NAI	C4N-C3N	-4.87	1.40	1.50
2	M	500	NAI	C4N-C3N	-4.84	1.40	1.50
2	J	500	NAI	C4N-C3N	-4.81	1.40	1.50
2	A	500	NAI	C4N-C3N	-4.81	1.40	1.50
2	G	500	NAI	C4N-C3N	-4.81	1.40	1.50
2	K	500	NAI	C4N-C3N	-4.79	1.40	1.50
2	G	500	NAI	C4N-C5N	-4.02	1.38	1.49
2	C	500	NAI	C4N-C5N	-3.99	1.38	1.49
2	L	500	NAI	C4N-C5N	-3.99	1.38	1.49
2	F	500	NAI	C4N-C5N	-3.98	1.38	1.49
2	E	500	NAI	C4N-C5N	-3.94	1.38	1.49
2	O	500	NAI	C4N-C5N	-3.93	1.38	1.49
2	H	500	NAI	C4N-C5N	-3.92	1.38	1.49
2	I	500	NAI	C4N-C5N	-3.92	1.38	1.49
2	D	500	NAI	C4N-C5N	-3.89	1.38	1.49
2	M	500	NAI	C4N-C5N	-3.89	1.38	1.49
2	K	500	NAI	C4N-C5N	-3.89	1.38	1.49
2	J	500	NAI	C4N-C5N	-3.89	1.38	1.49
2	A	500	NAI	C4N-C5N	-3.84	1.39	1.49
2	N	500	NAI	C4N-C5N	-3.77	1.39	1.49
2	B	500	NAI	C4N-C5N	-3.75	1.39	1.49
2	P	500	NAI	C4N-C5N	-3.73	1.39	1.49
3	I	550	HP7	C2-N1	-3.13	1.33	1.38
3	A	550	HP7	C2-N1	-3.03	1.33	1.38
3	D	550	HP7	C2-N1	-2.93	1.33	1.38
3	G	550	HP7	C2-N1	-2.91	1.33	1.38
3	O	550	HP7	C2-N1	-2.90	1.33	1.38
3	P	550	HP7	C2-N1	-2.87	1.34	1.38
3	K	550	HP7	C2-N1	-2.86	1.34	1.38
3	H	550	HP7	C2-N1	-2.79	1.34	1.38
3	E	550	HP7	C2-N1	-2.75	1.34	1.38
3	B	550	HP7	C2-N1	-2.69	1.34	1.38
3	N	550	HP7	PB-O3A	2.63	1.62	1.59
3	L	550	HP7	PA-O3A	2.62	1.62	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	550	HP7	C2-N1	-2.56	1.34	1.38
3	L	550	HP7	C2-N1	-2.54	1.34	1.38
3	C	550	HP7	C2-N1	-2.51	1.34	1.38
3	B	550	HP7	PA-O3A	2.48	1.62	1.59
3	F	550	HP7	C2-N1	-2.46	1.34	1.38
3	N	550	HP7	C2-N1	-2.44	1.34	1.38
3	M	550	HP7	C2-N1	-2.42	1.34	1.38
3	F	550	HP7	C4-N3	-2.41	1.34	1.38
3	E	550	HP7	PB-O3A	2.32	1.62	1.59
3	L	550	HP7	PB-O3A	2.32	1.62	1.59
3	K	550	HP7	PB-O3A	2.31	1.62	1.59
3	K	550	HP7	PA-O3A	2.28	1.62	1.59
3	A	550	HP7	PB-O3A	2.25	1.61	1.59
3	I	550	HP7	C4-N3	-2.25	1.34	1.38
3	J	550	HP7	C4-N3	-2.21	1.34	1.38
3	K	550	HP7	C4-N3	-2.16	1.34	1.38
3	M	550	HP7	PA-O3A	2.16	1.61	1.59
3	I	550	HP7	C5-C4	-2.15	1.39	1.43
3	A	550	HP7	C5-C4	-2.14	1.39	1.43
3	D	550	HP7	PB-O3A	2.14	1.61	1.59
3	A	550	HP7	C6-C5	2.12	1.40	1.35
2	C	500	NAI	C6N-N1N	-2.12	1.32	1.37
3	E	550	HP7	PA-O3A	2.11	1.61	1.59
3	G	550	HP7	C5-C4	-2.10	1.39	1.43
3	M	550	HP7	C6-C5	2.10	1.40	1.35
3	P	550	HP7	C5-C4	-2.10	1.39	1.43
3	O	550	HP7	PA-O3A	2.09	1.61	1.59
3	H	550	HP7	C4-N3	-2.08	1.35	1.38
2	A	500	NAI	C6N-C5N	2.08	1.39	1.33
3	L	550	HP7	C6-C5	2.08	1.39	1.35
3	G	550	HP7	C4-N3	-2.08	1.35	1.38
3	H	550	HP7	C5-C4	-2.08	1.39	1.43
3	C	550	HP7	C6-C5	2.07	1.39	1.35
3	G	550	HP7	PB-O3A	2.07	1.61	1.59
2	F	500	NAI	C6N-N1N	-2.06	1.32	1.37
3	I	550	HP7	C2-N3	-2.06	1.34	1.38
3	J	550	HP7	C6-C5	2.05	1.39	1.35
3	F	550	HP7	PA-O3A	2.04	1.61	1.59
2	M	500	NAI	C6N-C5N	2.04	1.39	1.33
2	E	500	NAI	C6N-N1N	-2.04	1.32	1.37
2	H	500	NAI	C6N-N1N	-2.03	1.32	1.37
3	D	550	HP7	PA-O3A	2.02	1.61	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	550	HP7	C4-N3	-2.02	1.35	1.38
3	B	550	HP7	C4-N3	-2.01	1.35	1.38
3	K	550	HP7	C5-C4	-2.01	1.39	1.43
3	G	550	HP7	PA-O3A	2.00	1.61	1.59

All (631) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	500	NAI	C5B-C4B-C3B	-7.15	89.48	115.21
2	D	500	NAI	C5B-C4B-C3B	-7.05	89.82	115.21
3	N	550	HP7	C4-N3-C2	-7.05	117.86	126.61
2	O	500	NAI	C5A-C4A-N3A	-6.91	117.20	126.72
2	H	500	NAI	O4D-C4D-C5D	-6.69	87.92	109.33
3	J	550	HP7	C4-N3-C2	-6.58	118.44	126.61
3	K	550	HP7	O5'-C1'-O3B	-6.58	102.77	111.36
2	F	500	NAI	C5A-C4A-N3A	-6.57	117.68	126.72
2	M	500	NAI	C5B-C4B-C3B	-6.56	91.58	115.21
2	K	500	NAI	O4D-C4D-C5D	-6.44	88.72	109.33
2	I	500	NAI	O4D-C4D-C5D	-6.38	88.90	109.33
3	A	550	HP7	C4-N3-C2	-6.23	118.87	126.61
3	L	550	HP7	O5'-C1'-O3B	-6.23	103.22	111.36
2	G	500	NAI	N3A-C2A-N1A	-6.23	119.15	128.58
2	H	500	NAI	C6N-N1N-C2N	6.20	125.95	119.32
2	H	500	NAI	O4B-C1B-N9A	6.14	119.87	108.09
2	A	500	NAI	C5A-C4A-N3A	-6.13	118.28	126.72
3	D	550	HP7	O5'-C1'-O3B	-6.04	103.47	111.36
2	N	500	NAI	N3A-C2A-N1A	-6.01	119.48	128.58
2	I	500	NAI	C5B-C4B-C3B	-6.00	93.63	115.21
3	M	550	HP7	O5'-C1'-O3B	-5.95	103.59	111.36
3	N	550	HP7	C8'-C7'-N2'	5.93	125.95	116.12
3	B	550	HP7	C4-N3-C2	-5.84	119.36	126.61
2	K	500	NAI	N3A-C2A-N1A	-5.75	119.88	128.58
2	F	500	NAI	C5B-C4B-C3B	-5.69	94.73	115.21
2	O	500	NAI	O5B-C5B-C4B	5.69	128.36	108.99
3	C	550	HP7	C4-N3-C2	-5.66	119.58	126.61
2	P	500	NAI	C5B-C4B-C3B	-5.66	94.84	115.21
2	N	500	NAI	C5B-C4B-C3B	-5.65	94.86	115.21
3	G	550	HP7	N3-C2-N1	5.65	122.24	114.89
2	L	500	NAI	N3A-C2A-N1A	-5.65	120.04	128.58
3	G	550	HP7	C4-N3-C2	-5.63	119.62	126.61
3	N	550	HP7	O7'-C7'-N2'	-5.61	112.08	121.98
3	M	550	HP7	N3-C2-N1	5.58	122.16	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	550	HP7	N3-C2-N1	5.56	122.13	114.89
3	M	550	HP7	C8'-C7'-N2'	5.55	125.33	116.12
2	C	500	NAI	C5A-N7A-C8A	5.52	112.12	103.45
3	O	550	HP7	N3-C2-N1	5.51	122.07	114.89
3	K	550	HP7	N3-C2-N1	5.50	122.06	114.89
3	N	550	HP7	C5-C4-N3	5.50	122.51	114.80
2	O	500	NAI	N3A-C2A-N1A	-5.48	120.29	128.58
2	A	500	NAI	N3A-C2A-N1A	-5.46	120.32	128.58
3	H	550	HP7	O5'-C1'-O3B	-5.45	104.23	111.36
2	K	500	NAI	C5A-N7A-C8A	5.43	111.99	103.45
3	H	550	HP7	C4-N3-C2	-5.43	119.88	126.61
3	A	550	HP7	C5-C4-N3	5.42	122.40	114.80
3	A	550	HP7	C8'-C7'-N2'	5.40	125.07	116.12
3	M	550	HP7	C4-N3-C2	-5.40	119.91	126.61
2	B	500	NAI	O4D-C1D-N1N	5.35	118.28	108.08
2	M	500	NAI	C4A-C5A-N7A	-5.35	104.47	110.58
2	C	500	NAI	C6N-N1N-C2N	5.29	124.98	119.32
2	B	500	NAI	C5B-C4B-C3B	-5.26	96.26	115.21
3	L	550	HP7	C1'-C2'-N2'	-5.26	102.09	110.92
3	G	550	HP7	C8'-C7'-N2'	5.17	124.69	116.12
2	O	500	NAI	C2A-N3A-C4A	5.16	124.44	111.83
2	O	500	NAI	O4D-C1D-N1N	5.12	117.84	108.08
2	E	500	NAI	C5A-C4A-N3A	-5.09	119.71	126.72
3	I	550	HP7	C6-C5-C4	-5.07	113.05	119.53
2	E	500	NAI	C5B-C4B-C3B	-5.07	96.96	115.21
2	D	500	NAI	O4D-C1D-N1N	5.04	117.70	108.08
3	H	550	HP7	C3'-C2'-N2'	-5.03	101.34	110.62
3	E	550	HP7	C4-N3-C2	-5.03	120.37	126.61
3	C	550	HP7	C5-C4-N3	5.00	121.81	114.80
2	K	500	NAI	N9A-C8A-N7A	-4.98	106.87	113.94
2	C	500	NAI	C5A-C4A-N3A	-4.96	119.88	126.72
2	E	500	NAI	N3A-C2A-N1A	-4.96	121.08	128.58
2	O	500	NAI	N3A-C4A-N9A	4.95	135.58	127.17
2	N	500	NAI	C6N-N1N-C2N	4.94	124.61	119.32
2	H	500	NAI	C3B-C2B-C1B	-4.93	92.13	101.46
2	P	500	NAI	C6N-N1N-C2N	4.93	124.59	119.32
2	L	500	NAI	C5B-C4B-C3B	-4.91	97.52	115.21
2	J	500	NAI	C5A-C4A-N3A	-4.89	119.98	126.72
2	F	500	NAI	C6N-N1N-C2N	4.87	124.53	119.32
2	A	500	NAI	C4A-C5A-N7A	-4.87	105.01	110.58
2	J	500	NAI	C6N-N1N-C2N	4.86	124.52	119.32
2	C	500	NAI	C4A-C5A-N7A	-4.86	105.03	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	550	HP7	C4-N3-C2	-4.83	120.62	126.61
3	B	550	HP7	N3-C2-N1	4.83	121.18	114.89
2	M	500	NAI	C3N-C7N-N7N	4.79	126.18	117.67
2	M	500	NAI	C5A-N7A-C8A	4.79	110.97	103.45
2	A	500	NAI	C5A-N7A-C8A	4.77	110.94	103.45
2	M	500	NAI	C5A-C4A-N3A	-4.76	120.17	126.72
2	J	500	NAI	N3A-C2A-N1A	-4.74	121.40	128.58
2	N	500	NAI	C1D-N1N-C2N	-4.74	113.33	121.14
3	D	550	HP7	C4-N3-C2	-4.73	120.75	126.61
2	D	500	NAI	N3A-C2A-N1A	-4.70	121.46	128.58
3	E	550	HP7	N3-C2-N1	4.70	121.01	114.89
2	O	500	NAI	O4D-C4D-C5D	-4.64	94.46	109.33
2	P	500	NAI	C5A-C4A-N3A	-4.63	120.34	126.72
3	H	550	HP7	N3-C2-N1	4.62	120.91	114.89
2	I	500	NAI	N3A-C4A-N9A	4.59	134.98	127.17
2	H	500	NAI	O3-PN-O2N	4.58	124.49	110.70
2	K	500	NAI	C5A-C4A-N3A	-4.58	120.41	126.72
3	I	550	HP7	C5-C4-N3	4.57	121.21	114.80
2	I	500	NAI	C5A-C4A-N3A	-4.55	120.44	126.72
2	I	500	NAI	O3-PN-O2N	4.53	124.34	110.70
2	C	500	NAI	C5B-C4B-C3B	-4.53	98.89	115.21
2	E	500	NAI	O4D-C1D-N1N	4.52	116.70	108.08
2	A	500	NAI	C2A-N3A-C4A	4.51	122.84	111.83
3	F	550	HP7	O4-C4-N3	-4.48	112.78	119.27
2	G	500	NAI	O1N-PN-O3	-4.47	95.19	107.27
3	K	550	HP7	C8'-C7'-N2'	4.43	123.47	116.12
2	J	500	NAI	C1D-N1N-C2N	-4.43	113.84	121.14
2	C	500	NAI	N9A-C8A-N7A	-4.43	107.65	113.94
2	B	500	NAI	N3A-C2A-N1A	-4.41	121.90	128.58
2	N	500	NAI	C2A-N3A-C4A	4.39	122.55	111.83
2	I	500	NAI	N3A-C2A-N1A	-4.38	121.96	128.58
3	O	550	HP7	C4-N3-C2	-4.37	121.19	126.61
2	B	500	NAI	O4D-C4D-C5D	-4.37	95.35	109.33
2	K	500	NAI	C2A-N3A-C4A	4.35	122.45	111.83
2	J	500	NAI	O4D-C4D-C5D	-4.27	95.67	109.33
2	H	500	NAI	O1N-PN-O2N	-4.27	92.60	112.44
2	H	500	NAI	C5B-C4B-C3B	-4.25	99.90	115.21
2	L	500	NAI	N3A-C4A-N9A	4.25	134.40	127.17
2	E	500	NAI	C4A-C5A-N7A	-4.21	105.76	110.58
2	D	500	NAI	O4D-C4D-C5D	-4.21	95.85	109.33
2	O	500	NAI	C5A-N7A-C8A	4.21	110.07	103.45
3	A	550	HP7	O7'-C7'-C8'	-4.21	114.56	122.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500	NAI	N3A-C2A-N1A	-4.19	122.24	128.58
2	D	500	NAI	N3A-C4A-N9A	4.17	134.27	127.17
2	L	500	NAI	C3B-C2B-C1B	-4.17	93.58	101.46
2	N	500	NAI	C5A-C4A-N3A	-4.16	120.99	126.72
3	N	550	HP7	N3-C2-N1	4.16	120.31	114.89
2	K	500	NAI	C4A-C5A-N7A	-4.11	105.89	110.58
2	G	500	NAI	C5B-C4B-C3B	-4.10	100.44	115.21
2	I	500	NAI	O1N-PN-O3	-4.10	96.19	107.27
2	B	500	NAI	C4A-C5A-N7A	-4.09	105.90	110.58
2	H	500	NAI	N3A-C2A-N1A	-4.09	122.39	128.58
2	D	500	NAI	C5A-C4A-N3A	-4.08	121.09	126.72
2	P	500	NAI	N3A-C2A-N1A	-4.08	122.40	128.58
2	G	500	NAI	O3-PN-O2N	4.07	122.94	110.70
3	J	550	HP7	C5-C4-N3	4.06	120.49	114.80
2	F	500	NAI	N3A-C4A-N9A	4.06	134.07	127.17
3	L	550	HP7	C4-N3-C2	-4.06	121.58	126.61
2	B	500	NAI	C5A-N7A-C8A	4.04	109.81	103.45
2	A	500	NAI	C3N-C7N-N7N	4.04	124.84	117.67
2	F	500	NAI	O3-PN-O2N	4.02	122.78	110.70
3	M	550	HP7	O'Q-C6'-O'P	-4.01	114.99	124.08
2	O	500	NAI	C4A-C5A-N7A	-4.00	106.01	110.58
2	H	500	NAI	C3N-C2N-N1N	-3.99	117.34	123.20
3	G	550	HP7	O2-C2-N1	-3.99	117.60	122.80
2	G	500	NAI	O5B-C5B-C4B	3.99	122.59	108.99
3	B	550	HP7	C5-C4-N3	3.98	120.38	114.80
3	E	550	HP7	O5'-C1'-C2'	3.96	118.08	110.59
2	F	500	NAI	C4A-C5A-N7A	-3.96	106.06	110.58
2	A	500	NAI	O1N-PN-O3	-3.94	96.63	107.27
2	K	500	NAI	O2A-PA-O5B	-3.92	89.80	107.57
2	K	500	NAI	N3A-C4A-N9A	3.92	133.83	127.17
3	B	550	HP7	C1'-C2'-N2'	-3.91	104.36	110.92
3	D	550	HP7	N3-C2-N1	3.91	119.98	114.89
3	H	550	HP7	O4-C4-C5	-3.90	118.43	125.16
2	J	500	NAI	C4D-O4D-C1D	-3.88	100.90	109.47
3	G	550	HP7	O5C-C5C-C4C	-3.88	95.78	108.99
2	K	500	NAI	C6A-C5A-N7A	3.87	139.56	132.09
2	C	500	NAI	O3-PN-O2N	3.87	122.35	110.70
2	A	500	NAI	O3-PN-O2N	3.87	122.34	110.70
2	E	500	NAI	C2A-N3A-C4A	3.86	121.26	111.83
2	E	500	NAI	O4B-C1B-C2B	-3.85	98.39	106.62
2	L	500	NAI	C5A-C4A-N3A	-3.83	121.44	126.72
2	F	500	NAI	O1N-PN-O5D	-3.83	90.22	107.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	500	NAI	C6N-N1N-C2N	3.82	123.40	119.32
2	A	500	NAI	O7N-C7N-C3N	-3.81	113.72	120.90
2	J	500	NAI	C2A-N3A-C4A	3.80	121.11	111.83
2	J	500	NAI	N3A-C4A-N9A	3.80	133.63	127.17
3	A	550	HP7	O2-C2-N1	-3.79	117.86	122.80
2	A	500	NAI	N3A-C4A-N9A	3.79	133.61	127.17
2	H	500	NAI	C5A-C4A-N3A	-3.78	121.52	126.72
2	G	500	NAI	C2A-N1A-C6A	3.77	124.92	118.73
2	K	500	NAI	C5B-C4B-C3B	-3.77	101.65	115.21
2	C	500	NAI	O4D-C4D-C5D	-3.77	97.27	109.33
2	F	500	NAI	O1N-PN-O3	-3.77	97.09	107.27
2	L	500	NAI	C2A-N3A-C4A	3.76	121.01	111.83
2	E	500	NAI	C5A-N7A-C8A	3.75	109.34	103.45
2	M	500	NAI	O7N-C7N-N7N	-3.73	114.53	122.89
3	C	550	HP7	O2-C2-N3	-3.72	114.62	121.49
3	F	550	HP7	O3'-C3'-C2'	-3.72	102.19	109.58
2	K	500	NAI	C3N-C2N-N1N	-3.71	117.75	123.20
3	G	550	HP7	C5-C4-N3	3.71	120.00	114.80
3	D	550	HP7	C5-C4-N3	3.70	119.98	114.80
3	J	550	HP7	C4'-C3'-C2'	-3.68	105.04	110.40
3	E	550	HP7	O2-C2-N1	-3.68	118.00	122.80
2	F	500	NAI	C3N-C2N-N1N	-3.67	117.82	123.20
2	L	500	NAI	C5A-N7A-C8A	3.66	109.20	103.45
2	P	500	NAI	N3A-C4A-N9A	3.65	133.38	127.17
2	C	500	NAI	N3A-C4A-N9A	3.64	133.37	127.17
2	L	500	NAI	N9A-C8A-N7A	-3.63	108.78	113.94
2	F	500	NAI	C5A-N7A-C8A	3.62	109.13	103.45
2	N	500	NAI	C4A-N9A-C1B	-3.61	118.20	126.63
3	A	550	HP7	N3-C2-N1	3.61	119.59	114.89
2	M	500	NAI	O2A-PA-O5B	-3.61	91.23	107.57
3	L	550	HP7	C5-C4-N3	3.60	119.84	114.80
2	G	500	NAI	C4A-N9A-C1B	-3.59	118.23	126.63
3	I	550	HP7	O5'-C5'-C4'	-3.59	102.40	109.48
2	J	500	NAI	C3D-C2D-C1D	-3.58	94.70	101.46
2	H	500	NAI	O1N-PN-O3	3.57	116.93	107.27
2	K	500	NAI	C4A-N9A-C8A	3.56	109.48	105.74
3	J	550	HP7	O4-C4-N3	-3.56	114.11	119.27
2	K	500	NAI	C4A-N9A-C1B	-3.56	118.31	126.63
2	L	500	NAI	O5B-C5B-C4B	3.56	121.11	108.99
2	N	500	NAI	O3-PN-O2N	3.56	121.41	110.70
3	E	550	HP7	O4-C4-C5	-3.56	119.03	125.16
2	I	500	NAI	O4D-C1D-N1N	3.54	114.84	108.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	500	NAI	C5A-N7A-C8A	3.54	109.01	103.45
2	D	500	NAI	O2D-C2D-C1D	-3.53	97.94	110.10
3	G	550	HP7	O3B-PB-O1B	-3.53	98.53	109.81
2	I	500	NAI	C6N-N1N-C2N	3.52	123.08	119.32
2	F	500	NAI	C1D-N1N-C2N	-3.52	115.35	121.14
3	K	550	HP7	C3'-C2'-N2'	-3.52	104.14	110.62
2	J	500	NAI	C5A-N7A-C8A	3.51	108.97	103.45
2	G	500	NAI	O4D-C4D-C5D	-3.51	98.10	109.33
2	I	500	NAI	C1D-N1N-C2N	-3.51	115.36	121.14
2	B	500	NAI	C6A-C5A-N7A	3.50	138.84	132.09
3	C	550	HP7	N3-C2-N1	3.47	119.41	114.89
3	F	550	HP7	O2-C2-N3	-3.47	115.10	121.49
2	G	500	NAI	C5A-N7A-C8A	3.46	108.89	103.45
2	N	500	NAI	C1B-N9A-C8A	3.46	134.77	127.09
2	B	500	NAI	O5B-C5B-C4B	3.45	120.75	108.99
3	B	550	HP7	C2C-C1C-N1	-3.45	103.64	113.25
3	M	550	HP7	O7'-C7'-C8'	-3.45	115.91	122.05
2	I	500	NAI	C2A-N3A-C4A	3.45	120.26	111.83
2	L	500	NAI	C4A-N9A-C8A	3.45	109.36	105.74
2	L	500	NAI	O4D-C1D-N1N	3.45	114.66	108.08
2	N	500	NAI	C6A-C5A-N7A	3.44	138.72	132.09
2	G	500	NAI	C2A-N3A-C4A	3.43	120.21	111.83
2	H	500	NAI	C5A-N7A-C8A	3.42	108.83	103.45
2	M	500	NAI	N3A-C2A-N1A	-3.41	123.41	128.58
3	C	550	HP7	O5'-C1'-O3B	-3.41	106.91	111.36
3	L	550	HP7	C1'-O5'-C5'	-3.41	106.65	112.23
3	A	550	HP7	C1C-N1-C2	-3.40	111.49	117.59
3	F	550	HP7	C4-N3-C2	-3.38	122.41	126.61
2	C	500	NAI	C3N-C2N-N1N	-3.38	118.25	123.20
3	P	550	HP7	O5'-C1'-O3B	-3.37	106.97	111.36
2	N	500	NAI	O3-PA-O1A	-3.36	100.59	110.70
3	M	550	HP7	O3C-C3C-C4C	-3.34	101.48	111.08
2	C	500	NAI	C2A-N3A-C4A	3.34	119.99	111.83
3	C	550	HP7	O'Q-C6'-O'P	-3.34	116.51	124.08
2	D	500	NAI	C6N-N1N-C2N	3.33	122.89	119.32
3	N	550	HP7	O5C-C5C-C4C	-3.33	97.65	108.99
3	H	550	HP7	O5'-C1'-C2'	3.33	116.89	110.59
2	F	500	NAI	O4D-C4D-C3D	3.32	111.75	105.15
2	B	500	NAI	C2D-C3D-C4D	-3.31	96.22	102.61
3	H	550	HP7	C5-C4-N3	3.31	119.43	114.80
2	K	500	NAI	O5D-C5D-C4D	3.31	120.25	108.99
3	H	550	HP7	O2A-PA-O1A	3.30	127.80	112.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	500	NAI	O1N-PN-O3	-3.30	98.36	107.27
2	N	500	NAI	N3A-C4A-N9A	3.26	132.72	127.17
2	G	500	NAI	N9A-C8A-N7A	-3.25	109.33	113.94
2	P	500	NAI	C5A-N7A-C8A	3.24	108.55	103.45
2	I	500	NAI	N9A-C8A-N7A	-3.24	109.34	113.94
2	K	500	NAI	O3D-C3D-C4D	-3.23	101.80	111.08
2	N	500	NAI	O4D-C4D-C5D	-3.23	98.99	109.33
2	J	500	NAI	C3N-C2N-N1N	-3.23	118.47	123.20
3	C	550	HP7	O4C-C4C-C3C	-3.22	98.76	105.15
2	F	500	NAI	O2B-C2B-C3B	-3.20	101.56	111.82
2	G	500	NAI	N3A-C4A-N9A	3.20	132.61	127.17
2	J	500	NAI	O4D-C1D-C2D	3.18	113.43	106.62
3	H	550	HP7	O3A-PA-O1A	-3.18	101.13	110.70
2	J	500	NAI	O4B-C1B-N9A	3.18	114.20	108.09
3	F	550	HP7	N3-C2-N1	3.18	119.03	114.89
3	F	550	HP7	C5-C4-N3	3.18	119.25	114.80
3	B	550	HP7	O2A-PA-O3A	3.16	115.82	107.27
2	L	500	NAI	C4B-O4B-C1B	-3.16	102.49	109.47
3	O	550	HP7	O5'-C1'-O3B	-3.16	107.24	111.36
2	M	500	NAI	O3-PN-O2N	3.16	120.20	110.70
3	D	550	HP7	O2-C2-N1	-3.15	118.69	122.80
2	A	500	NAI	O2A-PA-O3	-3.15	98.76	107.27
2	G	500	NAI	C5A-C4A-N3A	-3.14	122.39	126.72
2	N	500	NAI	C5A-N7A-C8A	3.14	108.38	103.45
2	F	500	NAI	C2A-N3A-C4A	3.14	119.50	111.83
3	L	550	HP7	N3-C2-N1	3.13	118.96	114.89
2	H	500	NAI	O2D-C2D-C1D	-3.12	99.37	110.10
3	C	550	HP7	C3'-C2'-N2'	-3.11	104.88	110.62
2	G	500	NAI	O3D-C3D-C4D	-3.11	102.14	111.08
2	D	500	NAI	C2A-N3A-C4A	3.11	119.42	111.83
2	D	500	NAI	C4B-O4B-C1B	-3.10	102.62	109.47
2	L	500	NAI	O1N-PN-O3	3.10	115.65	107.27
2	M	500	NAI	O1N-PN-O3	-3.09	98.91	107.27
2	I	500	NAI	C4A-N9A-C8A	3.08	108.97	105.74
3	E	550	HP7	C4'-C3'-C2'	-3.08	105.92	110.40
2	I	500	NAI	C4B-O4B-C1B	-3.08	102.67	109.47
2	H	500	NAI	C1D-N1N-C2N	-3.08	116.07	121.14
3	F	550	HP7	C8'-C7'-N2'	3.07	121.21	116.12
3	E	550	HP7	C5-C4-N3	3.06	119.08	114.80
3	H	550	HP7	O2-C2-N1	-3.05	118.83	122.80
2	P	500	NAI	C2A-N3A-C4A	3.04	119.26	111.83
3	N	550	HP7	O2C-C2C-C1C	-3.04	99.64	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	500	NAI	O1N-PN-O2N	-3.04	98.32	112.44
2	E	500	NAI	O3-PA-O1A	-3.04	101.57	110.70
3	K	550	HP7	O7'-C7'-N2'	-3.03	116.62	121.98
3	I	550	HP7	O5C-C5C-C4C	-3.03	98.67	108.99
2	E	500	NAI	C1D-N1N-C2N	-3.03	116.15	121.14
2	L	500	NAI	O4D-C4D-C5D	-3.02	99.65	109.33
2	E	500	NAI	C6N-N1N-C2N	3.02	122.55	119.32
3	C	550	HP7	C8'-C7'-N2'	3.01	121.12	116.12
2	B	500	NAI	C6N-N1N-C2N	3.01	122.54	119.32
2	C	500	NAI	C4B-O4B-C1B	-3.00	102.85	109.47
3	C	550	HP7	O2C-C2C-C3C	-2.99	102.23	111.82
2	E	500	NAI	O4B-C1B-N9A	2.99	113.83	108.09
2	H	500	NAI	C4A-C5A-N7A	-2.98	107.17	110.58
2	P	500	NAI	C1D-N1N-C2N	-2.98	116.23	121.14
2	J	500	NAI	C4A-C5A-N7A	-2.97	107.19	110.58
2	L	500	NAI	O4B-C1B-N9A	2.96	113.78	108.09
2	M	500	NAI	C1D-N1N-C2N	-2.96	116.26	121.14
3	K	550	HP7	C5-C6-N1	-2.95	117.04	121.84
2	M	500	NAI	C5A-C4A-N9A	2.95	109.02	105.81
2	A	500	NAI	N9A-C8A-N7A	-2.95	109.76	113.94
3	C	550	HP7	O4-C4-N3	-2.94	115.01	119.27
2	C	500	NAI	O2A-PA-O3	-2.93	99.34	107.27
2	F	500	NAI	O4B-C4B-C3B	2.92	110.95	105.15
2	O	500	NAI	O3B-C3B-C4B	-2.92	102.70	111.08
2	N	500	NAI	O4B-C4B-C5B	2.91	118.67	109.33
3	D	550	HP7	C3C-C2C-C1C	2.91	106.97	101.46
3	L	550	HP7	O4-C4-C5	-2.91	120.14	125.16
2	H	500	NAI	N3A-C4A-N9A	2.89	132.08	127.17
3	P	550	HP7	N3-C2-N1	2.89	118.65	114.89
3	J	550	HP7	O2A-PA-O1A	2.89	125.87	112.44
3	O	550	HP7	O2C-C2C-C1C	-2.88	100.19	110.10
2	O	500	NAI	O3-PN-O2N	2.88	119.36	110.70
3	F	550	HP7	C4'-C3'-C2'	2.87	114.58	110.40
2	M	500	NAI	C2A-N3A-C4A	2.87	118.83	111.83
3	M	550	HP7	O4C-C1C-N1	2.85	114.83	108.36
2	N	500	NAI	O5B-PA-O1A	2.85	120.24	108.94
2	H	500	NAI	C2A-N1A-C6A	2.85	123.42	118.73
3	A	550	HP7	O2C-C2C-C3C	-2.84	102.72	111.82
2	H	500	NAI	O4B-C4B-C5B	2.83	118.41	109.33
2	A	500	NAI	C6A-C5A-N7A	2.83	137.54	132.09
2	B	500	NAI	C1D-N1N-C2N	-2.83	116.48	121.14
3	D	550	HP7	O5'-C5'-C4'	-2.83	103.90	109.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	NAI	O4D-C1D-N1N	2.82	113.47	108.08
2	B	500	NAI	C2B-C1B-N9A	-2.82	106.29	113.30
2	E	500	NAI	N3A-C4A-N9A	2.81	131.95	127.17
3	A	550	HP7	C3'-C2'-N2'	-2.79	105.47	110.62
2	G	500	NAI	C1B-N9A-C8A	2.79	133.28	127.09
2	G	500	NAI	O1N-PN-O5D	-2.77	95.00	107.57
2	K	500	NAI	O4B-C1B-N9A	2.77	113.40	108.09
2	O	500	NAI	O2A-PA-O5B	-2.76	95.04	107.57
2	L	500	NAI	O7N-C7N-N7N	-2.76	116.70	122.89
2	D	500	NAI	C2A-N1A-C6A	2.76	123.26	118.73
2	L	500	NAI	C4A-N9A-C1B	-2.76	120.18	126.63
2	B	500	NAI	C2A-N1A-C6A	2.76	123.26	118.73
2	G	500	NAI	C4D-O4D-C1D	2.75	115.55	109.47
2	O	500	NAI	C6A-C5A-N7A	2.74	137.38	132.09
3	B	550	HP7	C5C-C4C-C3C	-2.74	105.34	115.21
3	C	550	HP7	C1'-C2'-N2'	2.74	115.51	110.92
2	E	500	NAI	C3N-C2N-N1N	-2.73	119.19	123.20
2	O	500	NAI	C6N-N1N-C2N	2.72	122.23	119.32
2	L	500	NAI	C3N-C7N-N7N	2.72	122.50	117.67
2	M	500	NAI	N9A-C8A-N7A	-2.72	110.08	113.94
2	F	500	NAI	O3-PA-O1A	-2.72	102.53	110.70
3	A	550	HP7	C4'-C3'-C2'	2.72	114.36	110.40
2	O	500	NAI	C5B-C4B-C3B	-2.70	105.48	115.21
3	P	550	HP7	O5C-C5C-C4C	-2.70	99.80	108.99
3	N	550	HP7	O2-C2-N1	-2.70	119.29	122.80
2	P	500	NAI	O2A-PA-O5B	-2.70	95.35	107.57
3	C	550	HP7	O7'-C7'-N2'	-2.69	117.22	121.98
2	F	500	NAI	O2A-PA-O1A	-2.69	99.92	112.44
3	C	550	HP7	O5'-C1'-C2'	2.69	115.68	110.59
3	G	550	HP7	O7'-C7'-C8'	-2.69	117.27	122.05
2	K	500	NAI	O4B-C4B-C3B	2.68	110.48	105.15
2	P	500	NAI	O3D-C3D-C2D	-2.68	103.23	111.82
2	M	500	NAI	C1B-N9A-C8A	2.67	133.03	127.09
2	D	500	NAI	C3B-C2B-C1B	-2.67	96.41	101.46
3	G	550	HP7	C1'-O5'-C5'	2.67	116.61	112.23
2	O	500	NAI	N9A-C8A-N7A	-2.67	110.15	113.94
2	B	500	NAI	C4B-O4B-C1B	-2.67	103.58	109.47
2	H	500	NAI	C2A-N3A-C4A	2.66	118.33	111.83
2	M	500	NAI	C6A-C5A-N7A	2.65	137.20	132.09
3	N	550	HP7	O'Q-C6'-O'P	-2.65	118.08	124.08
2	N	500	NAI	C6A-C5A-C4A	-2.64	113.57	117.18
2	H	500	NAI	O7N-C7N-C3N	-2.63	115.93	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	500	NAI	C6A-C5A-N7A	2.63	137.15	132.09
3	C	550	HP7	O3'-C3'-C2'	2.62	114.80	109.58
2	G	500	NAI	C4A-N9A-C8A	2.62	108.49	105.74
2	C	500	NAI	O2A-PA-O5B	-2.62	95.71	107.57
3	B	550	HP7	O3A-PA-O1A	-2.61	102.85	110.70
2	P	500	NAI	C4A-C5A-N7A	-2.60	107.61	110.58
2	H	500	NAI	PN-O5D-C5D	-2.60	106.48	121.35
3	B	550	HP7	O4C-C1C-N1	2.60	114.24	108.36
2	B	500	NAI	PA-O5B-C5B	-2.59	106.49	121.35
3	E	550	HP7	C2C-C3C-C4C	-2.59	97.60	102.61
3	M	550	HP7	O2C-C2C-C1C	-2.59	101.19	110.10
2	B	500	NAI	C4D-O4D-C1D	-2.59	103.75	109.47
3	E	550	HP7	O5'-C1'-O3B	-2.59	107.98	111.36
2	L	500	NAI	C5A-C6A-N6A	-2.59	116.88	123.29
3	N	550	HP7	O4-C4-C5	-2.59	120.70	125.16
3	O	550	HP7	O2-C2-N1	-2.58	119.43	122.80
2	F	500	NAI	C4B-O4B-C1B	-2.58	103.76	109.47
3	J	550	HP7	C3'-C2'-N2'	-2.58	105.86	110.62
2	I	500	NAI	PN-O5D-C5D	-2.58	106.56	121.35
2	L	500	NAI	PA-O5B-C5B	-2.58	106.58	121.35
2	I	500	NAI	PA-O5B-C5B	-2.57	106.61	121.35
2	C	500	NAI	C4A-N9A-C8A	2.57	108.44	105.74
2	C	500	NAI	O4B-C4B-C3B	2.57	110.25	105.15
3	P	550	HP7	C8'-C7'-N2'	2.56	120.37	116.12
2	K	500	NAI	PN-O5D-C5D	-2.56	106.67	121.35
2	B	500	NAI	PN-O5D-C5D	-2.56	106.67	121.35
3	A	550	HP7	O2B-PB-O3A	2.56	114.19	107.27
3	N	550	HP7	C5-C6-N1	-2.55	117.69	121.84
2	M	500	NAI	C6N-N1N-C2N	2.55	122.05	119.32
2	E	500	NAI	PA-O5B-C5B	-2.55	106.74	121.35
2	F	500	NAI	C6A-C5A-C4A	2.55	120.66	117.18
2	D	500	NAI	C5A-N7A-C8A	2.55	107.45	103.45
3	E	550	HP7	O7'-C7'-C8'	-2.54	117.52	122.05
2	O	500	NAI	PN-O5D-C5D	-2.54	106.78	121.35
2	F	500	NAI	C5D-C4D-C3D	-2.54	106.06	115.21
3	F	550	HP7	O'Q-C6'-C5'	2.54	122.81	113.64
3	P	550	HP7	C2C-C3C-C4C	-2.54	97.70	102.61
2	E	500	NAI	PN-O5D-C5D	-2.54	106.80	121.35
3	G	550	HP7	O2A-PA-O3A	2.54	114.13	107.27
2	N	500	NAI	C4A-C5A-N7A	-2.53	107.69	110.58
3	J	550	HP7	C5C-C4C-C3C	-2.53	106.10	115.21
2	P	500	NAI	O7N-C7N-N7N	-2.53	117.22	122.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	500	NAI	O2D-C2D-C3D	-2.53	103.72	111.82
3	I	550	HP7	O3A-PA-O1A	-2.52	103.12	110.70
2	M	500	NAI	PN-O5D-C5D	-2.52	106.91	121.35
2	B	500	NAI	N9A-C8A-N7A	-2.52	110.36	113.94
2	L	500	NAI	PN-O5D-C5D	-2.52	106.94	121.35
3	B	550	HP7	C2'-N2'-C7'	2.51	128.99	123.11
2	J	500	NAI	PA-O5B-C5B	-2.51	106.96	121.35
2	D	500	NAI	PN-O5D-C5D	-2.51	106.97	121.35
3	C	550	HP7	C5C-C4C-C3C	-2.51	106.18	115.21
2	G	500	NAI	O5B-PA-O1A	2.51	118.87	108.94
2	J	500	NAI	PN-O5D-C5D	-2.51	106.99	121.35
2	H	500	NAI	PA-O5B-C5B	-2.50	107.04	121.35
2	D	500	NAI	PA-O5B-C5B	-2.50	107.05	121.35
2	A	500	NAI	C2D-C1D-N1N	2.49	119.44	113.31
2	C	500	NAI	PA-O5B-C5B	-2.49	107.09	121.35
2	C	500	NAI	C1D-N1N-C2N	-2.49	117.04	121.14
2	B	500	NAI	O4B-C4B-C5B	2.49	117.30	109.33
2	A	500	NAI	C5B-C4B-C3B	-2.49	106.26	115.21
2	J	500	NAI	N9A-C8A-N7A	-2.49	110.41	113.94
2	D	500	NAI	O3-PA-O1A	-2.48	103.23	110.70
3	F	550	HP7	O2A-PA-O1A	2.48	124.00	112.44
2	F	500	NAI	PA-O5B-C5B	-2.48	107.14	121.35
3	A	550	HP7	O4-C4-C5	-2.48	120.89	125.16
2	G	500	NAI	PN-O5D-C5D	-2.48	107.16	121.35
3	O	550	HP7	O4C-C4C-C3C	-2.48	100.24	105.15
3	J	550	HP7	O5'-C1'-C2'	2.47	115.27	110.59
2	B	500	NAI	C2A-N3A-C4A	2.47	117.87	111.83
2	A	500	NAI	C6N-N1N-C2N	2.47	121.96	119.32
3	J	550	HP7	O5'-C1'-O3B	-2.46	108.15	111.36
3	I	550	HP7	O4C-C4C-C3C	-2.46	100.27	105.15
2	P	500	NAI	O4B-C1B-C2B	-2.46	101.36	106.62
3	A	550	HP7	O2C-C2C-C1C	-2.45	101.65	110.10
2	D	500	NAI	C2D-C1D-N1N	-2.45	107.27	113.31
3	I	550	HP7	O2B-PB-O3B	2.45	116.67	106.70
3	G	550	HP7	O4-C4-C5	-2.45	120.94	125.16
3	A	550	HP7	O4'-C4'-C5'	-2.45	104.17	109.76
2	N	500	NAI	PN-O5D-C5D	-2.44	107.36	121.35
2	C	500	NAI	PN-O5D-C5D	-2.44	107.36	121.35
2	M	500	NAI	PA-O5B-C5B	-2.44	107.38	121.35
3	C	550	HP7	O2-C2-N1	2.44	125.97	122.80
3	M	550	HP7	O5C-C5C-C4C	-2.43	100.70	108.99
3	N	550	HP7	O2B-PB-O1B	2.43	123.76	112.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	500	NAI	C6N-N1N-C2N	2.43	121.92	119.32
2	P	500	NAI	PN-O5D-C5D	-2.43	107.42	121.35
2	N	500	NAI	C3N-C2N-N1N	-2.43	119.64	123.20
2	N	500	NAI	PA-O5B-C5B	-2.43	107.44	121.35
2	F	500	NAI	PN-O5D-C5D	-2.43	107.44	121.35
3	M	550	HP7	C5-C4-N3	2.42	118.19	114.80
2	B	500	NAI	C3N-C7N-N7N	2.42	121.97	117.67
2	P	500	NAI	PA-O5B-C5B	-2.42	107.47	121.35
2	D	500	NAI	O7N-C7N-N7N	-2.42	117.46	122.89
2	K	500	NAI	PA-O5B-C5B	-2.41	107.52	121.35
3	I	550	HP7	C8'-C7'-N2'	2.41	120.12	116.12
2	M	500	NAI	O3D-C3D-C4D	-2.41	104.16	111.08
2	F	500	NAI	N3A-C2A-N1A	-2.41	124.94	128.58
3	J	550	HP7	O2A-PA-O5C	-2.41	96.65	107.57
2	O	500	NAI	PA-O5B-C5B	-2.41	107.55	121.35
3	E	550	HP7	O2C-C2C-C1C	-2.41	101.82	110.10
2	A	500	NAI	PN-O5D-C5D	-2.40	107.59	121.35
2	C	500	NAI	C6A-C5A-N7A	2.40	136.71	132.09
2	L	500	NAI	O4B-C4B-C5B	2.39	117.00	109.33
2	P	500	NAI	O4B-C4B-C5B	2.39	116.99	109.33
3	J	550	HP7	C5-C6-N1	-2.39	117.96	121.84
2	C	500	NAI	O1N-PN-O3	-2.39	100.82	107.27
2	K	500	NAI	O4D-C1D-N1N	2.39	112.64	108.08
3	H	550	HP7	C1'-C2'-N2'	2.39	114.92	110.92
3	C	550	HP7	O2B-PB-O1B	2.38	123.52	112.44
3	M	550	HP7	C5-C6-N1	-2.37	117.98	121.84
3	L	550	HP7	O5C-C5C-C4C	-2.37	100.92	108.99
2	F	500	NAI	C4D-O4D-C1D	-2.37	104.23	109.47
3	D	550	HP7	O4-C4-C5	-2.37	121.07	125.16
3	J	550	HP7	O3'-C3'-C4'	2.36	115.95	110.38
2	O	500	NAI	O4B-C1B-C2B	-2.36	101.57	106.62
2	L	500	NAI	C2A-N1A-C6A	2.35	122.60	118.73
3	F	550	HP7	O2-C2-N1	2.35	125.86	122.80
3	D	550	HP7	O2A-PA-O1A	2.35	123.38	112.44
2	M	500	NAI	C4A-N9A-C1B	-2.35	121.14	126.63
3	M	550	HP7	O3B-PB-O1B	-2.35	102.31	109.81
2	G	500	NAI	PA-O5B-C5B	-2.34	107.94	121.35
2	A	500	NAI	PA-O5B-C5B	-2.34	107.94	121.35
2	L	500	NAI	O3-PA-O1A	-2.34	103.67	110.70
2	B	500	NAI	O4B-C4B-C3B	2.33	109.77	105.15
2	B	500	NAI	O3-PA-O1A	-2.32	103.72	110.70
2	J	500	NAI	C2D-C3D-C4D	-2.32	98.12	102.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	500	NAI	C5A-C4A-N9A	2.32	108.34	105.81
2	J	500	NAI	C3B-C2B-C1B	-2.31	97.08	101.46
3	I	550	HP7	O2C-C2C-C1C	-2.31	102.14	110.10
2	A	500	NAI	O1N-PN-O2N	-2.31	101.69	112.44
2	P	500	NAI	C2A-N1A-C6A	2.31	122.53	118.73
3	K	550	HP7	O2C-C2C-C1C	-2.31	102.16	110.10
2	N	500	NAI	N9A-C8A-N7A	-2.30	110.67	113.94
3	P	550	HP7	O2-C2-N3	-2.30	117.25	121.49
2	P	500	NAI	O4D-C4D-C5D	-2.29	101.98	109.33
2	G	500	NAI	O1N-PN-O2N	-2.29	101.77	112.44
2	J	500	NAI	O3-PN-O2N	2.29	117.60	110.70
3	C	550	HP7	O'Q-C6'-C5'	2.29	121.91	113.64
3	H	550	HP7	C8'-C7'-N2'	2.28	119.90	116.12
2	A	500	NAI	C1D-N1N-C2N	-2.28	117.39	121.14
3	B	550	HP7	C3C-C2C-C1C	2.28	105.77	101.46
3	B	550	HP7	O5C-C5C-C4C	-2.28	101.24	108.99
2	B	500	NAI	C5A-C4A-N3A	-2.28	123.58	126.72
2	K	500	NAI	C1B-N9A-C8A	2.28	132.15	127.09
3	N	550	HP7	C6-N1-C2	2.27	123.77	121.00
2	O	500	NAI	O5B-PA-O1A	2.27	117.94	108.94
3	M	550	HP7	O2-C2-N3	-2.27	117.30	121.49
3	G	550	HP7	C3C-C2C-C1C	2.27	105.75	101.46
2	I	500	NAI	C3B-C2B-C1B	-2.27	97.18	101.46
3	C	550	HP7	C5-C6-N1	-2.26	118.16	121.84
3	K	550	HP7	C2C-C1C-N1	-2.26	106.96	113.25
3	O	550	HP7	O2B-PB-O1B	2.25	122.93	112.44
3	B	550	HP7	O5'-C1'-O3B	-2.25	108.42	111.36
3	C	550	HP7	C6-N1-C2	2.25	123.74	121.00
3	C	550	HP7	O2A-PA-O1A	2.25	122.90	112.44
2	I	500	NAI	O4B-C1B-N9A	2.25	112.40	108.09
2	L	500	NAI	C6A-C5A-N7A	2.24	136.41	132.09
3	K	550	HP7	C3'-C4'-C5'	2.24	113.15	109.30
3	G	550	HP7	O7'-C7'-N2'	-2.24	118.03	121.98
3	P	550	HP7	O5'-C5'-C4'	-2.24	105.07	109.48
3	N	550	HP7	O3A-PA-O1A	-2.23	103.99	110.70
3	O	550	HP7	O2A-PA-O1A	2.23	122.82	112.44
2	J	500	NAI	O1N-PN-O2N	-2.22	102.11	112.44
3	B	550	HP7	O'Q-C6'-C5'	2.22	121.65	113.64
3	J	550	HP7	O4'-C4'-C3'	-2.22	105.14	110.38
3	H	550	HP7	C1C-N1-C2	2.22	121.58	117.59
2	G	500	NAI	O4D-C1D-C2D	-2.22	101.87	106.62
3	N	550	HP7	O4C-C1C-N1	2.22	113.38	108.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	500	NAI	O4B-C1B-N9A	2.21	112.34	108.09
3	M	550	HP7	O5C-PA-O1A	-2.21	100.17	108.94
3	H	550	HP7	O2C-C2C-C1C	-2.21	102.49	110.10
2	L	500	NAI	N6A-C6A-N1A	2.21	123.30	118.38
3	B	550	HP7	O'Q-C6'-O'P	-2.21	119.07	124.08
3	H	550	HP7	O5C-C5C-C4C	-2.20	101.50	108.99
2	F	500	NAI	O4D-C4D-C5D	-2.20	102.29	109.33
2	J	500	NAI	C6A-C5A-N7A	2.20	136.32	132.09
2	A	500	NAI	C3D-C2D-C1D	2.19	105.61	101.46
3	A	550	HP7	O'Q-C6'-O'P	-2.19	119.10	124.08
2	M	500	NAI	O5B-PA-O1A	2.19	117.62	108.94
2	C	500	NAI	C2A-N1A-C6A	2.19	122.33	118.73
3	C	550	HP7	C4'-C3'-C2'	-2.19	107.22	110.40
3	K	550	HP7	C6-C5-C4	2.19	122.33	119.53
2	C	500	NAI	C2B-C1B-N9A	-2.19	107.87	113.30
2	I	500	NAI	C4A-C5A-N7A	-2.18	108.09	110.58
2	H	500	NAI	N9A-C8A-N7A	-2.18	110.84	113.94
2	A	500	NAI	O2A-PA-O5B	-2.18	97.68	107.57
2	P	500	NAI	C3N-C2N-N1N	-2.18	120.00	123.20
2	J	500	NAI	O5D-C5D-C4D	-2.18	101.58	108.99
2	G	500	NAI	O4B-C4B-C3B	2.17	109.47	105.15
3	A	550	HP7	O2A-PA-O3A	2.17	113.14	107.27
3	L	550	HP7	C2'-N2'-C7'	2.17	128.18	123.11
2	N	500	NAI	O4D-C1D-N1N	2.17	112.22	108.08
3	A	550	HP7	C6-N1-C2	2.16	123.63	121.00
2	G	500	NAI	C1D-N1N-C2N	-2.16	117.58	121.14
2	I	500	NAI	O2A-PA-O3	-2.16	101.44	107.27
2	F	500	NAI	C5A-C4A-N9A	2.16	108.17	105.81
2	P	500	NAI	N9A-C8A-N7A	-2.16	110.87	113.94
3	G	550	HP7	O2B-PB-O1B	2.16	122.49	112.44
2	C	500	NAI	O3D-C3D-C2D	-2.15	104.92	111.82
2	K	500	NAI	C2D-C1D-N1N	-2.15	108.03	113.31
2	I	500	NAI	C2D-C3D-C4D	-2.15	98.46	102.61
3	N	550	HP7	C1C-N1-C2	-2.14	113.75	117.59
3	I	550	HP7	O4-C4-C5	-2.14	121.47	125.16
3	A	550	HP7	O3'-C3'-C2'	-2.14	105.33	109.58
2	M	500	NAI	N3A-C4A-N9A	2.14	130.80	127.17
2	G	500	NAI	C6A-C5A-N7A	2.14	136.21	132.09
3	K	550	HP7	O2-C2-N3	-2.14	117.55	121.49
2	G	500	NAI	N6A-C6A-N1A	2.13	123.12	118.38
3	G	550	HP7	C4'-C3'-C2'	2.12	113.49	110.40
3	M	550	HP7	O3A-PA-O1A	-2.12	104.32	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	550	HP7	C3'-C4'-C5'	-2.12	105.65	109.30
2	D	500	NAI	O5D-PN-O2N	2.12	117.34	108.94
2	O	500	NAI	O1N-PN-O2N	-2.12	102.59	112.44
3	A	550	HP7	O2A-PA-O1A	2.11	122.28	112.44
2	E	500	NAI	C2A-N1A-C6A	2.11	122.20	118.73
3	P	550	HP7	O3B-PB-O1B	-2.11	103.06	109.81
2	F	500	NAI	C2B-C3B-C4B	-2.11	98.54	102.61
3	L	550	HP7	O2-C2-N3	-2.11	117.61	121.49
2	D	500	NAI	N9A-C8A-N7A	-2.10	110.95	113.94
2	O	500	NAI	O2A-PA-O1A	-2.10	102.66	112.44
3	A	550	HP7	C6-C5-C4	-2.10	116.85	119.53
2	H	500	NAI	C3N-C7N-N7N	2.10	121.40	117.67
3	I	550	HP7	O3C-C3C-C2C	2.10	118.54	111.82
3	I	550	HP7	O5'-C1'-O3B	-2.10	108.62	111.36
3	N	550	HP7	O2A-PA-O3A	2.10	112.94	107.27
3	J	550	HP7	O2-C2-N3	-2.10	117.62	121.49
3	M	550	HP7	C3C-C2C-C1C	2.09	105.42	101.46
3	G	550	HP7	O3A-PA-O1A	-2.09	104.42	110.70
2	I	500	NAI	C3N-C7N-N7N	2.09	121.38	117.67
3	I	550	HP7	O2A-PA-O1A	2.09	122.15	112.44
3	M	550	HP7	O2A-PA-O3A	2.08	112.91	107.27
3	B	550	HP7	O2B-PB-O1B	2.08	122.14	112.44
2	F	500	NAI	C2B-C1B-N9A	2.08	118.47	113.30
2	A	500	NAI	C5A-C4A-N9A	2.08	108.08	105.81
3	E	550	HP7	O4'-C4'-C3'	2.08	115.28	110.38
2	B	500	NAI	O3-PN-O2N	2.08	116.95	110.70
2	D	500	NAI	C1D-N1N-C2N	-2.07	117.72	121.14
3	N	550	HP7	C5C-C4C-C3C	-2.07	107.75	115.21
3	M	550	HP7	O4'-C4'-C3'	-2.07	105.49	110.38
3	H	550	HP7	C5C-C4C-C3C	-2.07	107.76	115.21
3	C	550	HP7	O2A-PA-O3A	2.07	112.86	107.27
3	D	550	HP7	O'Q-C6'-C5'	2.07	121.10	113.64
2	E	500	NAI	C3N-C7N-N7N	2.06	121.33	117.67
3	G	550	HP7	O2B-PB-O3A	-2.06	101.71	107.27
2	M	500	NAI	O4D-C4D-C5D	-2.06	102.75	109.33
3	M	550	HP7	C1'-C2'-N2'	2.06	114.36	110.92
3	I	550	HP7	C3'-C4'-C5'	2.05	112.83	109.30
3	F	550	HP7	O2C-C2C-C3C	-2.05	105.25	111.82
2	G	500	NAI	C3N-C7N-N7N	2.05	121.30	117.67
3	M	550	HP7	O2A-PA-O1A	2.04	121.95	112.44
2	K	500	NAI	C4B-O4B-C1B	-2.04	104.95	109.47
2	N	500	NAI	C2B-C1B-N9A	2.04	118.38	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	500	NAI	C4A-C5A-N7A	-2.04	108.25	110.58
2	E	500	NAI	O7N-C7N-C3N	-2.04	117.06	120.90
3	D	550	HP7	O5C-C5C-C4C	-2.03	102.08	108.99
3	L	550	HP7	O5'-C5'-C6'	-2.03	99.79	106.14
3	L	550	HP7	O3B-PB-O1B	-2.03	103.33	109.81
2	F	500	NAI	O7N-C7N-C3N	-2.02	117.10	120.90
3	H	550	HP7	C5-C6-N1	-2.02	118.56	121.84
3	D	550	HP7	O'Q-C6'-O'P	-2.01	119.53	124.08
2	A	500	NAI	O1N-PN-O5D	-2.00	98.49	107.57

There are no chirality outliers.

All (271) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	NAI	C5D-O5D-PN-O3
2	B	500	NAI	C5B-O5B-PA-O1A
2	B	500	NAI	C5B-O5B-PA-O2A
2	B	500	NAI	C5B-O5B-PA-O3
2	C	500	NAI	C5B-O5B-PA-O3
2	C	500	NAI	C5D-O5D-PN-O3
2	C	500	NAI	C5D-O5D-PN-O1N
2	C	500	NAI	C5D-O5D-PN-O2N
2	D	500	NAI	C5B-O5B-PA-O1A
2	D	500	NAI	C5B-O5B-PA-O2A
2	D	500	NAI	C5B-O5B-PA-O3
2	E	500	NAI	C5B-O5B-PA-O2A
2	E	500	NAI	C5B-O5B-PA-O3
2	F	500	NAI	C5B-O5B-PA-O1A
2	F	500	NAI	C5B-O5B-PA-O2A
2	F	500	NAI	C5B-O5B-PA-O3
2	F	500	NAI	PN-O3-PA-O5B
2	F	500	NAI	O4B-C4B-C5B-O5B
2	F	500	NAI	C3B-C4B-C5B-O5B
2	F	500	NAI	C5D-O5D-PN-O3
2	G	500	NAI	C5B-O5B-PA-O1A
2	G	500	NAI	C5B-O5B-PA-O3
2	G	500	NAI	C5D-O5D-PN-O3
2	H	500	NAI	C5B-O5B-PA-O1A
2	H	500	NAI	C5B-O5B-PA-O2A
2	H	500	NAI	C5B-O5B-PA-O3
2	H	500	NAI	PN-O3-PA-O5B
2	I	500	NAI	C5B-O5B-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	I	500	NAI	C5B-O5B-PA-O2A
2	I	500	NAI	C5B-O5B-PA-O3
2	I	500	NAI	C5D-O5D-PN-O1N
2	J	500	NAI	C5B-O5B-PA-O1A
2	J	500	NAI	C5B-O5B-PA-O2A
2	J	500	NAI	C5B-O5B-PA-O3
2	J	500	NAI	PN-O3-PA-O5B
2	K	500	NAI	C5B-O5B-PA-O1A
2	K	500	NAI	C5B-O5B-PA-O2A
2	K	500	NAI	C5B-O5B-PA-O3
2	K	500	NAI	PN-O3-PA-O5B
2	L	500	NAI	C5B-O5B-PA-O2A
2	L	500	NAI	C5B-O5B-PA-O3
2	L	500	NAI	PN-O3-PA-O5B
2	L	500	NAI	C5D-O5D-PN-O3
2	L	500	NAI	C5D-O5D-PN-O1N
2	L	500	NAI	C5D-O5D-PN-O2N
2	M	500	NAI	C5B-O5B-PA-O1A
2	M	500	NAI	C5B-O5B-PA-O2A
2	M	500	NAI	C5B-O5B-PA-O3
2	M	500	NAI	C5D-O5D-PN-O3
2	M	500	NAI	C5D-O5D-PN-O1N
2	M	500	NAI	C5D-O5D-PN-O2N
2	M	500	NAI	O4D-C4D-C5D-O5D
2	N	500	NAI	C5B-O5B-PA-O1A
2	N	500	NAI	C5B-O5B-PA-O2A
2	N	500	NAI	C5B-O5B-PA-O3
2	N	500	NAI	PN-O3-PA-O5B
2	N	500	NAI	C5D-O5D-PN-O1N
2	O	500	NAI	C5B-O5B-PA-O1A
2	O	500	NAI	C5B-O5B-PA-O2A
2	O	500	NAI	C5B-O5B-PA-O3
2	O	500	NAI	O4B-C4B-C5B-O5B
2	O	500	NAI	C5D-O5D-PN-O3
2	O	500	NAI	C5D-O5D-PN-O1N
2	P	500	NAI	C5B-O5B-PA-O1A
2	P	500	NAI	C5B-O5B-PA-O2A
2	P	500	NAI	C5B-O5B-PA-O3
3	A	550	HP7	C1'-O3B-PB-O3A
3	B	550	HP7	C1'-O3B-PB-O3A
3	C	550	HP7	C1'-O3B-PB-O3A
3	D	550	HP7	C1'-O3B-PB-O3A

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Mol	Chain	Res	Type	Atoms
3	E	550	HP7	C5C-O5C-PA-O2A
3	F	550	HP7	O4C-C4C-C5C-O5C
3	G	550	HP7	C5C-O5C-PA-O1A
3	G	550	HP7	C5C-O5C-PA-O2A
3	G	550	HP7	C1'-O3B-PB-O3A
3	I	550	HP7	C1'-O3B-PB-O3A
3	M	550	HP7	C1'-O3B-PB-O3A
3	N	550	HP7	C5C-O5C-PA-O1A
3	N	550	HP7	C5C-O5C-PA-O2A
3	O	550	HP7	C5C-O5C-PA-O2A
3	O	550	HP7	C5C-O5C-PA-O3A
3	O	550	HP7	C1'-O3B-PB-O3A
2	B	500	NAI	C3B-C4B-C5B-O5B
2	D	500	NAI	C3B-C4B-C5B-O5B
2	E	500	NAI	C3B-C4B-C5B-O5B
2	G	500	NAI	O4B-C4B-C5B-O5B
2	I	500	NAI	O4B-C4B-C5B-O5B
2	I	500	NAI	C3B-C4B-C5B-O5B
2	J	500	NAI	C3B-C4B-C5B-O5B
2	L	500	NAI	O4D-C4D-C5D-O5D
2	M	500	NAI	C3B-C4B-C5B-O5B
2	N	500	NAI	O4B-C4B-C5B-O5B
2	N	500	NAI	C3B-C4B-C5B-O5B
2	O	500	NAI	C3B-C4B-C5B-O5B
2	P	500	NAI	C3B-C4B-C5B-O5B
3	L	550	HP7	O4C-C4C-C5C-O5C
3	P	550	HP7	C8'-C7'-N2'-C2'
2	B	500	NAI	O4B-C4B-C5B-O5B
2	C	500	NAI	O4B-C4B-C5B-O5B
2	C	500	NAI	O4D-C4D-C5D-O5D
2	D	500	NAI	O4B-C4B-C5B-O5B
2	E	500	NAI	O4B-C4B-C5B-O5B
2	G	500	NAI	C3B-C4B-C5B-O5B
2	J	500	NAI	O4B-C4B-C5B-O5B
2	L	500	NAI	C3B-C4B-C5B-O5B
2	M	500	NAI	O4B-C4B-C5B-O5B
2	M	500	NAI	C3D-C4D-C5D-O5D
2	O	500	NAI	O4D-C4D-C5D-O5D
2	P	500	NAI	O4B-C4B-C5B-O5B
3	I	550	HP7	O4C-C4C-C5C-O5C
2	C	500	NAI	C3B-C4B-C5B-O5B
2	K	500	NAI	O4B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
2	K	500	NAI	C3B-C4B-C5B-O5B
2	L	500	NAI	C3D-C4D-C5D-O5D
2	P	500	NAI	O4D-C4D-C5D-O5D
3	P	550	HP7	O7'-C7'-N2'-C2'
2	H	500	NAI	C3B-C4B-C5B-O5B
2	H	500	NAI	O4D-C4D-C5D-O5D
2	I	500	NAI	O4D-C4D-C5D-O5D
3	F	550	HP7	C3C-C4C-C5C-O5C
3	L	550	HP7	C8'-C7'-N2'-C2'
2	A	500	NAI	C3B-C4B-C5B-O5B
2	H	500	NAI	O4B-C4B-C5B-O5B
2	E	500	NAI	O4D-C4D-C5D-O5D
2	L	500	NAI	O4B-C4B-C5B-O5B
2	N	500	NAI	O4D-C4D-C5D-O5D
2	A	500	NAI	O4D-C4D-C5D-O5D
2	G	500	NAI	C3D-C4D-C5D-O5D
3	M	550	HP7	O4C-C4C-C5C-O5C
2	P	500	NAI	C2D-C1D-N1N-C2N
2	K	500	NAI	PN-O3-PA-O1A
2	K	500	NAI	O4D-C4D-C5D-O5D
2	A	500	NAI	C3D-C4D-C5D-O5D
3	L	550	HP7	C3C-C4C-C5C-O5C
2	P	500	NAI	C2D-C1D-N1N-C6N
3	L	550	HP7	O7'-C7'-N2'-C2'
2	A	500	NAI	PN-O3-PA-O5B
2	B	500	NAI	PN-O3-PA-O5B
2	C	500	NAI	PN-O3-PA-O5B
2	E	500	NAI	PN-O3-PA-O5B
2	G	500	NAI	PN-O3-PA-O5B
2	I	500	NAI	PN-O3-PA-O5B
2	M	500	NAI	PN-O3-PA-O5B
2	O	500	NAI	PN-O3-PA-O5B
2	P	500	NAI	PN-O3-PA-O5B
2	C	500	NAI	C3D-C4D-C5D-O5D
3	D	550	HP7	C1'-O3B-PB-O1B
3	G	550	HP7	C1'-O3B-PB-O1B
3	O	550	HP7	C1'-O3B-PB-O1B
2	B	500	NAI	O4D-C1D-N1N-C6N
2	E	500	NAI	O4D-C1D-N1N-C6N
2	P	500	NAI	O4D-C1D-N1N-C2N
2	A	500	NAI	O4B-C4B-C5B-O5B
3	D	550	HP7	O4C-C4C-C5C-O5C

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Mol	Chain	Res	Type	Atoms
2	C	500	NAI	C2B-C1B-N9A-C8A
2	G	500	NAI	C2B-C1B-N9A-C8A
2	H	500	NAI	C2B-C1B-N9A-C8A
2	L	500	NAI	C2B-C1B-N9A-C8A
2	N	500	NAI	C2B-C1B-N9A-C8A
2	P	500	NAI	C2B-C1B-N9A-C8A
2	D	500	NAI	PA-O3-PN-O2N
3	M	550	HP7	PB-O3A-PA-O2A
3	D	550	HP7	C8'-C7'-N2'-C2'
2	P	500	NAI	O4D-C1D-N1N-C6N
2	A	500	NAI	C5B-O5B-PA-O3
2	B	500	NAI	C5D-O5D-PN-O2N
2	C	500	NAI	C5B-O5B-PA-O2A
2	G	500	NAI	C5B-O5B-PA-O2A
3	E	550	HP7	C5C-O5C-PA-O1A
3	E	550	HP7	C5C-O5C-PA-O3A
3	G	550	HP7	C5C-O5C-PA-O3A
3	N	550	HP7	C5C-O5C-PA-O3A
3	O	550	HP7	C5C-O5C-PA-O1A
2	E	500	NAI	O4D-C1D-N1N-C2N
2	I	500	NAI	O4D-C1D-N1N-C2N
2	N	500	NAI	O4D-C1D-N1N-C6N
2	O	500	NAI	O4D-C1D-N1N-C6N
2	D	500	NAI	C2D-C1D-N1N-C2N
2	O	500	NAI	C2D-C1D-N1N-C2N
2	B	500	NAI	O4D-C1D-N1N-C2N
2	O	500	NAI	O4D-C1D-N1N-C2N
2	C	500	NAI	C2D-C1D-N1N-C2N
2	E	500	NAI	C2D-C1D-N1N-C2N
2	E	500	NAI	C2D-C1D-N1N-C6N
2	H	500	NAI	C2D-C1D-N1N-C2N
3	G	550	HP7	PB-O3A-PA-O2A
2	J	500	NAI	O4D-C1D-N1N-C2N
2	O	500	NAI	C3D-C4D-C5D-O5D
2	E	500	NAI	C2B-C1B-N9A-C8A
2	B	500	NAI	C2D-C1D-N1N-C6N
2	F	500	NAI	C2D-C1D-N1N-C2N
2	O	500	NAI	C2D-C1D-N1N-C6N
2	C	500	NAI	O4D-C1D-N1N-C2N
2	L	500	NAI	O4D-C1D-N1N-C2N
2	N	500	NAI	O4D-C1D-N1N-C2N
2	B	500	NAI	C2D-C1D-N1N-C2N

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Mol	Chain	Res	Type	Atoms
2	A	500	NAI	O4D-C1D-N1N-C2N
2	D	500	NAI	O4D-C1D-N1N-C2N
2	F	500	NAI	O4D-C1D-N1N-C2N
2	G	500	NAI	O4D-C1D-N1N-C2N
2	H	500	NAI	O4D-C1D-N1N-C2N
2	K	500	NAI	O4D-C1D-N1N-C2N
2	M	500	NAI	O4D-C1D-N1N-C2N
3	D	550	HP7	O7'-C7'-N2'-C2'
2	G	500	NAI	C2D-C1D-N1N-C2N
2	M	500	NAI	C2D-C1D-N1N-C2N
2	K	500	NAI	O4B-C1B-N9A-C8A
2	I	500	NAI	O4D-C1D-N1N-C6N
3	P	550	HP7	O4C-C4C-C5C-O5C
3	D	550	HP7	C3'-C2'-N2'-C7'
2	P	500	NAI	PA-O3-PN-O1N
2	C	500	NAI	O4D-C1D-N1N-C6N
2	D	500	NAI	O4D-C1D-N1N-C6N
2	J	500	NAI	O4D-C1D-N1N-C6N
2	M	500	NAI	O4D-C1D-N1N-C6N
2	H	500	NAI	O4B-C1B-N9A-C8A
2	I	500	NAI	C2D-C1D-N1N-C2N
2	N	500	NAI	C2D-C1D-N1N-C2N
2	J	500	NAI	C2B-C1B-N9A-C8A
2	L	500	NAI	O4D-C1D-N1N-C6N
2	A	500	NAI	C2D-C1D-N1N-C2N
2	J	500	NAI	C2D-C1D-N1N-C2N
2	L	500	NAI	C2D-C1D-N1N-C2N
3	B	550	HP7	C1'-O3B-PB-O2B
3	C	550	HP7	C1'-O3B-PB-O1B
3	I	550	HP7	C1'-O3B-PB-O1B
3	K	550	HP7	C1'-O3B-PB-O1B
3	N	550	HP7	C1'-O3B-PB-O1B
2	F	500	NAI	O4D-C1D-N1N-C6N
2	I	500	NAI	C2B-C1B-N9A-C8A
2	M	500	NAI	C2B-C1B-N9A-C8A
2	C	500	NAI	C2D-C1D-N1N-C6N
2	D	500	NAI	C2D-C1D-N1N-C6N
2	F	500	NAI	C2D-C1D-N1N-C6N
2	K	500	NAI	C2D-C1D-N1N-C2N
2	N	500	NAI	C2D-C1D-N1N-C6N
3	J	550	HP7	C3'-C2'-N2'-C7'
2	L	500	NAI	O4B-C1B-N9A-C8A

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Mol	Chain	Res	Type	Atoms
2	D	500	NAI	O4D-C4D-C5D-O5D
2	A	500	NAI	C2B-C1B-N9A-C8A
2	K	500	NAI	C2B-C1B-N9A-C8A
2	I	500	NAI	PA-O3-PN-O1N
2	M	500	NAI	PA-O3-PN-O1N
2	O	500	NAI	PA-O3-PN-O1N
3	G	550	HP7	PB-O3A-PA-O1A
3	M	550	HP7	PA-O3A-PB-O1B
3	O	550	HP7	PB-O3A-PA-O2A
3	O	550	HP7	PA-O3A-PB-O1B
3	K	550	HP7	C3'-C2'-N2'-C7'
3	M	550	HP7	C3C-C4C-C5C-O5C
2	B	500	NAI	C2B-C1B-N9A-C8A
2	F	500	NAI	C2B-C1B-N9A-C8A
2	O	500	NAI	C2B-C1B-N9A-C8A
2	M	500	NAI	C2B-C1B-N9A-C4A
2	M	500	NAI	C2D-C1D-N1N-C6N
3	E	550	HP7	O4C-C4C-C5C-O5C
2	N	500	NAI	O4B-C1B-N9A-C8A
2	A	500	NAI	O4D-C1D-N1N-C6N
2	H	500	NAI	O4D-C1D-N1N-C6N
2	D	500	NAI	C2B-C1B-N9A-C8A
2	J	500	NAI	O4B-C1B-N9A-C8A
2	B	500	NAI	PA-O3-PN-O1N
2	D	500	NAI	PA-O3-PN-O1N
2	E	500	NAI	PA-O3-PN-O1N
2	F	500	NAI	PA-O3-PN-O1N
2	G	500	NAI	PA-O3-PN-O1N
2	H	500	NAI	PA-O3-PN-O1N
2	N	500	NAI	PA-O3-PN-O1N
3	M	550	HP7	PB-O3A-PA-O1A
2	B	500	NAI	O4D-C4D-C5D-O5D
2	J	500	NAI	O4D-C4D-C5D-O5D

There are no ring outliers.

31 monomers are involved in 109 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	550	HP7	1	0
2	D	500	NAI	7	0
3	K	550	HP7	6	0
3	P	550	HP7	1	0

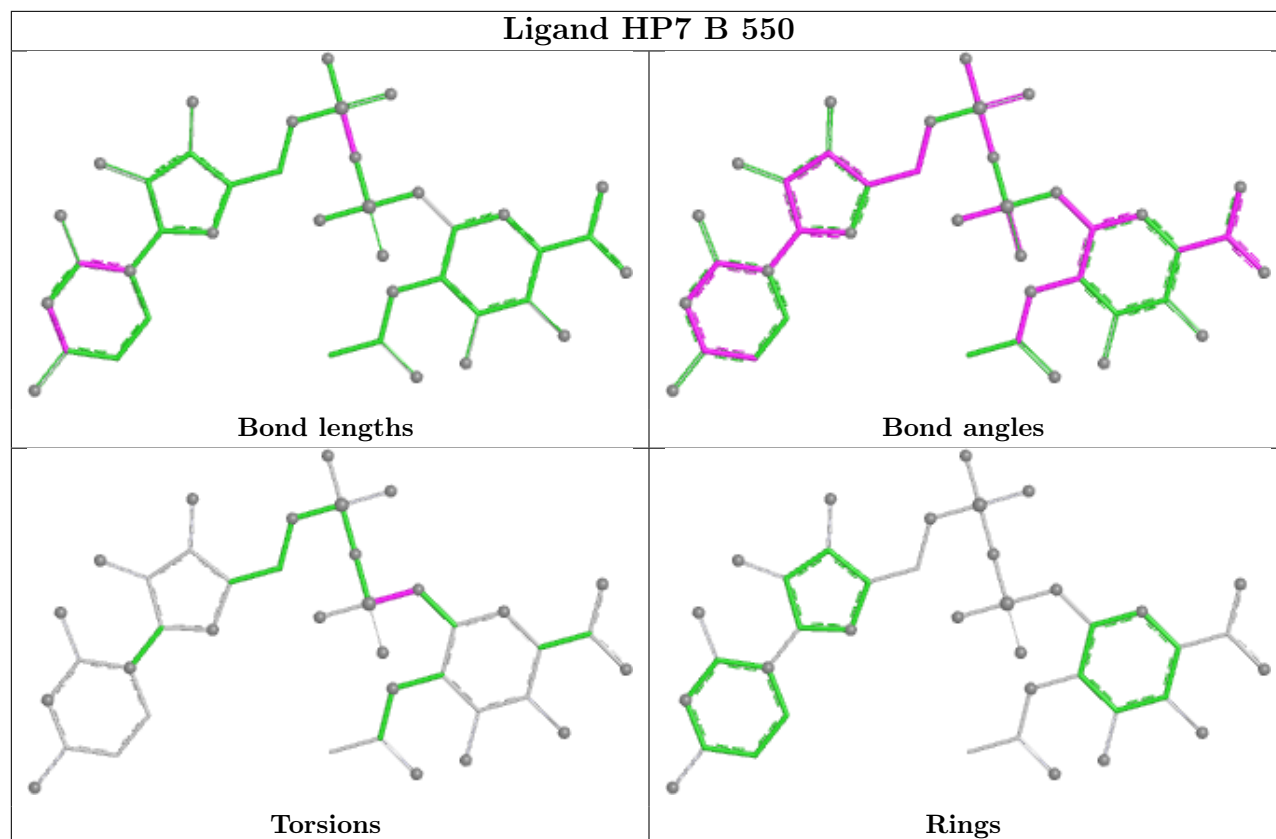
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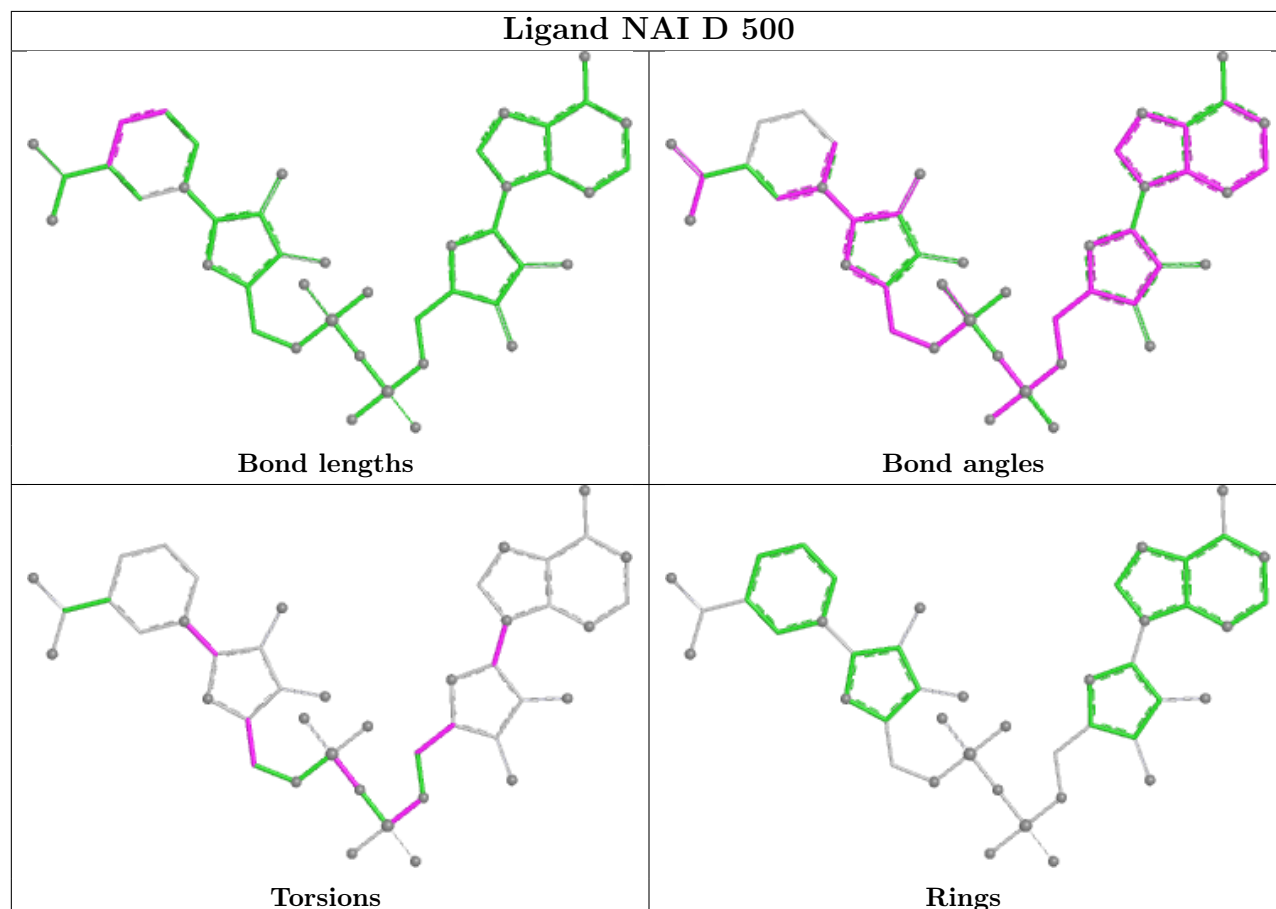
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	500	NAI	8	0
2	I	500	NAI	12	0
3	O	550	HP7	2	0
2	L	500	NAI	6	0
2	E	500	NAI	7	0
3	N	550	HP7	1	0
3	J	550	HP7	3	0
2	M	500	NAI	4	0
3	E	550	HP7	5	0
2	K	500	NAI	4	0
2	P	500	NAI	5	0
3	I	550	HP7	3	0
2	O	500	NAI	3	0
2	J	500	NAI	7	0
2	F	500	NAI	4	0
3	A	550	HP7	2	0
3	F	550	HP7	2	0
2	B	500	NAI	6	0
3	M	550	HP7	4	0
3	G	550	HP7	2	0
3	D	550	HP7	1	0
2	C	500	NAI	6	0
3	H	550	HP7	3	0
2	A	500	NAI	1	0
2	G	500	NAI	4	0
2	N	500	NAI	4	0
3	C	550	HP7	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.

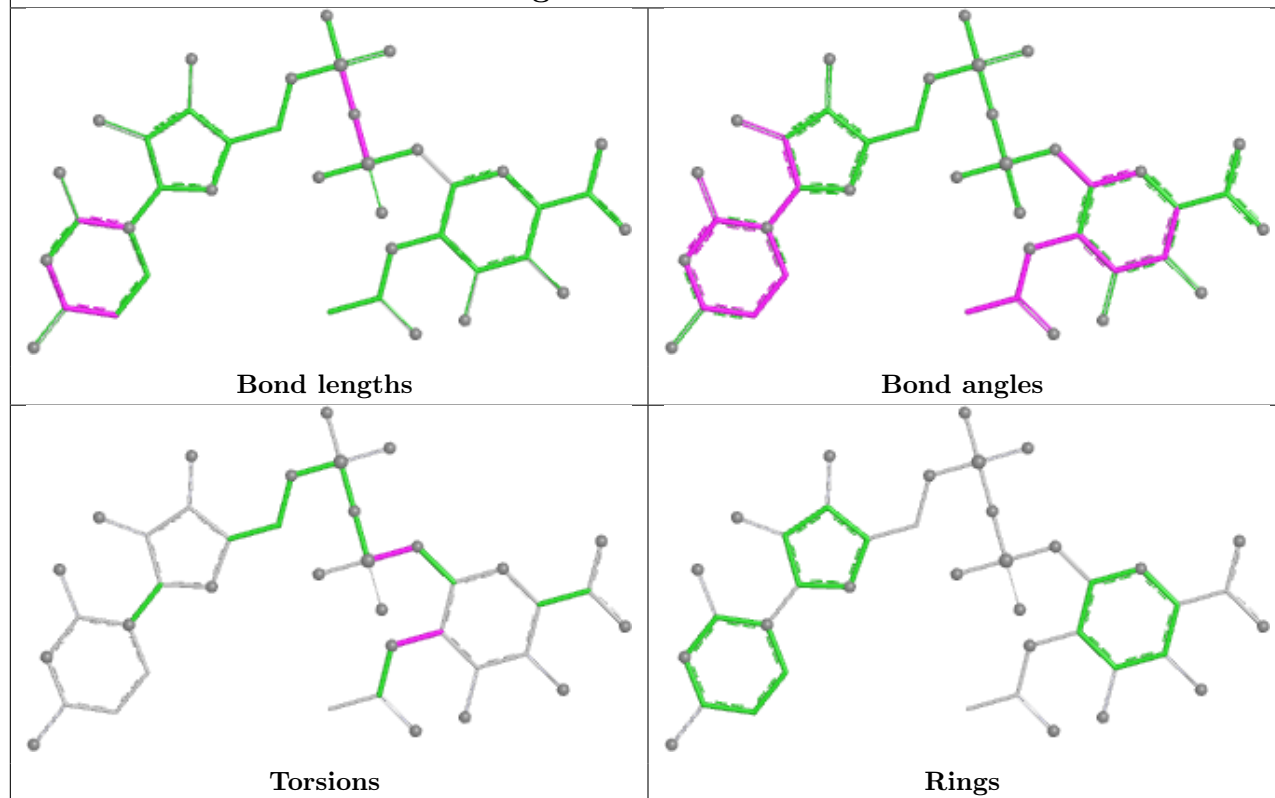
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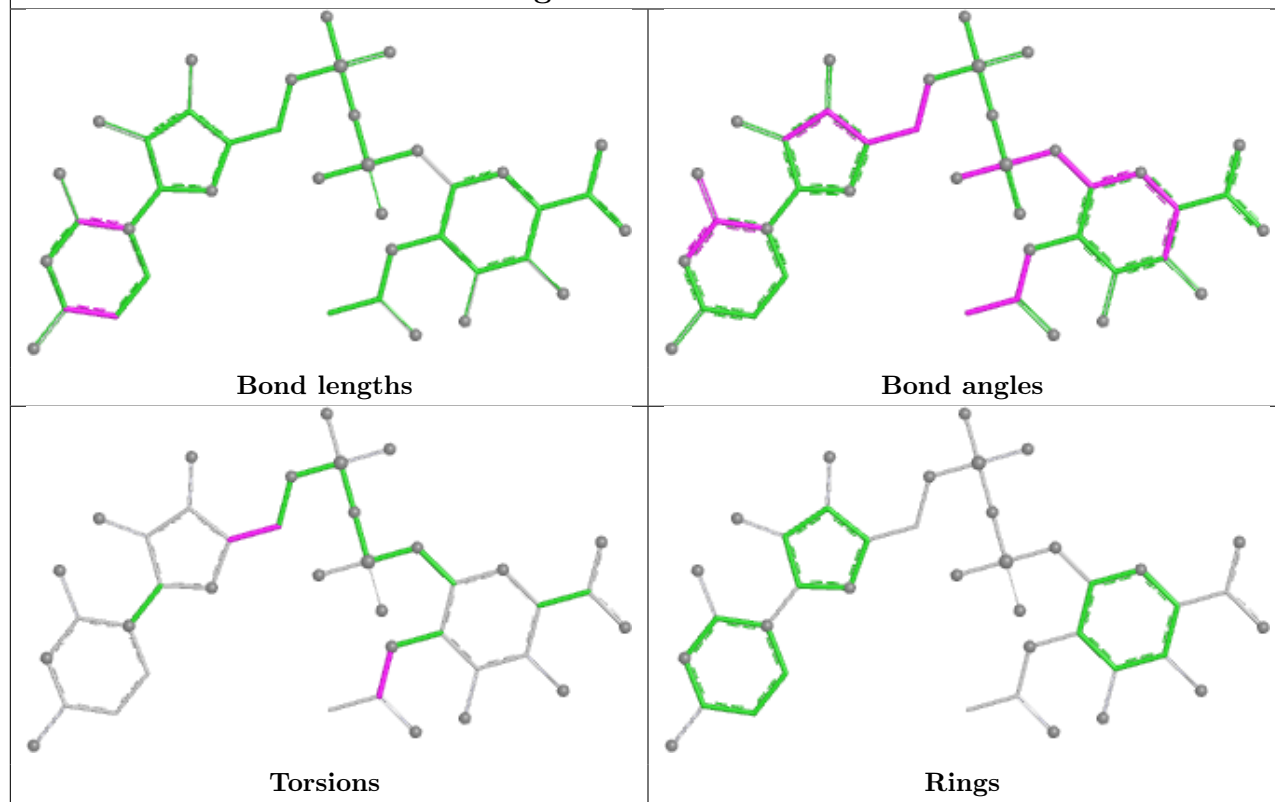
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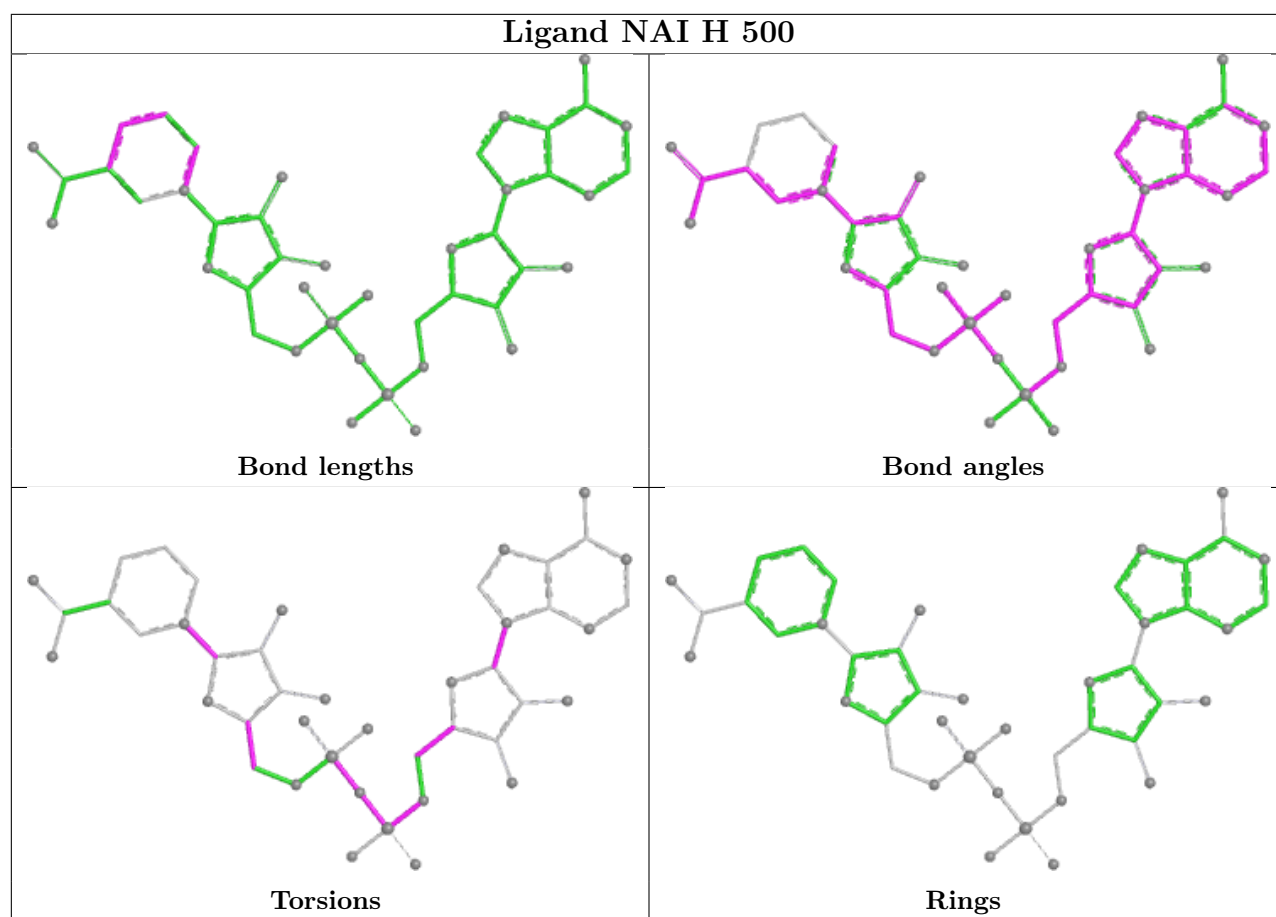


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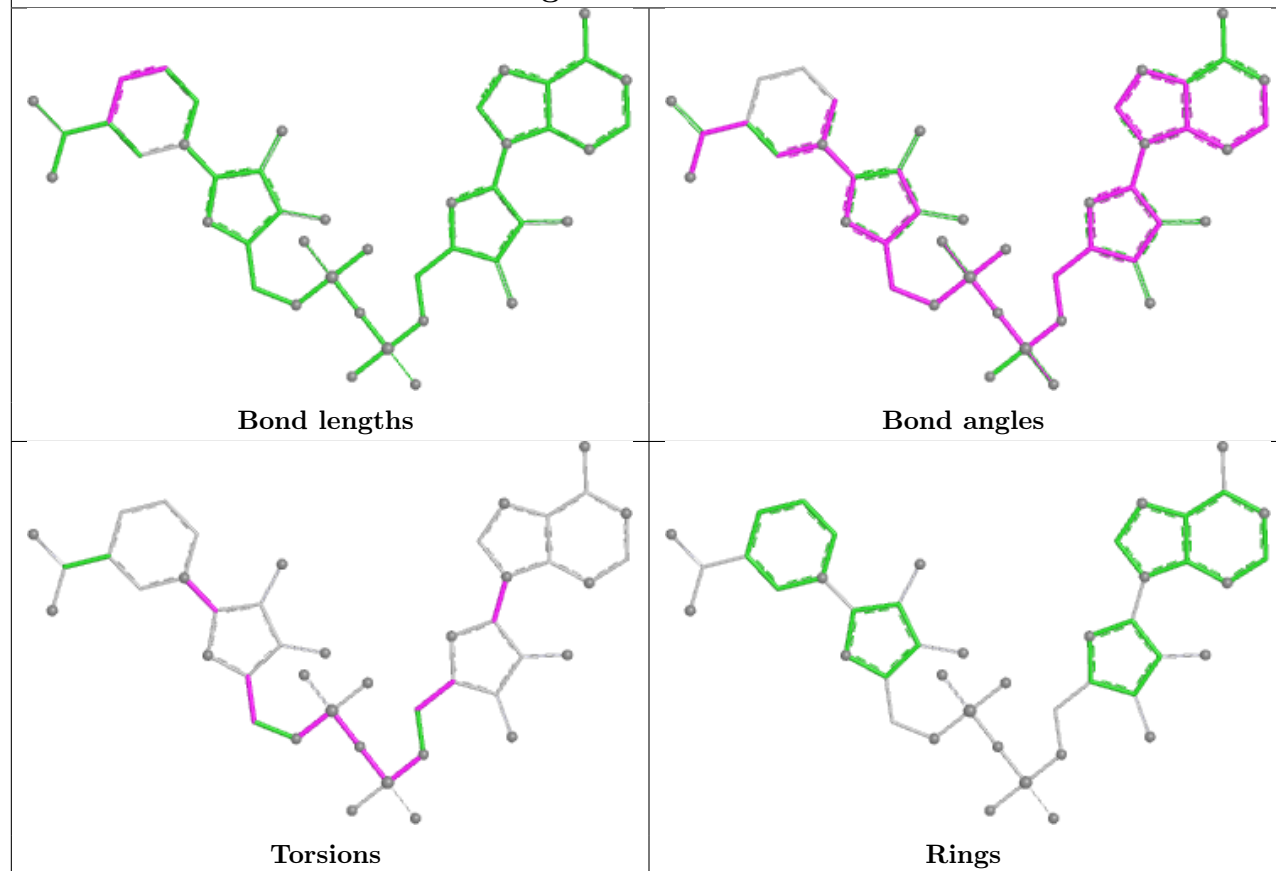


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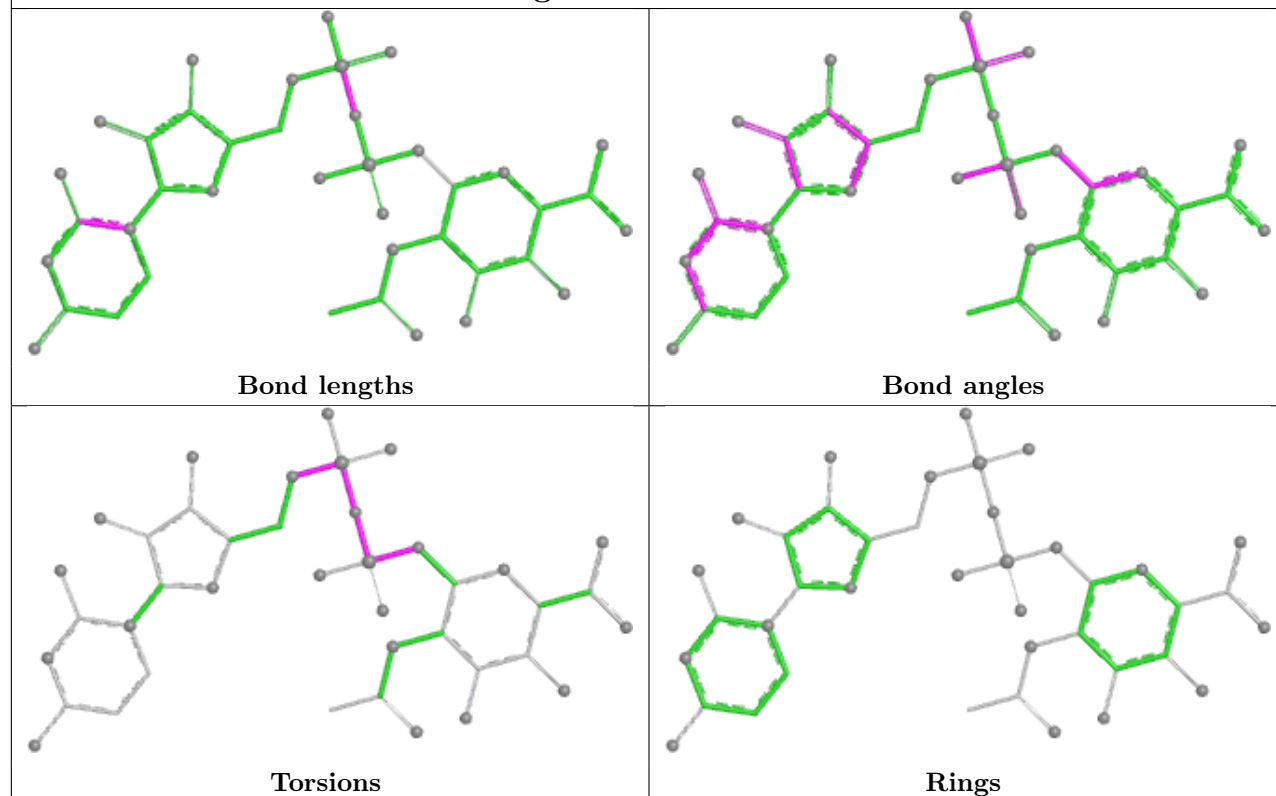


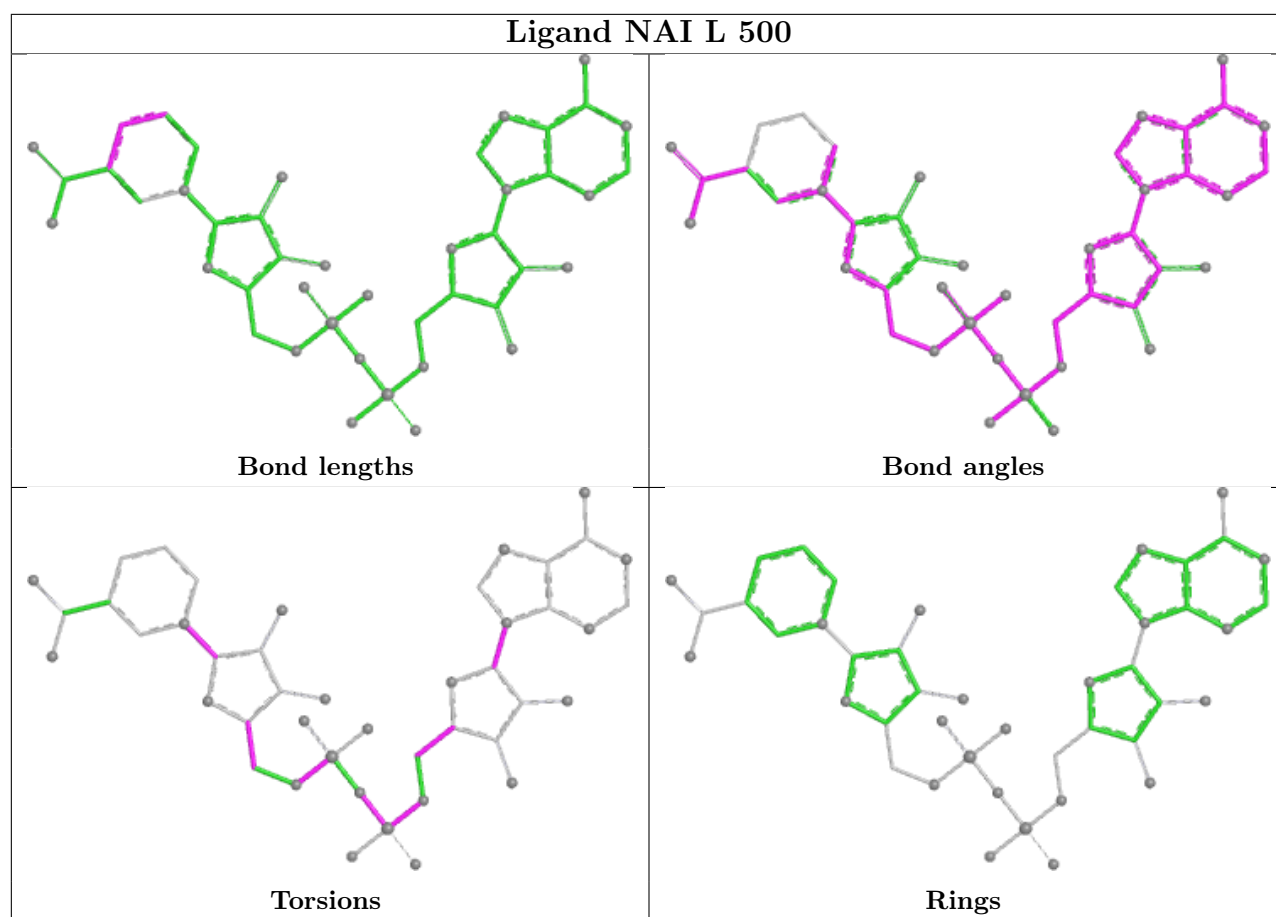


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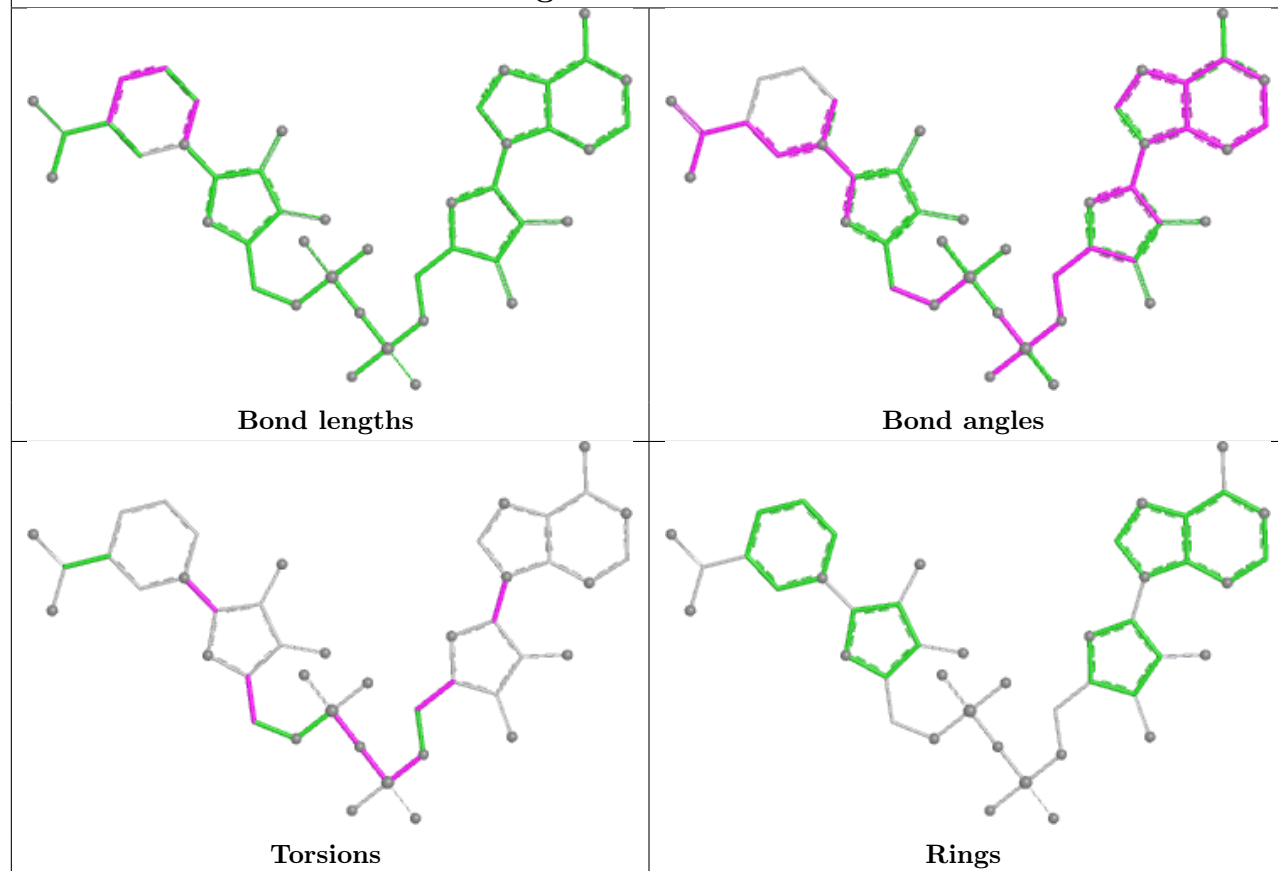


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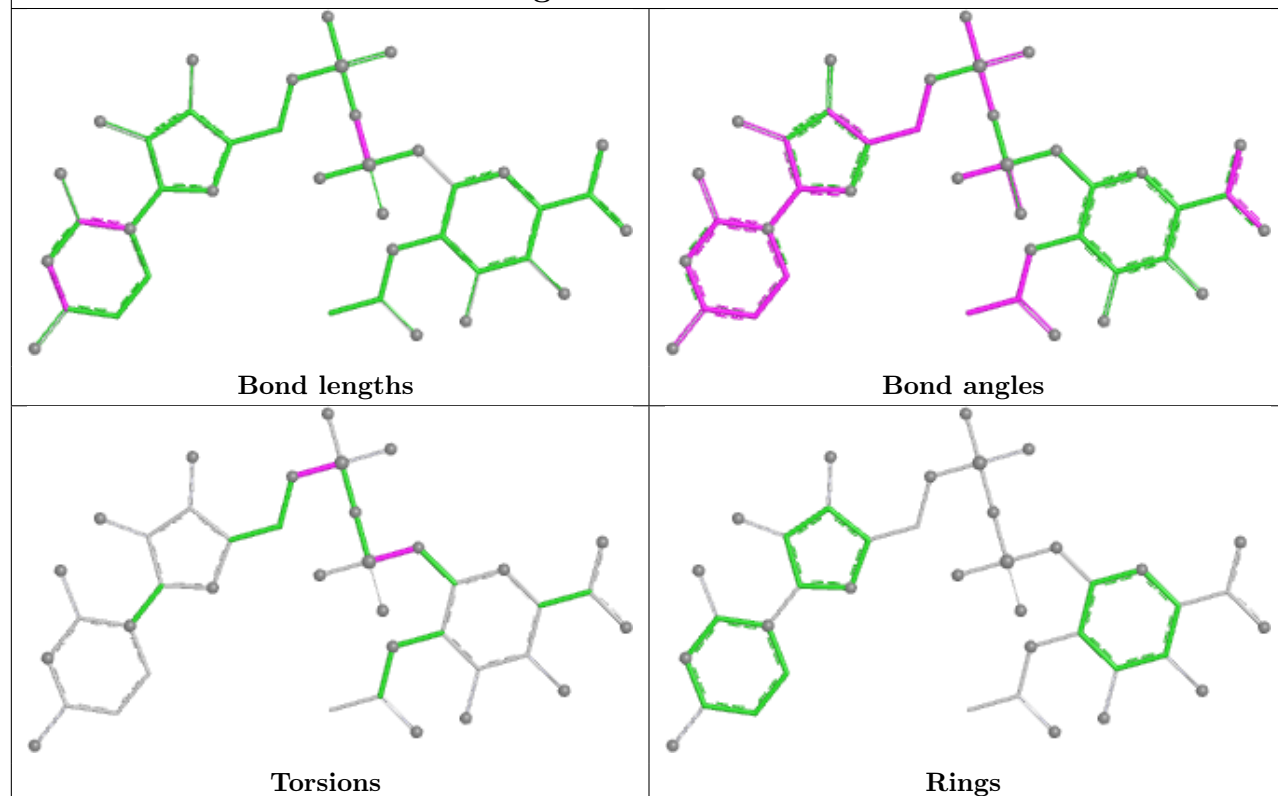




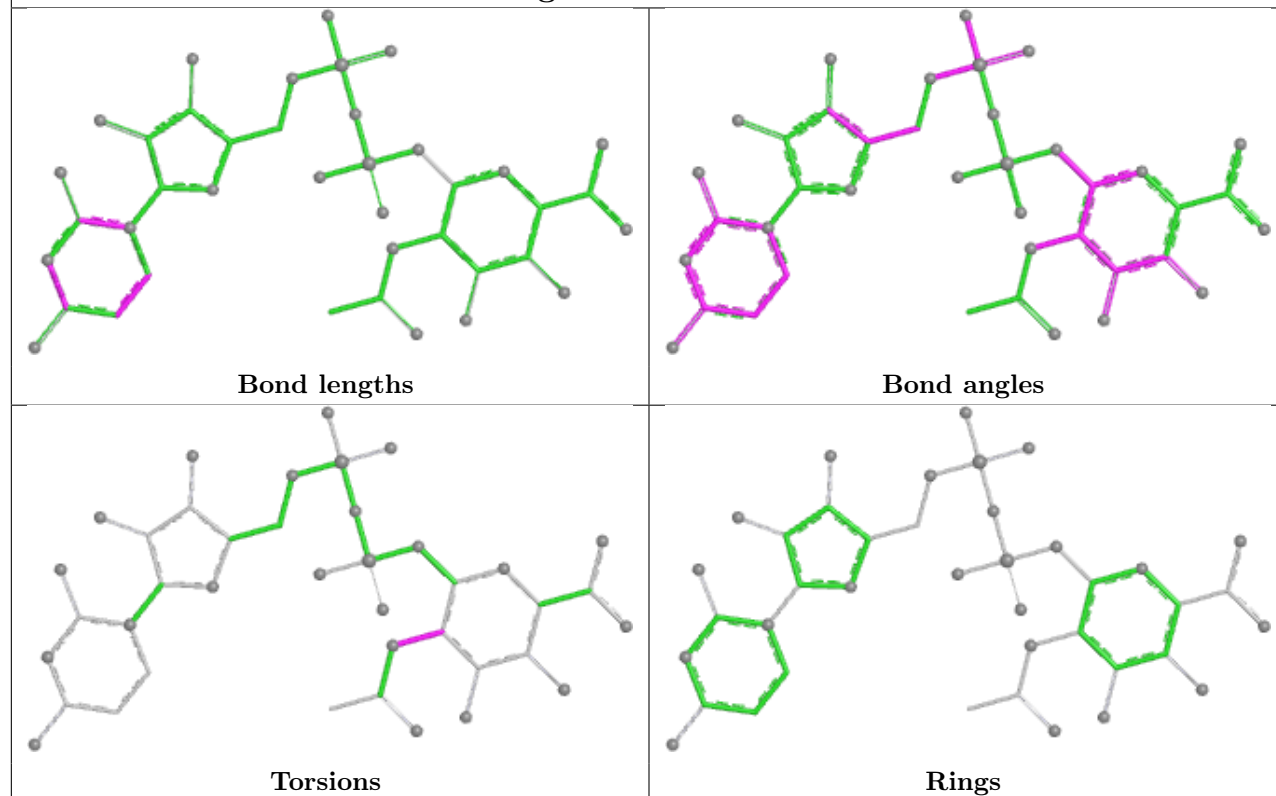
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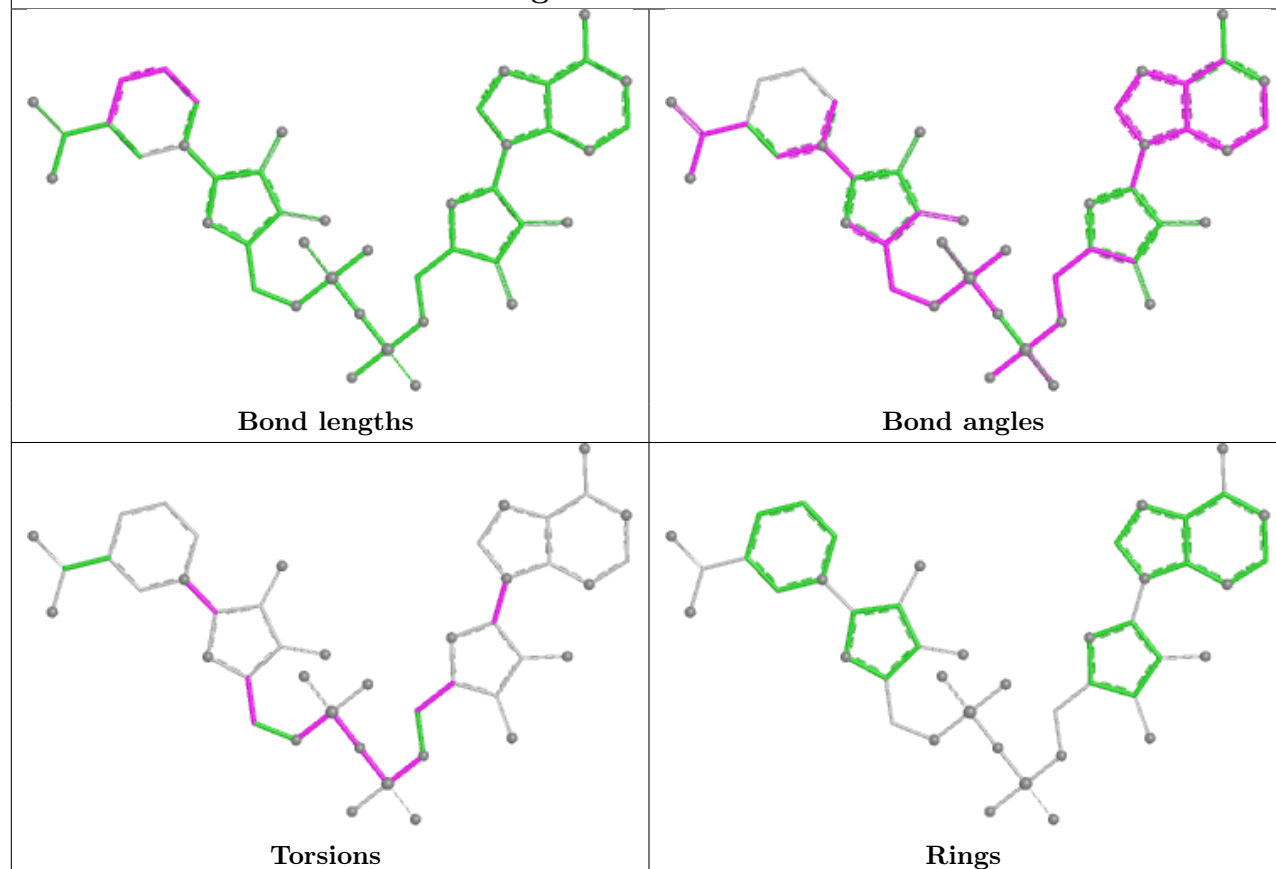
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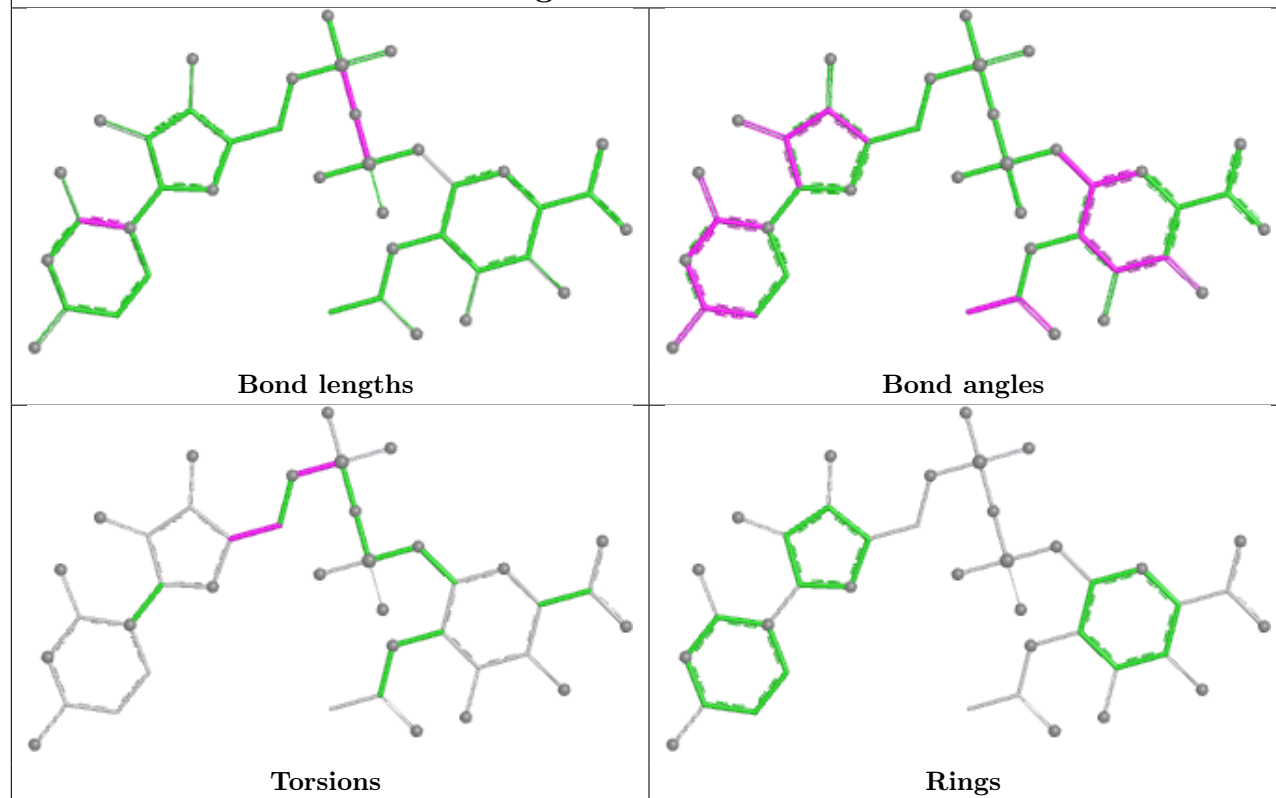
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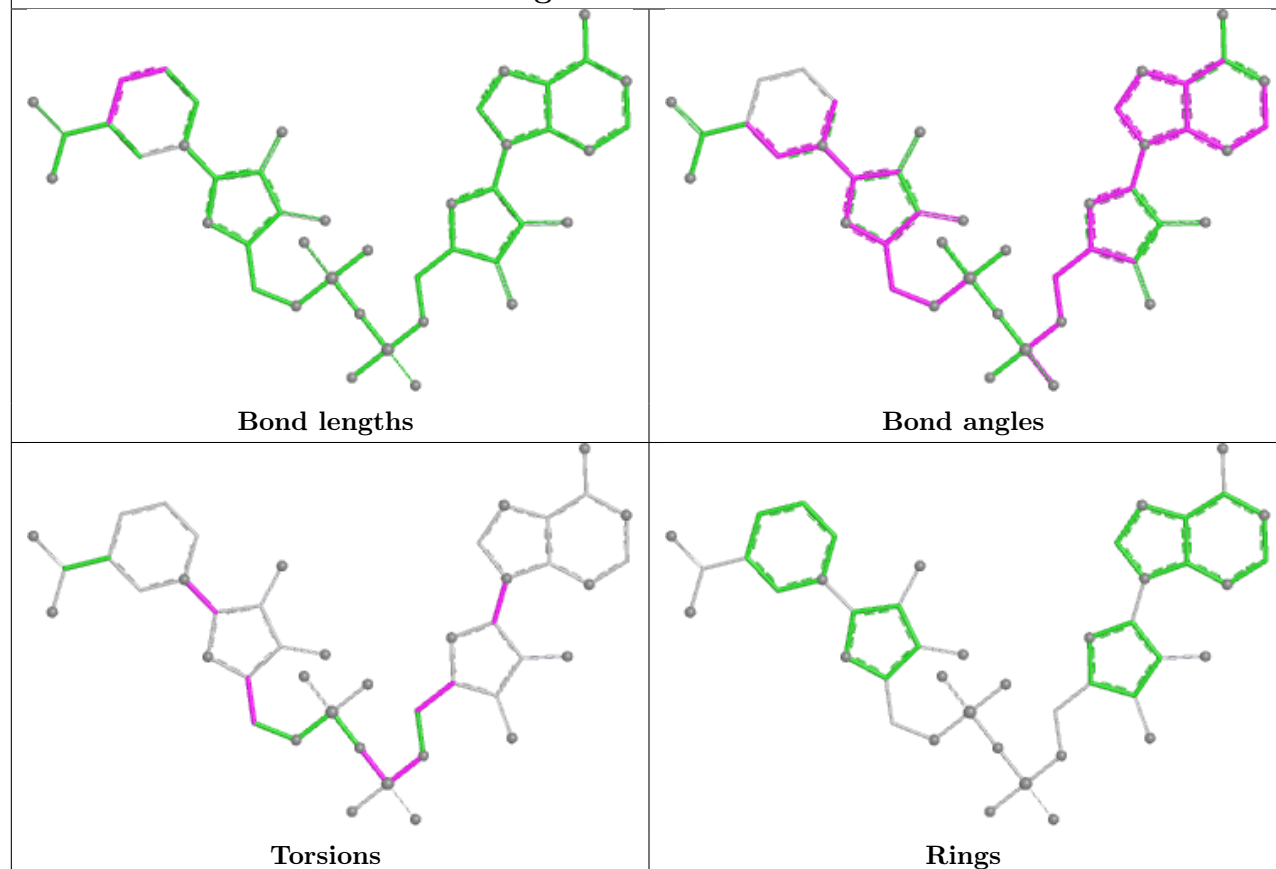
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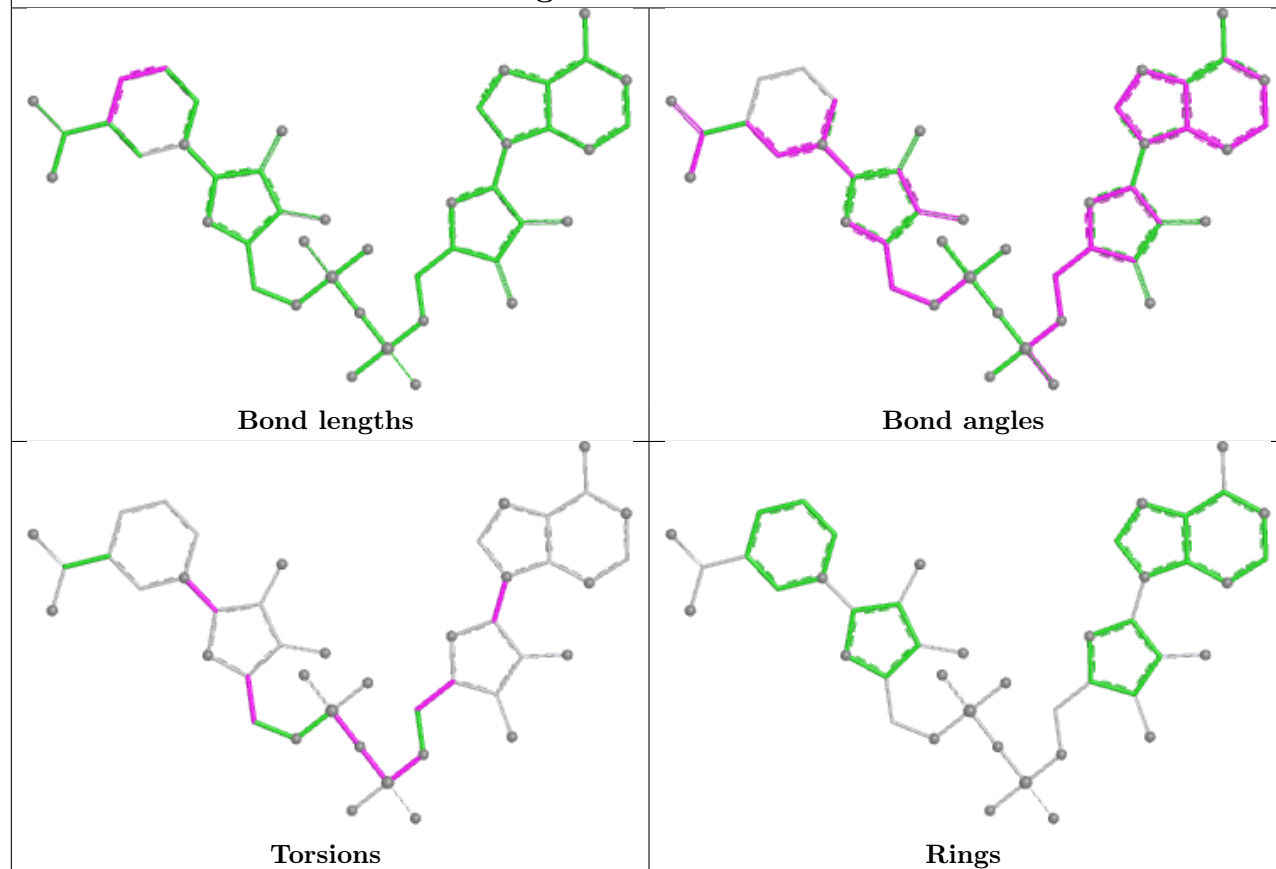
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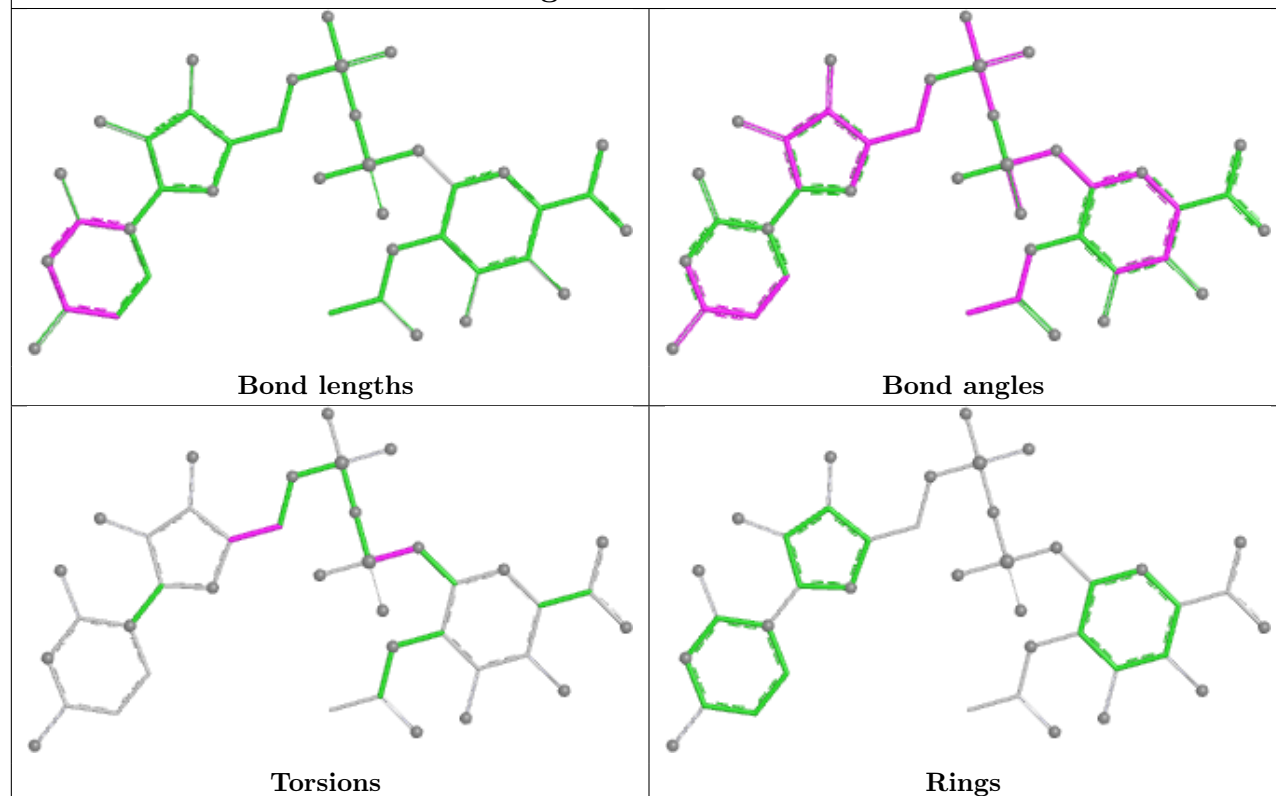
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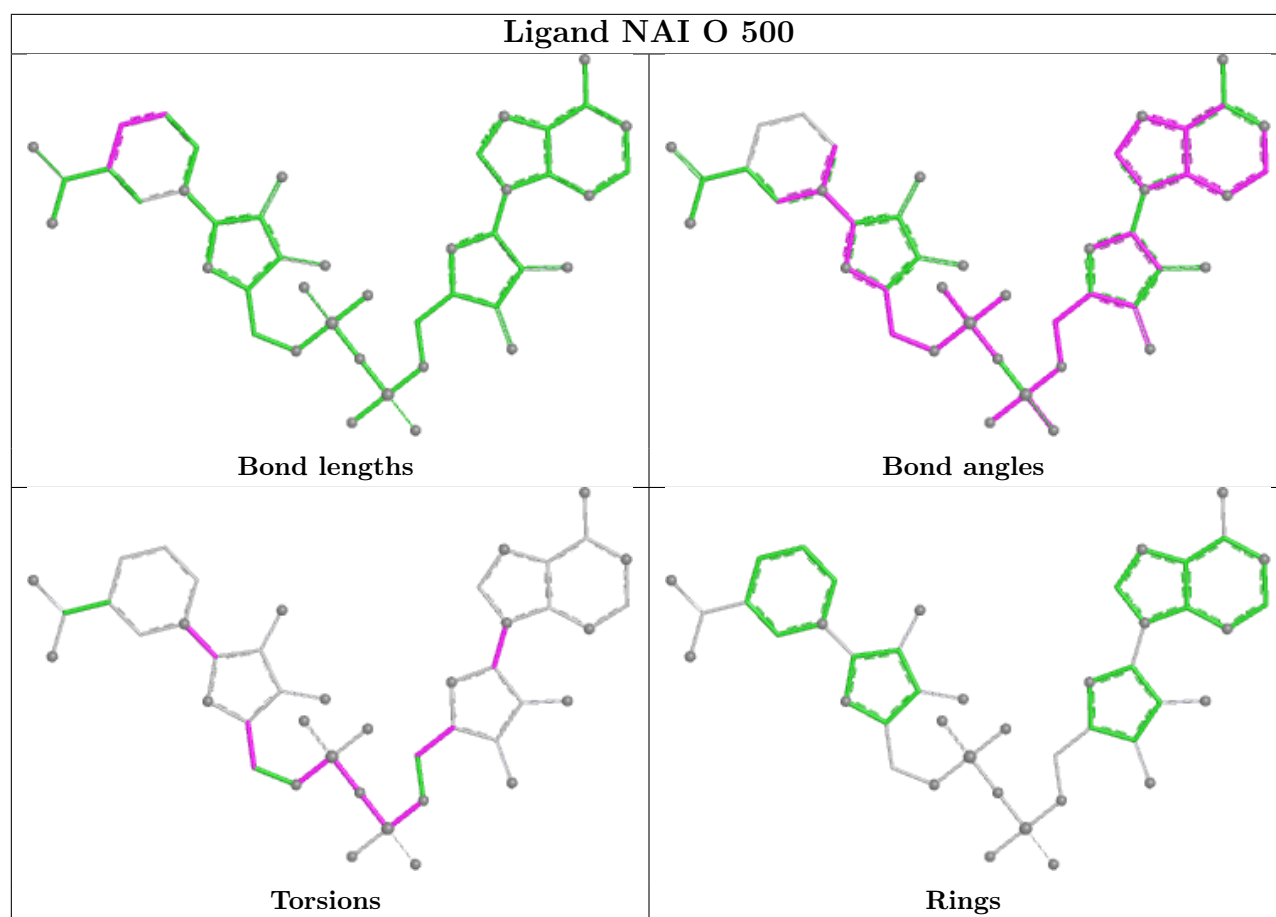


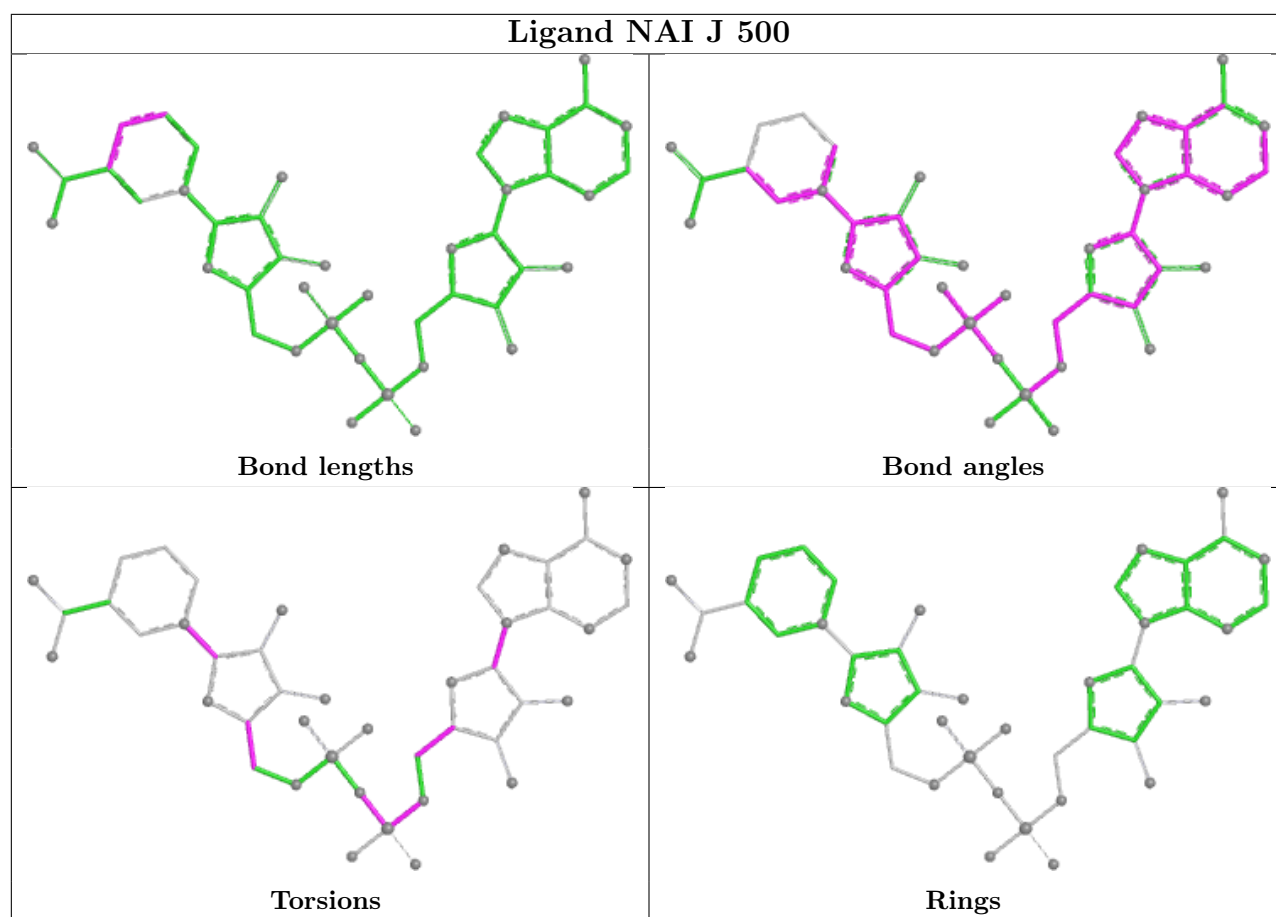
Ligand NAI P 500



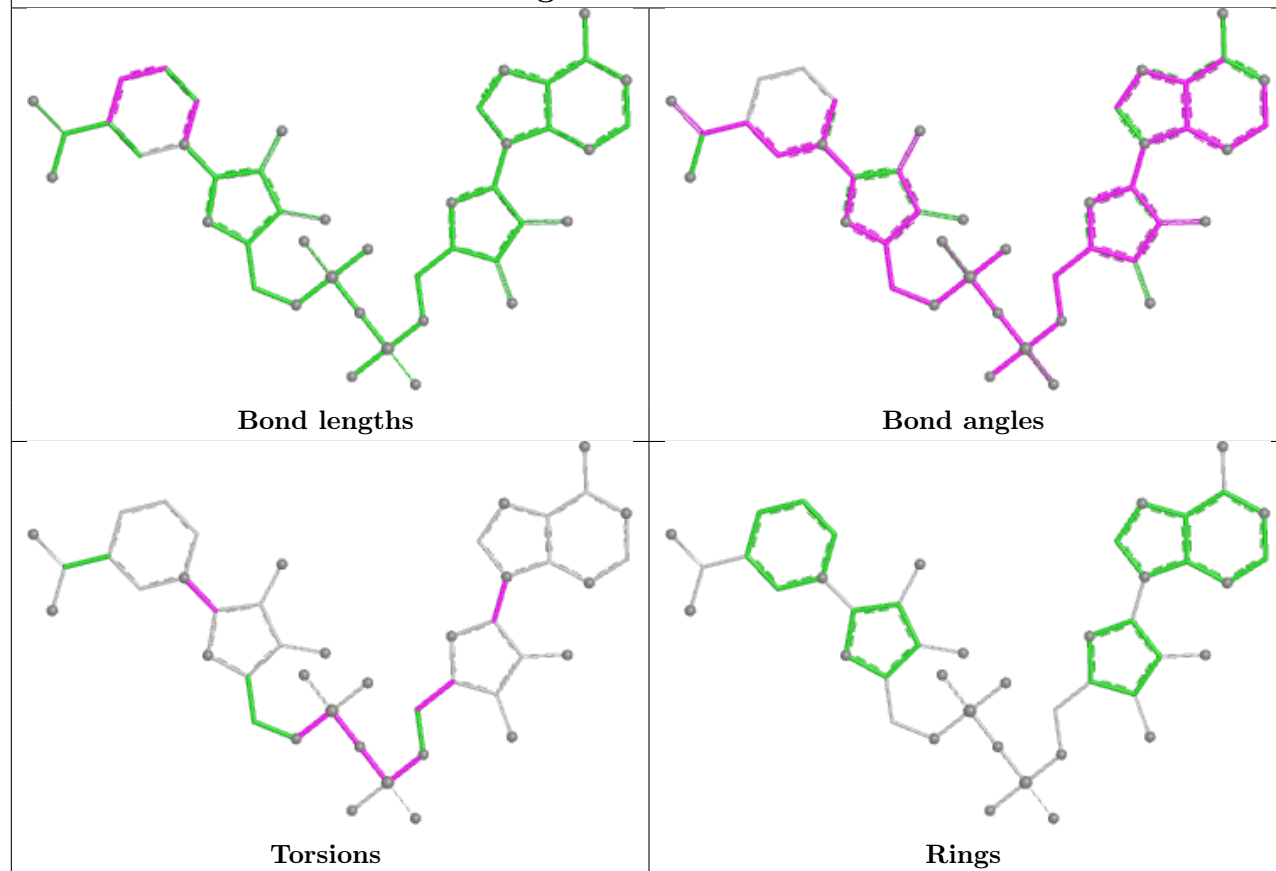
Ligand HP7 I 550



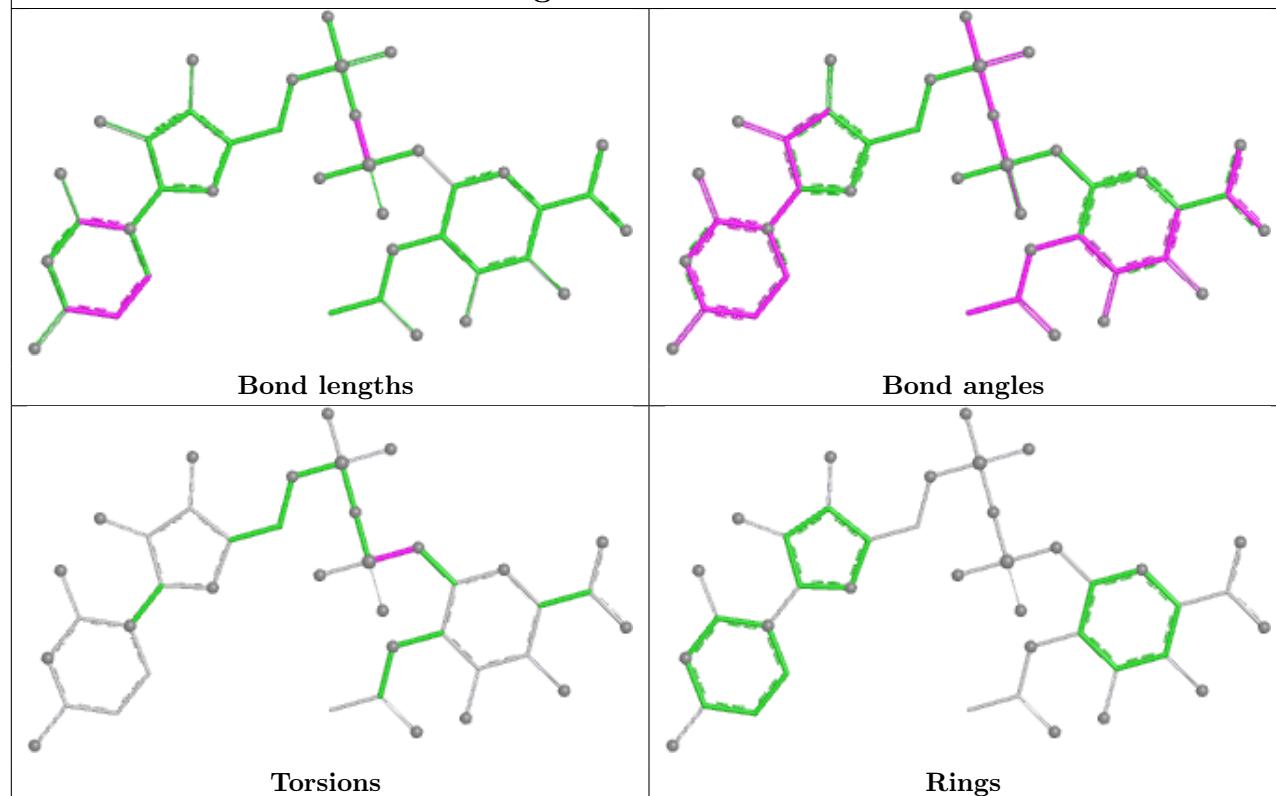




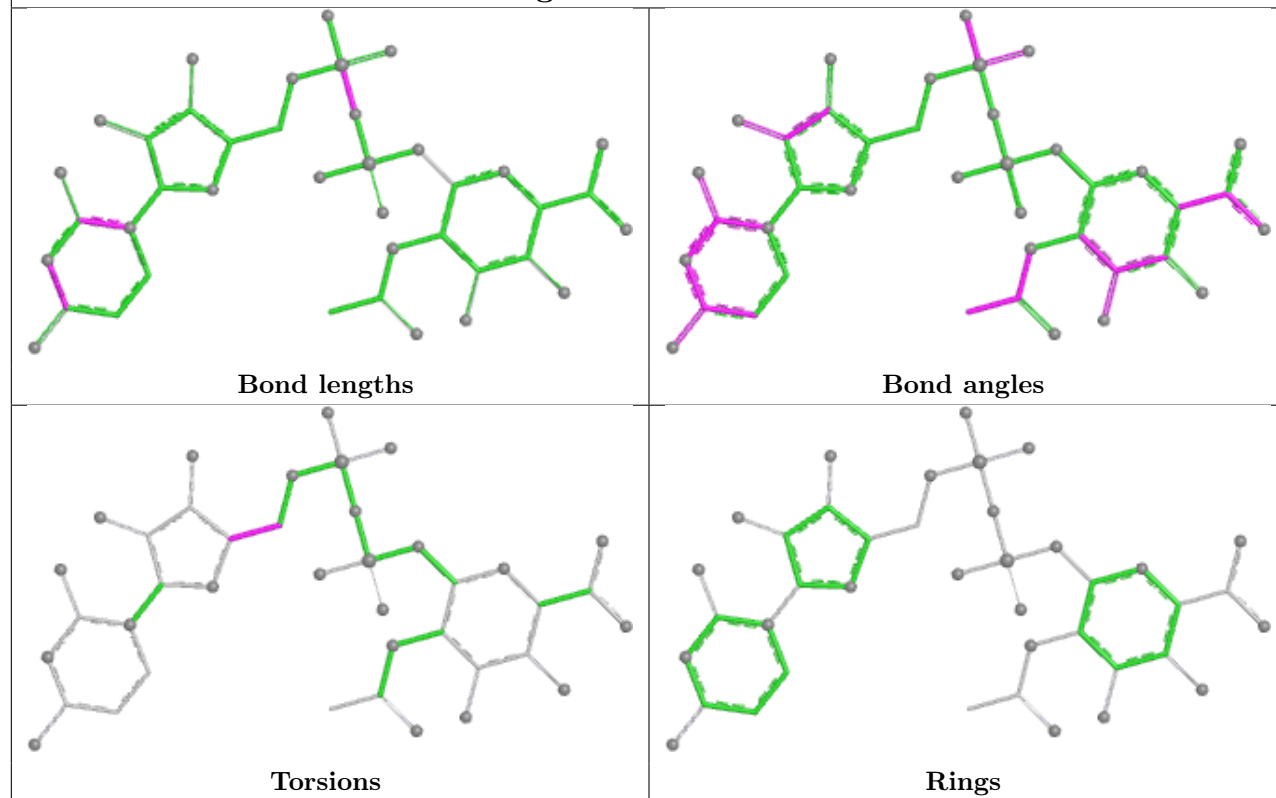
Ligand NAI F 500



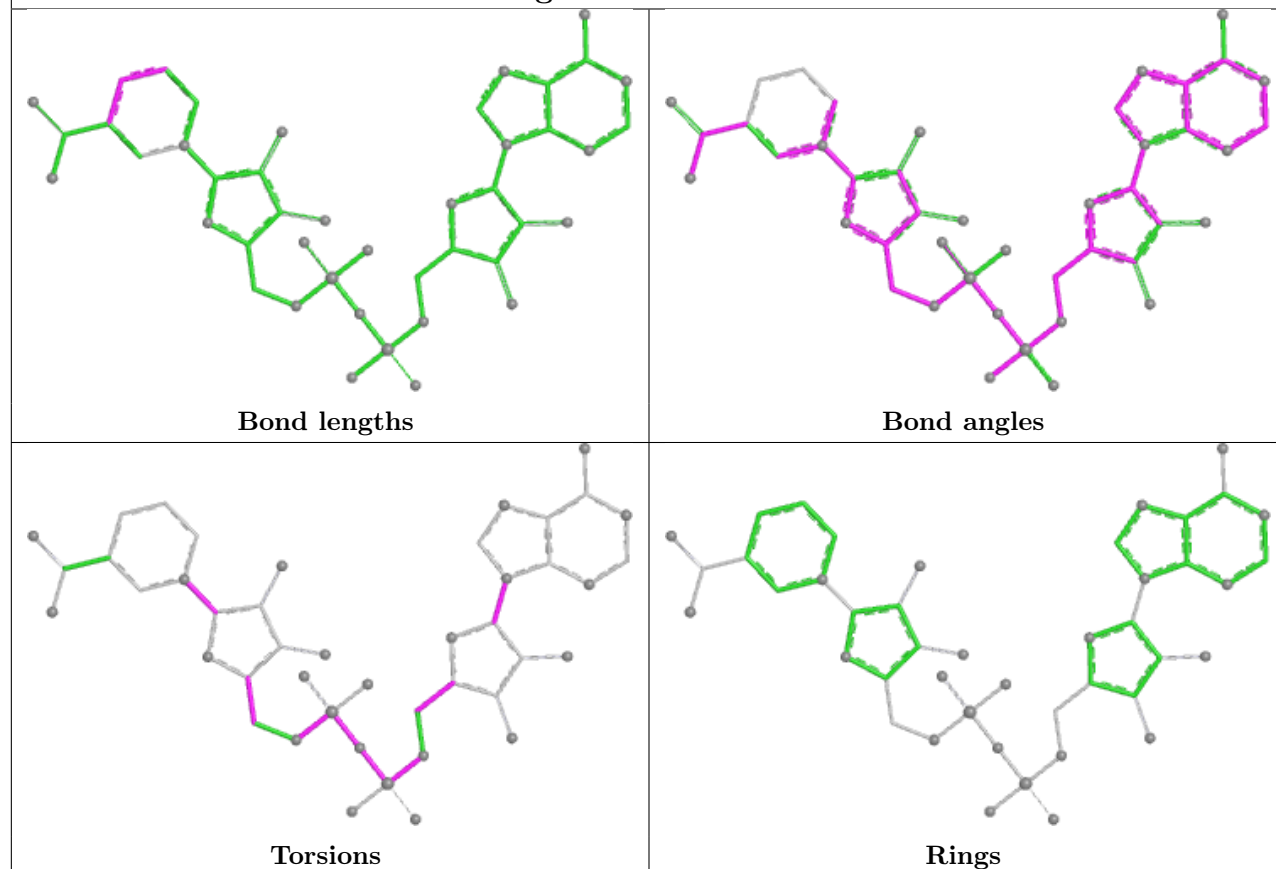
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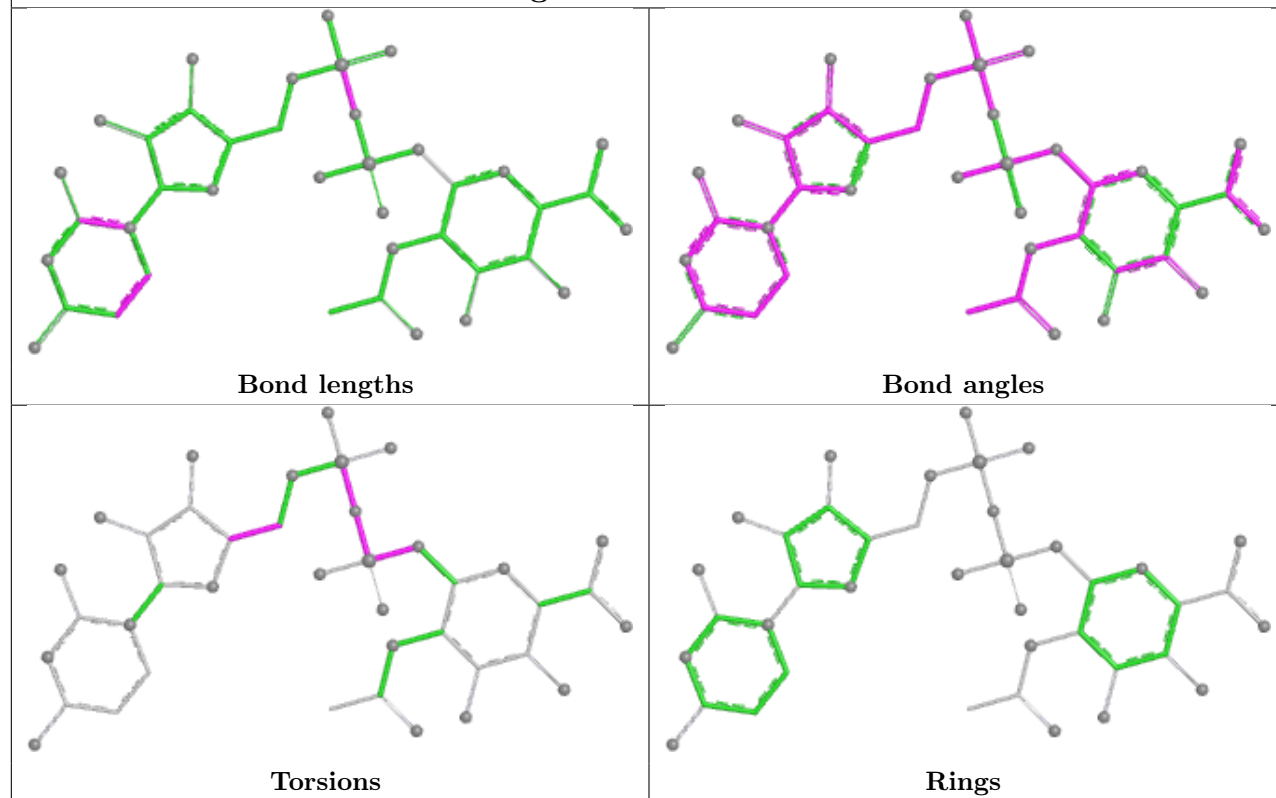
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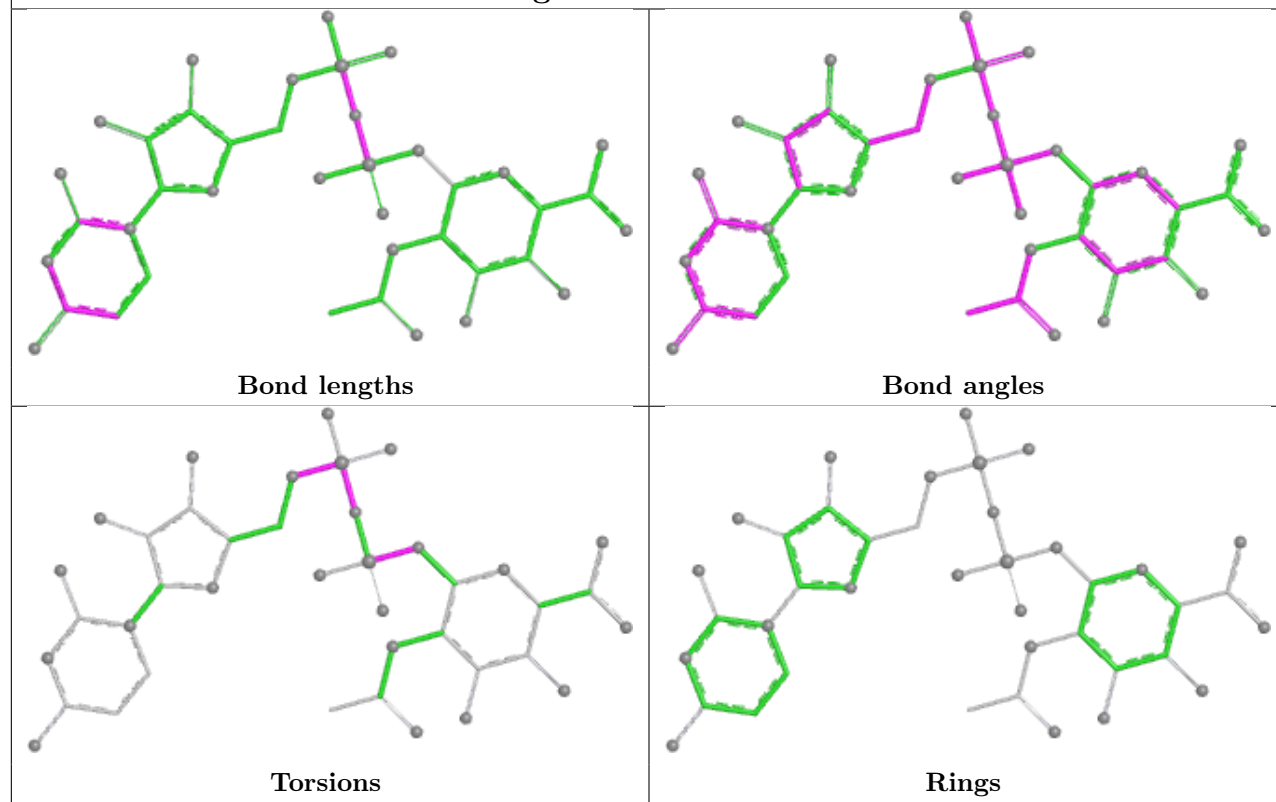
Ligand NAI B 500



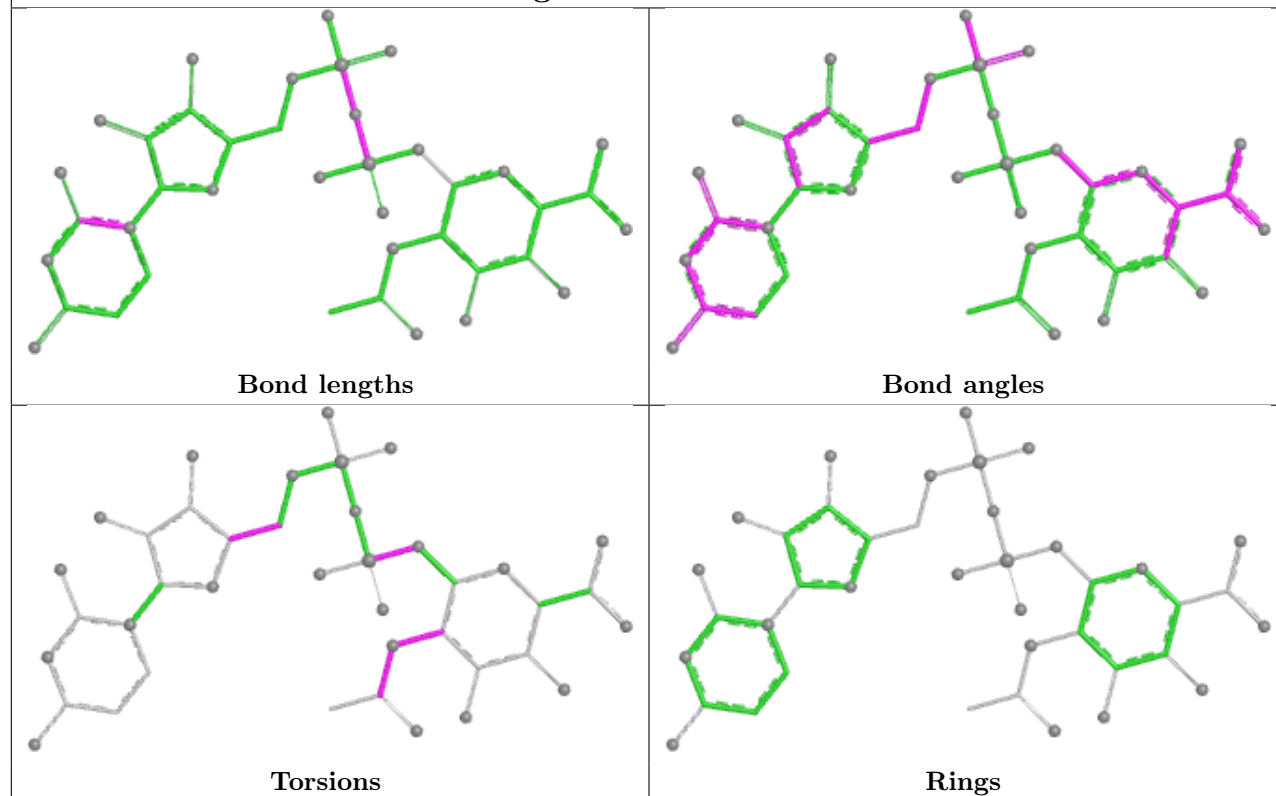
Ligand HP7 M 550



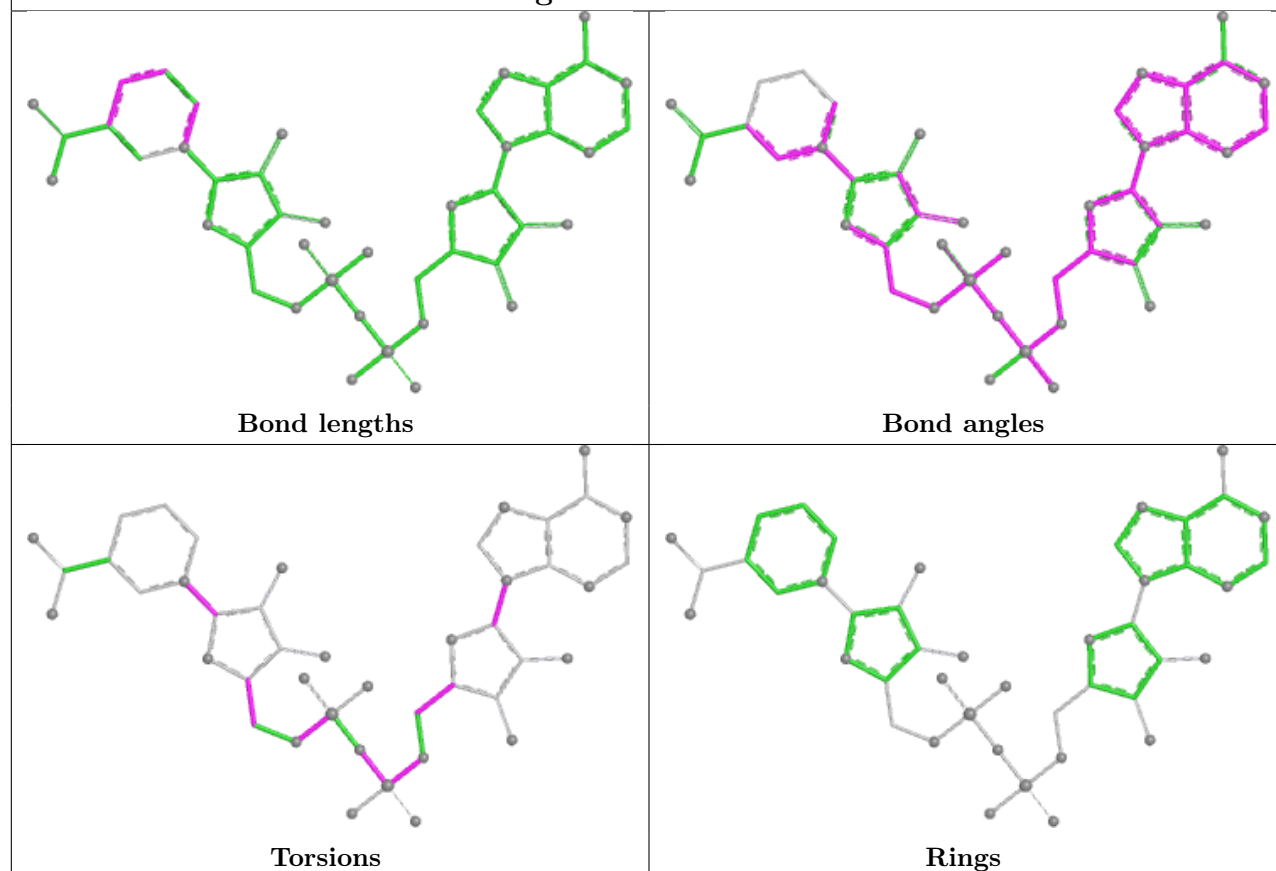
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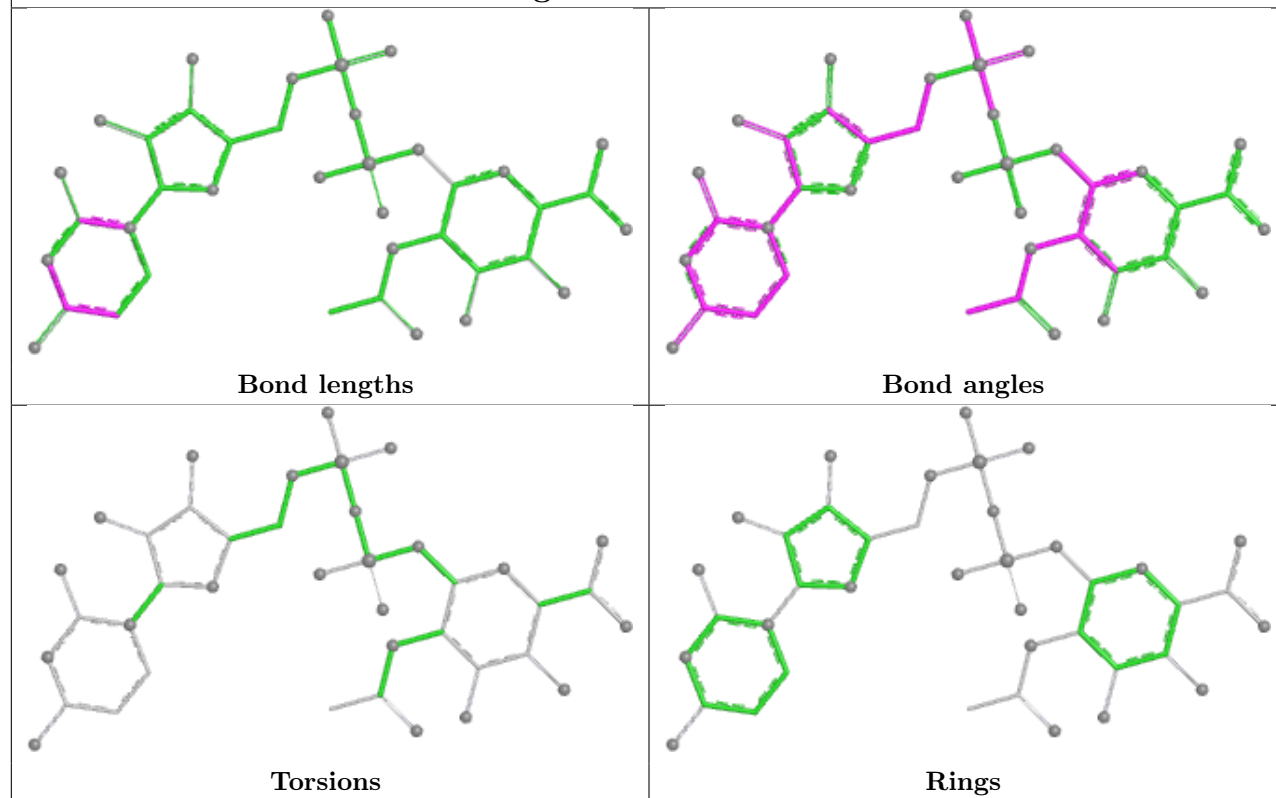
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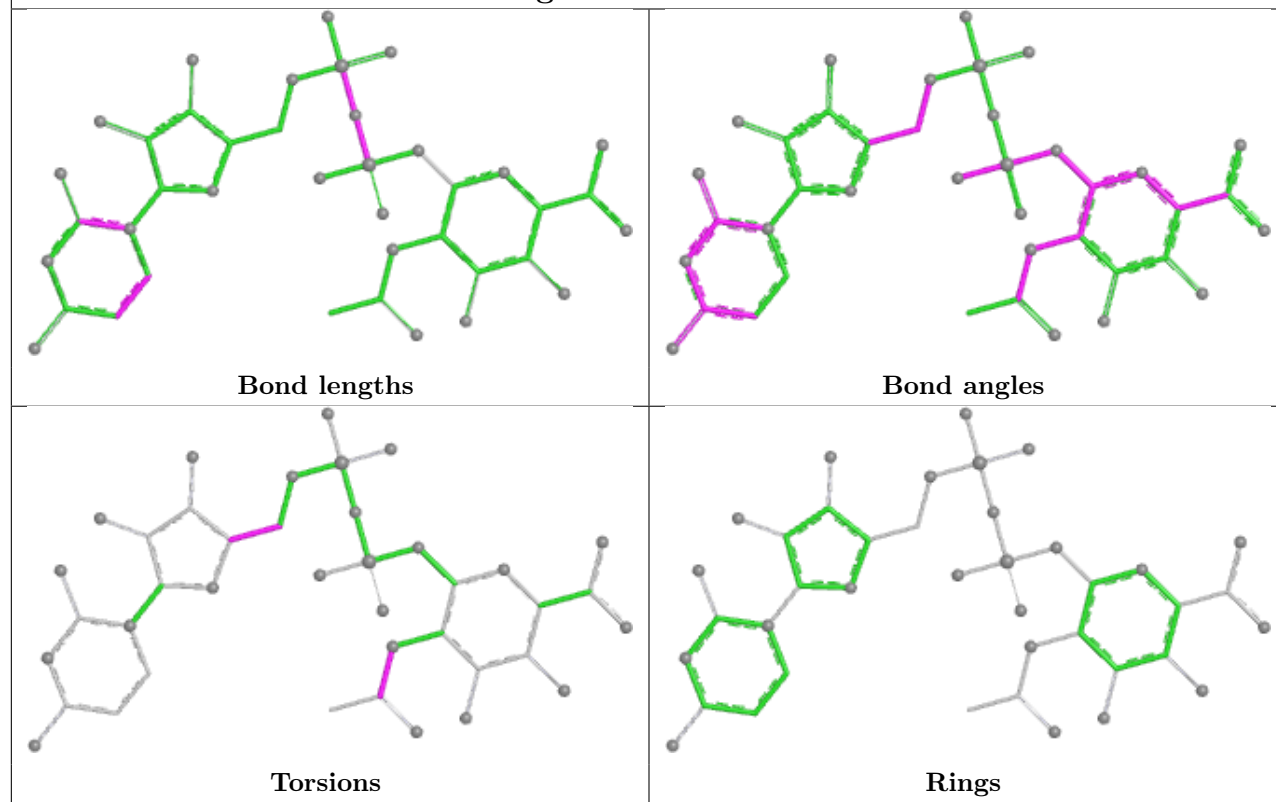
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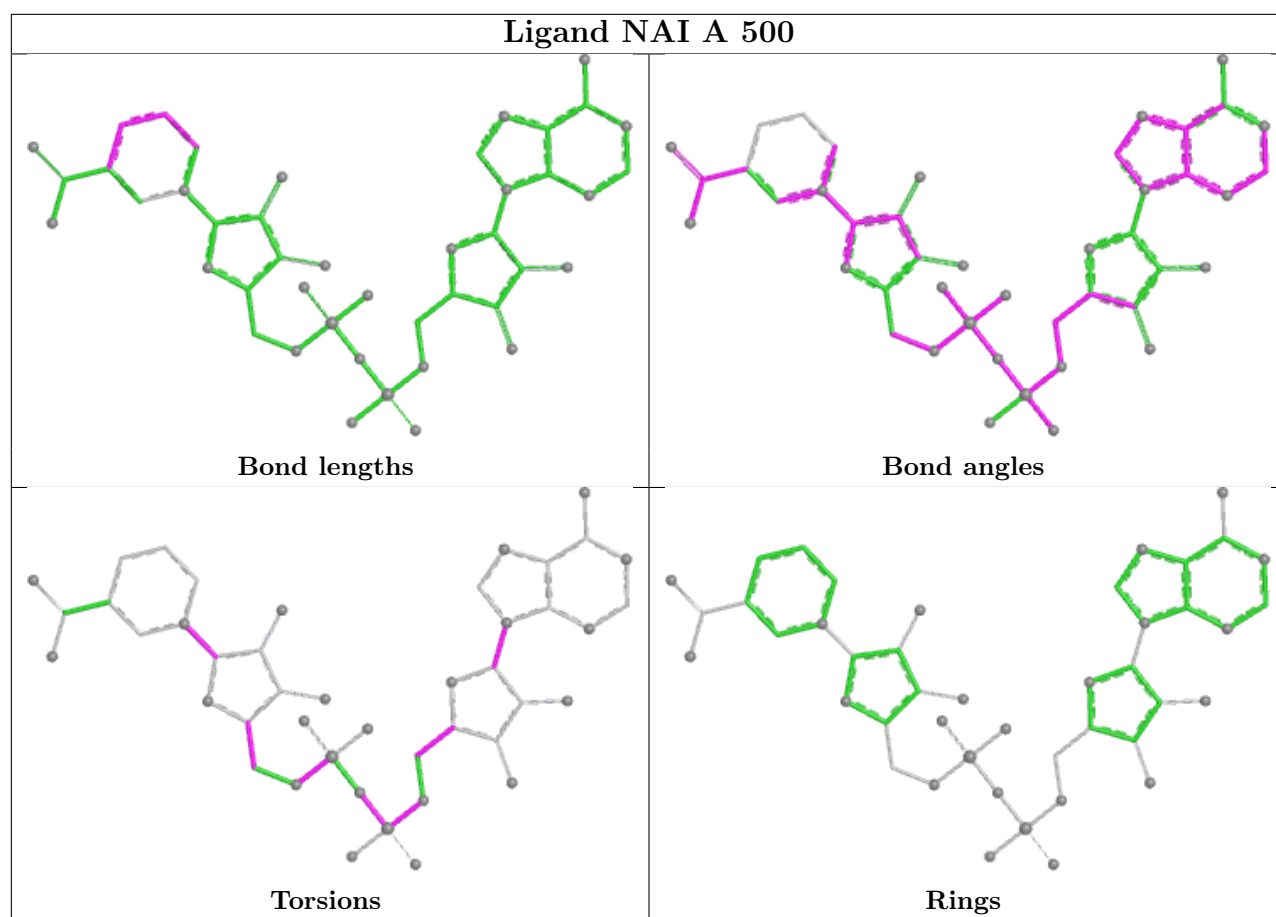


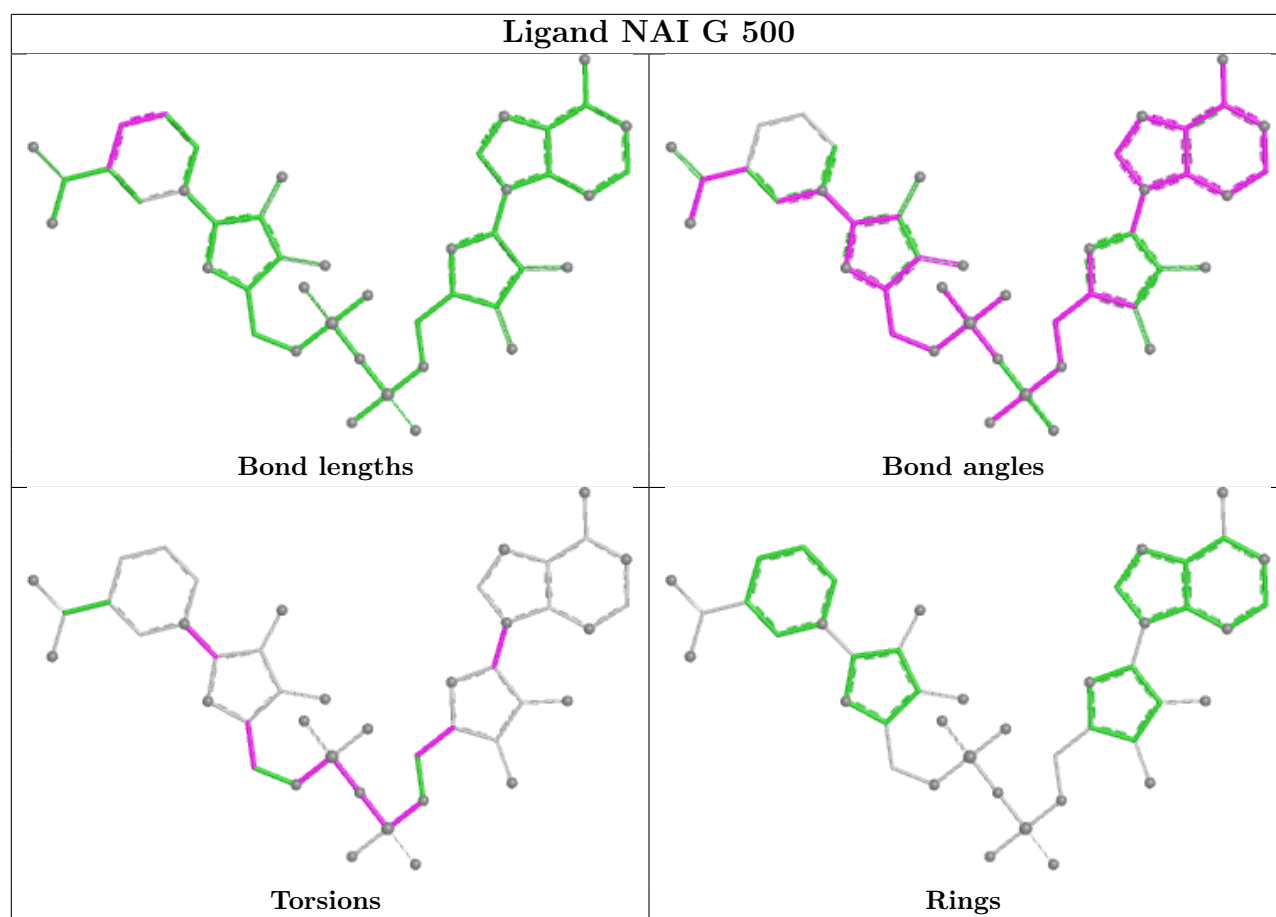
Ligand HP7 H 550

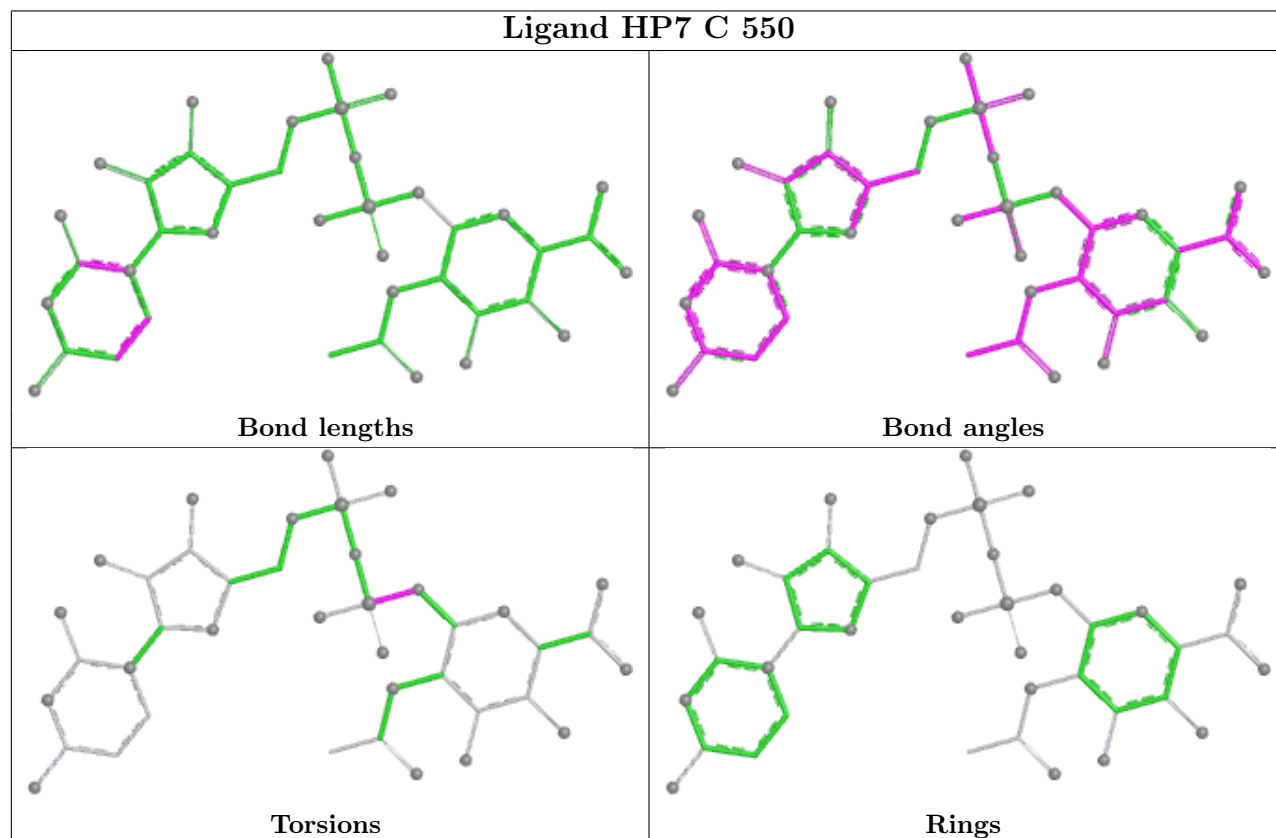
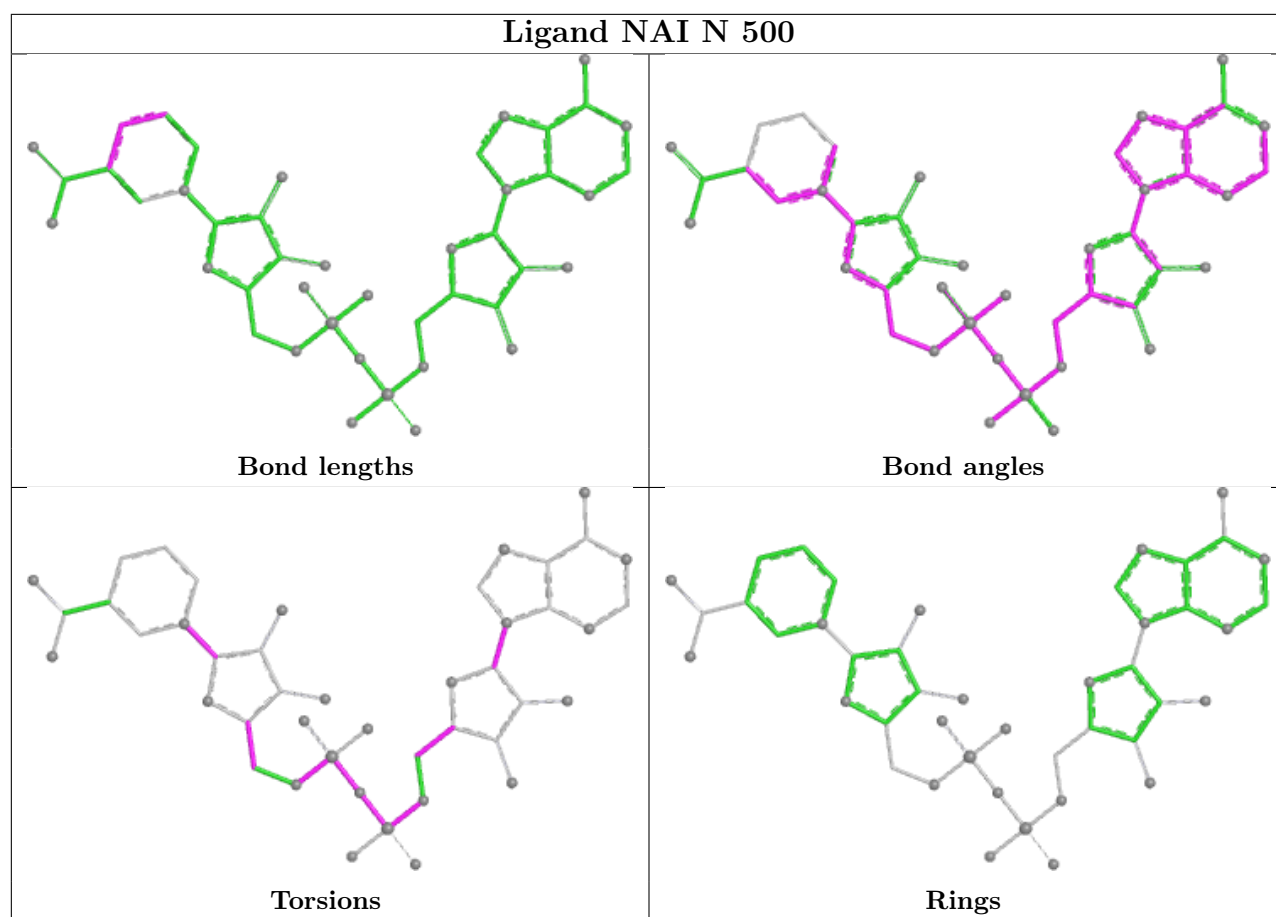


Ligand HP7 L 550









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	346/370 (93%)	-0.48	0 100 100	16, 29, 45, 62	0
1	B	329/370 (88%)	-0.24	1 (0%) 90 92	12, 37, 68, 94	2 (0%)
1	C	347/370 (93%)	-0.34	2 (0%) 85 88	13, 34, 62, 82	0
1	D	343/370 (92%)	-0.12	11 (3%) 50 54	14, 39, 75, 90	1 (0%)
1	E	321/370 (86%)	0.06	4 (1%) 76 80	16, 46, 74, 89	0
1	F	327/370 (88%)	-0.18	3 (0%) 81 84	16, 38, 69, 87	0
1	G	342/370 (92%)	-0.43	2 (0%) 85 88	13, 31, 59, 75	0
1	H	342/370 (92%)	-0.19	5 (1%) 72 76	10, 36, 72, 88	1 (0%)
1	I	342/370 (92%)	-0.09	3 (0%) 81 84	17, 39, 72, 91	0
1	J	346/370 (93%)	-0.13	5 (1%) 73 77	20, 40, 73, 86	0
1	K	322/370 (87%)	-0.02	6 (1%) 66 70	15, 42, 75, 97	0
1	L	321/370 (86%)	0.12	12 (3%) 45 50	16, 47, 82, 93	1 (0%)
1	M	346/370 (93%)	-0.41	4 (1%) 76 80	12, 31, 61, 84	0
1	N	342/370 (92%)	-0.29	1 (0%) 90 92	13, 34, 69, 80	0
1	O	334/370 (90%)	-0.21	1 (0%) 90 92	16, 39, 64, 86	0
1	P	322/370 (87%)	-0.10	6 (1%) 66 70	16, 40, 74, 93	0
All	All	5372/5920 (90%)	-0.19	66 (1%) 76 80	10, 37, 72, 97	5 (0%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	P	279	PRO	5.8
1	E	303	LEU	5.4
1	L	30	ALA	5.2
1	D	299	PHE	4.4
1	K	33	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	297	TYR	4.1
1	D	291	TYR	3.6
1	G	316	CYS	3.5
1	E	316	CYS	3.5
1	L	300	GLY	3.4
1	H	291	TYR	3.4
1	D	317	GLU	3.3
1	C	299	PHE	3.2
1	O	5	PRO	3.1
1	K	39	VAL	3.1
1	L	303	LEU	3.1
1	M	8	ASP	3.0
1	D	30	ALA	3.0
1	M	299	PHE	3.0
1	P	30	ALA	2.9
1	N	33	GLY	2.9
1	P	28	ALA	2.9
1	L	309	ILE	2.8
1	P	33	GLY	2.8
1	H	33	GLY	2.8
1	I	54	ALA	2.8
1	F	300	GLY	2.7
1	L	58	ALA	2.7
1	L	279	PRO	2.6
1	L	33	GLY	2.6
1	L	36	ALA	2.6
1	J	287	ARG	2.6
1	I	73	ALA	2.5
1	D	295	SER	2.5
1	L	11	ILE	2.5
1	D	294	THR	2.5
1	G	315	ASP	2.4
1	M	5	PRO	2.4
1	L	54	ALA	2.4
1	H	296	VAL	2.4
1	B	281	PRO	2.4
1	E	54	ALA	2.4
1	P	9	ARG	2.4
1	F	316	CYS	2.3
1	K	300	GLY	2.3
1	J	39	VAL	2.3
1	D	296	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	279	PRO	2.2
1	D	33	GLY	2.2
1	L	69	ALA	2.2
1	J	316	CYS	2.2
1	L	315	ASP	2.2
1	F	33	GLY	2.2
1	K	36	ALA	2.2
1	P	51	ALA	2.2
1	C	33	GLY	2.1
1	I	36	ALA	2.1
1	D	293	THR	2.1
1	J	319	GLU	2.1
1	K	35	ARG	2.1
1	H	57	GLY	2.1
1	K	57	GLY	2.1
1	J	5	PRO	2.0
1	H	316	CYS	2.0
1	M	7	THR	2.0
1	D	298	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HP7	E	550	40/40	0.91	0.10	32,64,100,100	0
3	HP7	P	550	40/40	0.92	0.10	28,48,100,100	0
3	HP7	L	550	40/40	0.93	0.10	20,56,100,100	0
3	HP7	O	550	40/40	0.93	0.10	22,56,100,100	0

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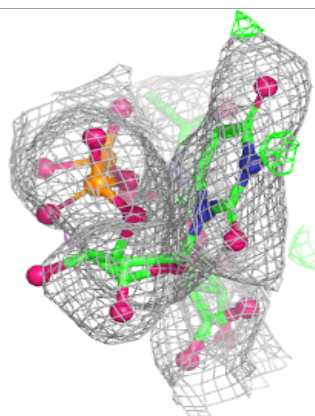
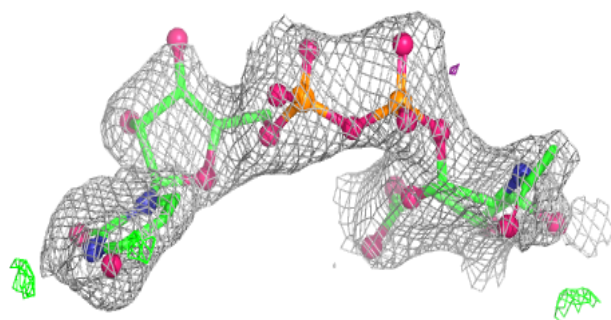
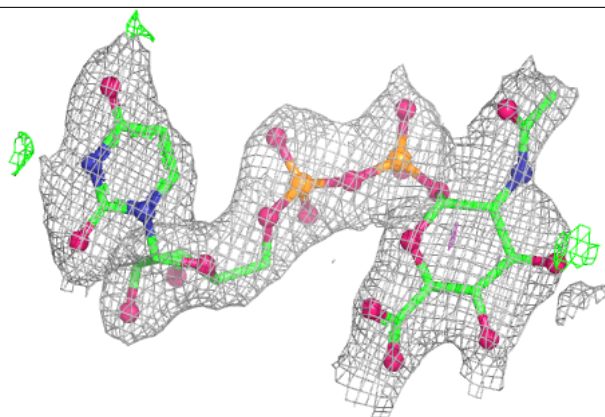
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HP7	F	550	40/40	0.93	0.10	24,43,100,100	0
3	HP7	K	550	40/40	0.94	0.09	17,53,100,100	0
3	HP7	B	550	40/40	0.94	0.08	25,45,100,100	0
3	HP7	D	550	40/40	0.95	0.09	23,47,99,100	0
2	NAI	L	500	44/44	0.95	0.09	23,40,63,100	0
2	NAI	B	500	44/44	0.95	0.08	21,36,58,79	0
3	HP7	H	550	40/40	0.95	0.07	21,34,59,90	0
2	NAI	N	500	44/44	0.96	0.07	17,32,48,63	0
2	NAI	O	500	44/44	0.96	0.07	19,35,52,63	0
3	HP7	I	550	40/40	0.96	0.07	19,40,82,100	0
3	HP7	J	550	40/40	0.96	0.07	14,36,75,100	0
2	NAI	E	500	44/44	0.96	0.07	23,43,87,98	0
3	HP7	C	550	40/40	0.96	0.07	17,30,76,100	0
2	NAI	K	500	44/44	0.96	0.07	18,33,53,100	0
2	NAI	D	500	44/44	0.96	0.07	20,36,52,70	0
2	NAI	J	500	44/44	0.97	0.07	18,37,60,78	0
2	NAI	A	500	44/44	0.97	0.06	19,25,31,45	0
2	NAI	C	500	44/44	0.97	0.06	14,28,44,71	0
3	HP7	G	550	40/40	0.97	0.06	14,32,77,100	0
2	NAI	M	500	44/44	0.97	0.07	15,32,49,84	0
2	NAI	F	500	44/44	0.97	0.06	15,28,43,64	0
2	NAI	G	500	44/44	0.97	0.06	17,28,38,57	0
2	NAI	P	500	44/44	0.97	0.06	24,37,54,73	0
3	HP7	A	550	40/40	0.97	0.06	11,25,50,100	0
3	HP7	M	550	40/40	0.97	0.06	17,31,42,59	0
3	HP7	N	550	40/40	0.97	0.05	15,27,50,56	0
2	NAI	H	500	44/44	0.97	0.07	21,34,60,100	0
2	NAI	I	500	44/44	0.97	0.06	20,35,46,59	0

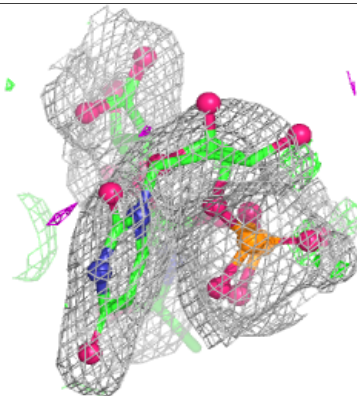
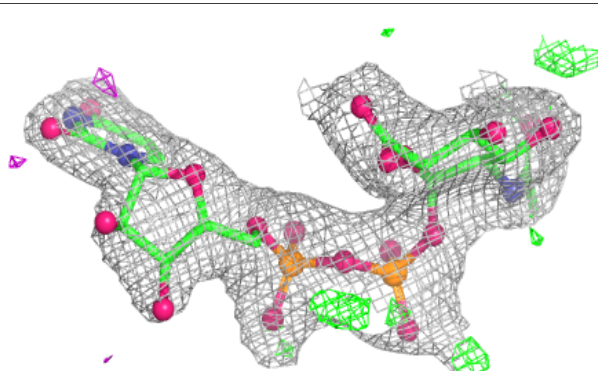
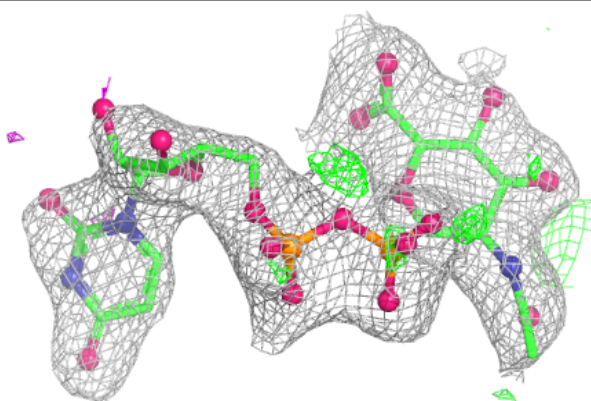
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HP7 E 550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

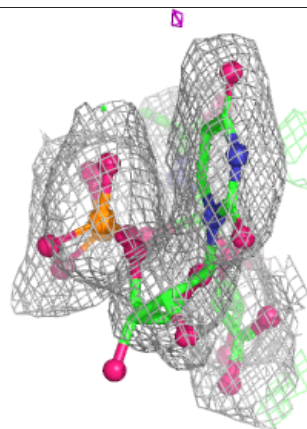
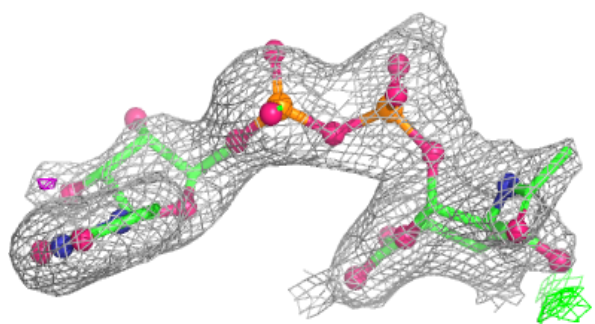
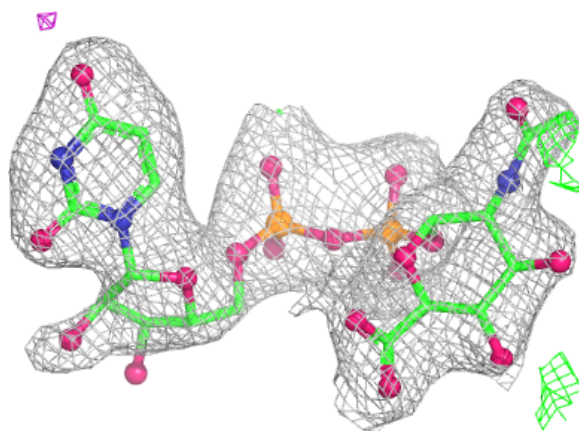
**Electron density around HP7 P 550:**

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and green (positive)



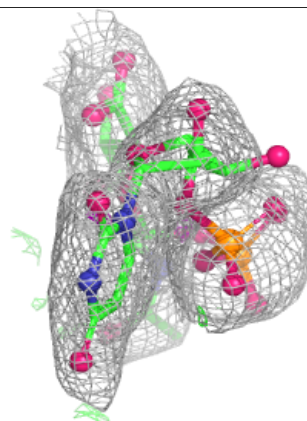
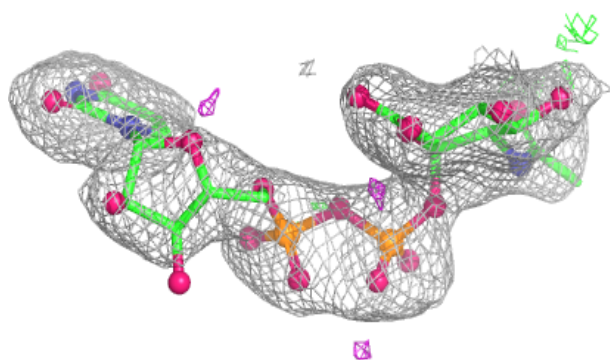
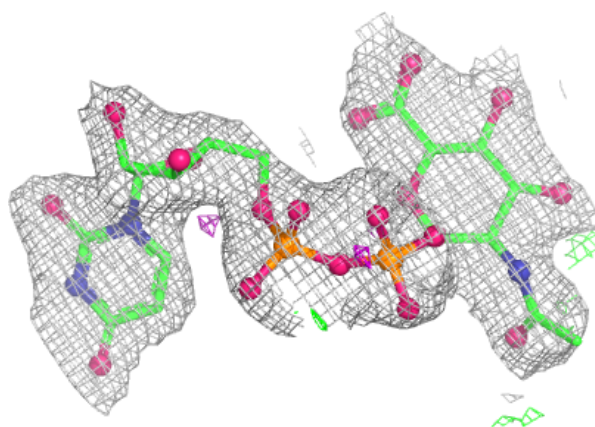
Electron density around HP7 L 550:

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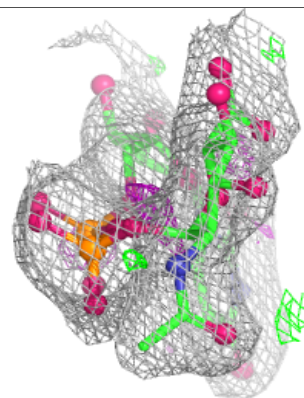
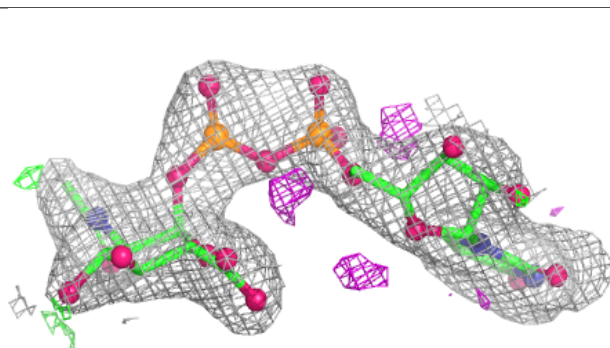
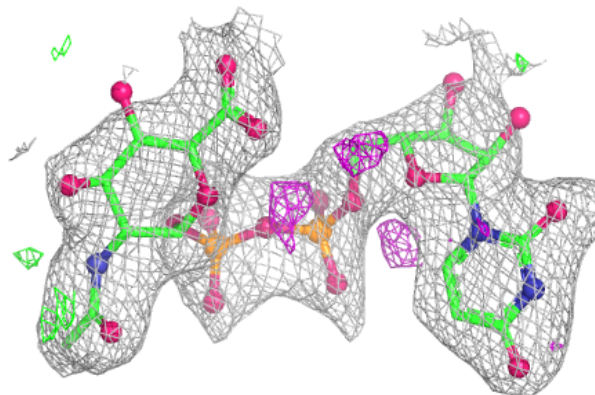


Electron density around HP7 O 550:

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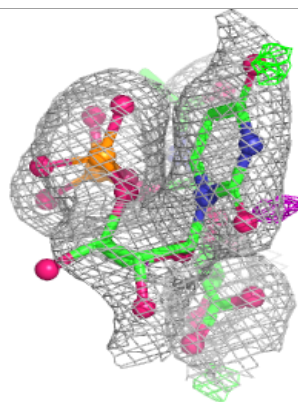
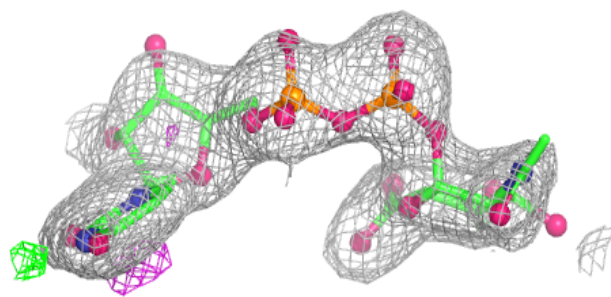
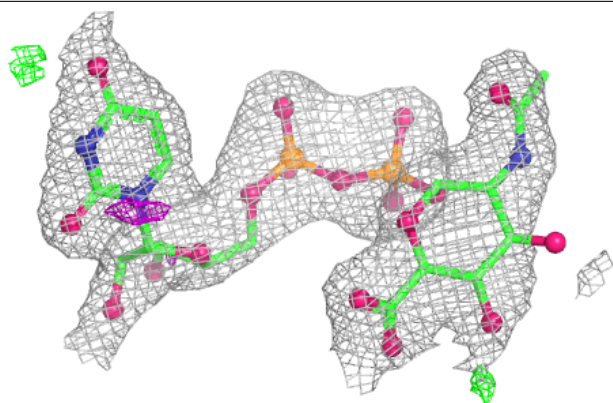
**Electron density around HP7 F 550:**

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and green (positive)

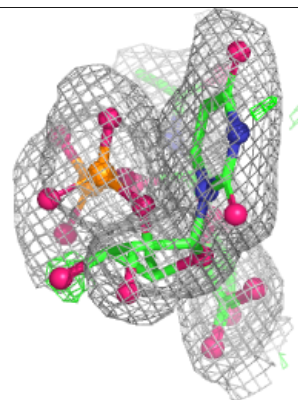
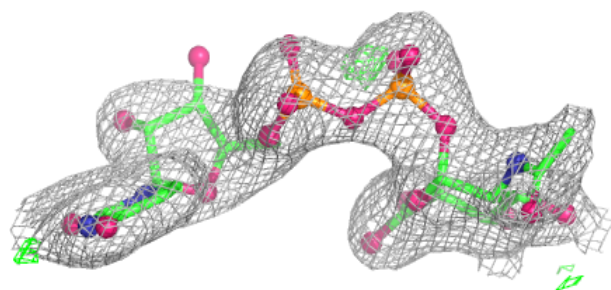
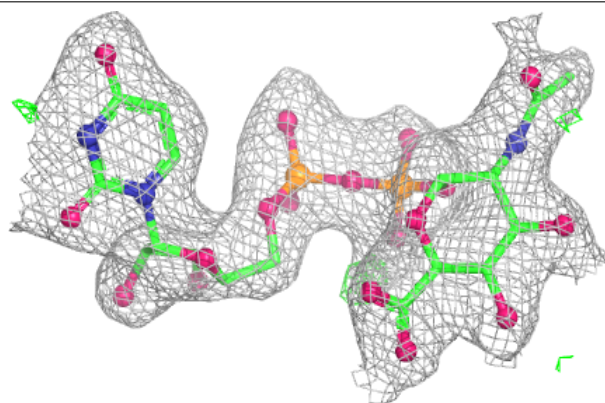


Electron density around HP7 K 550:

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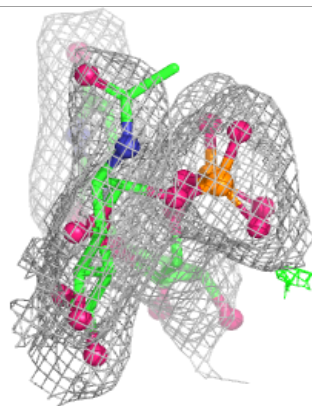
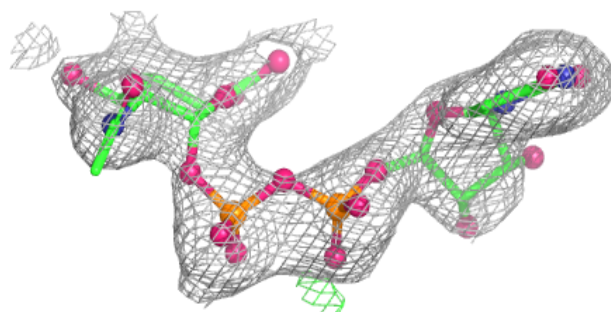
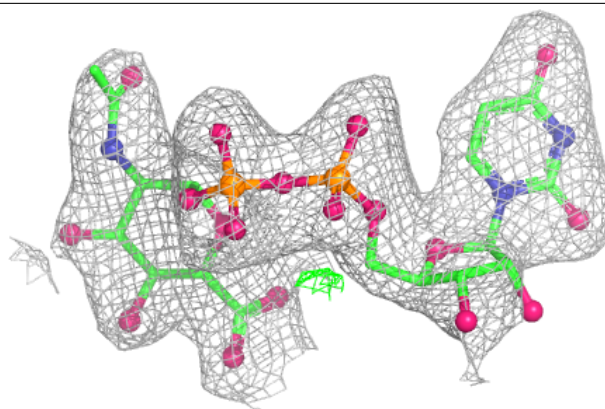
**Electron density around HP7 B 550:**

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and green (positive)

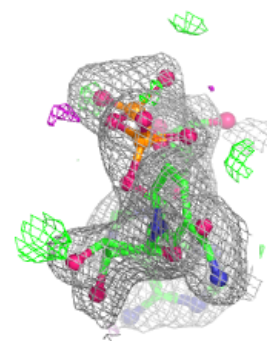
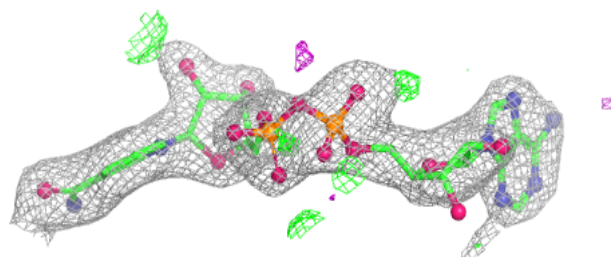
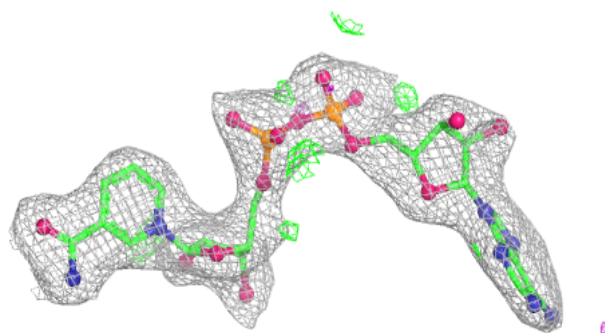


Electron density around HP7 D 550:

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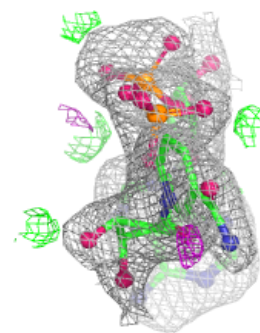
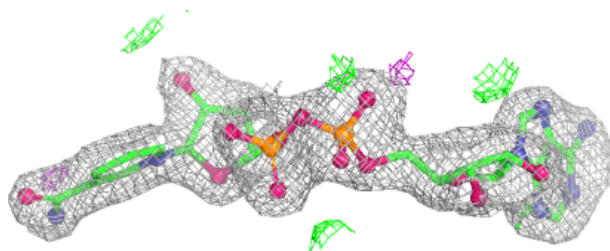
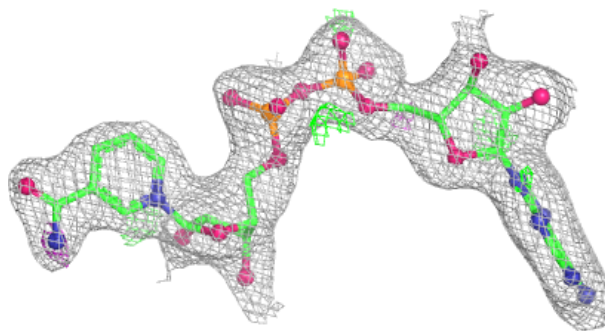
**Electron density around NAI L 500:**

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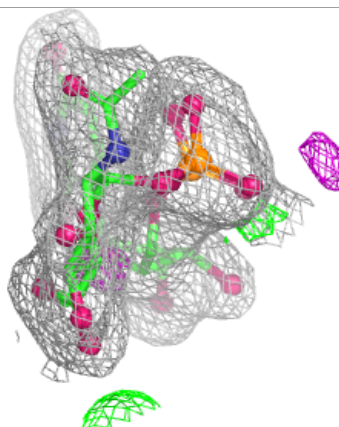
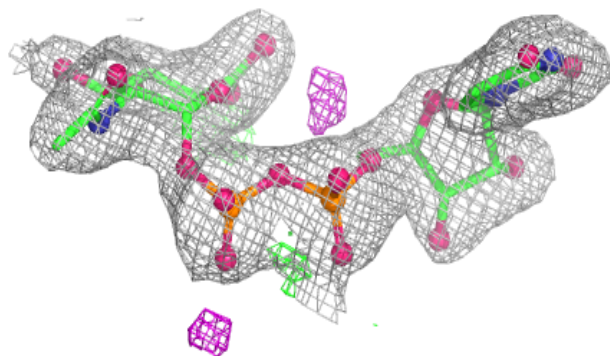
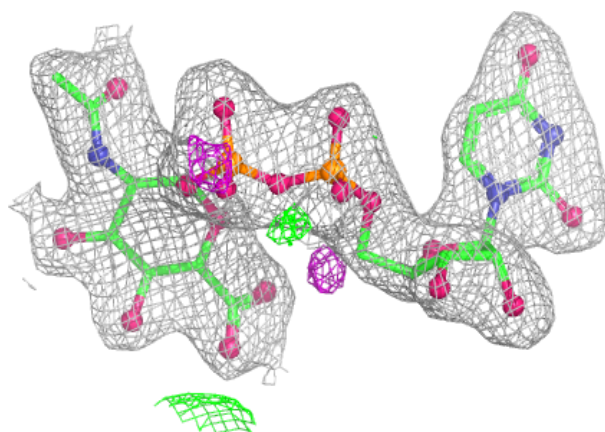


Electron density around NAI B 500:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
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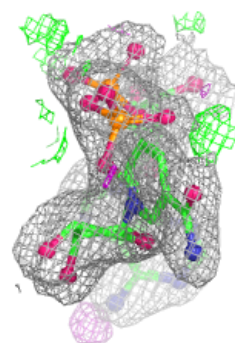
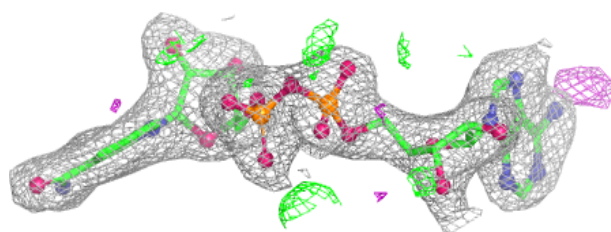
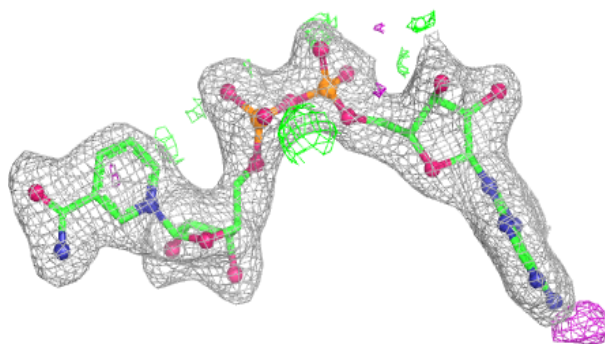
**Electron density around HP7 H 550:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

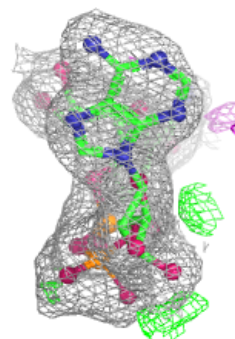
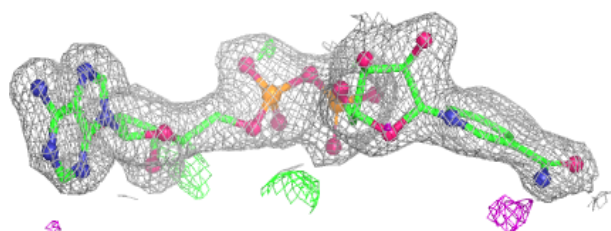
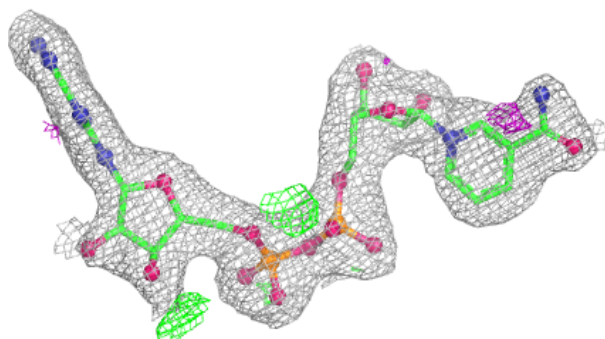


Electron density around NAI N 500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

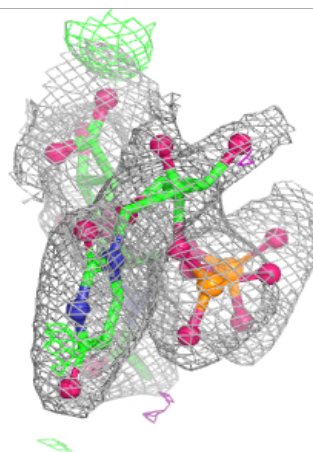
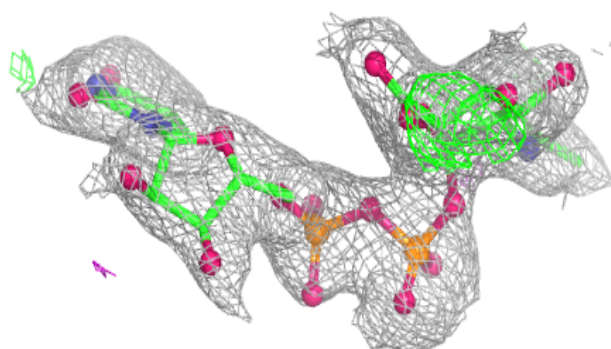
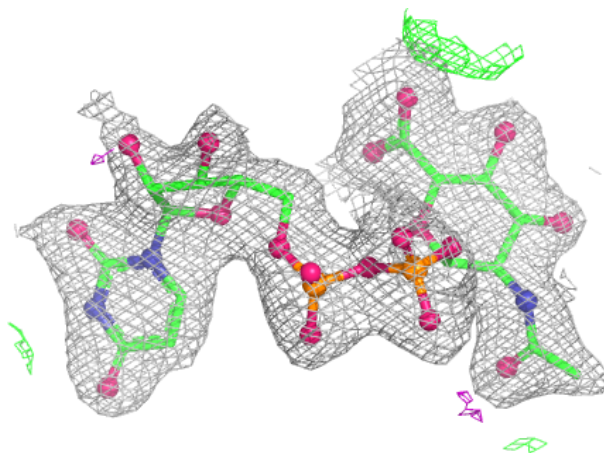
**Electron density around NAI O 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



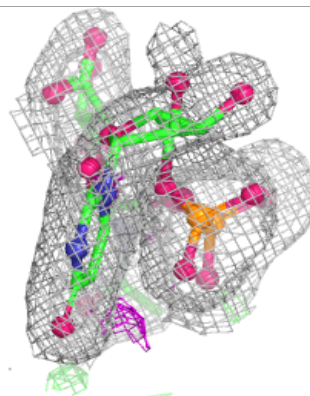
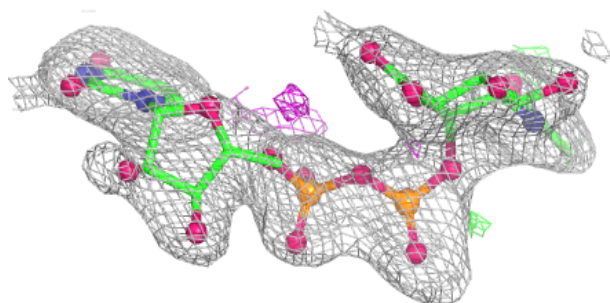
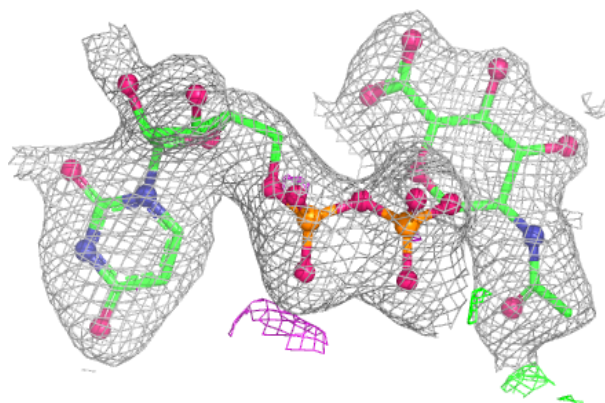
Electron density around HP7 I 550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

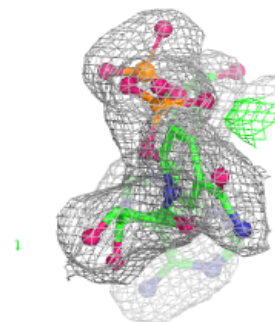
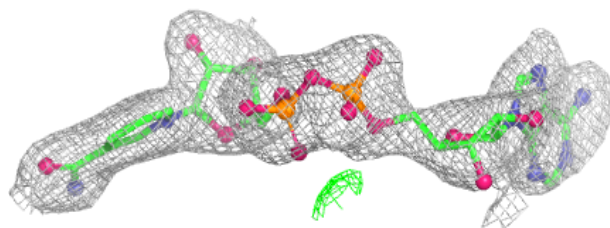
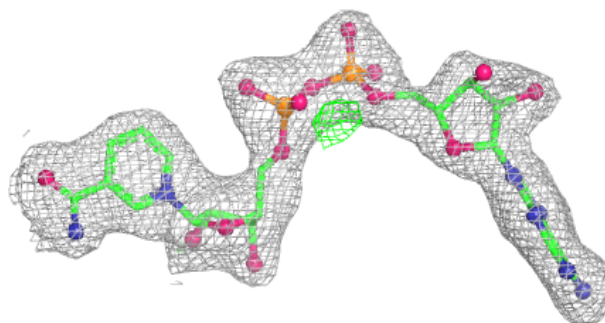


Electron density around HP7 J 550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

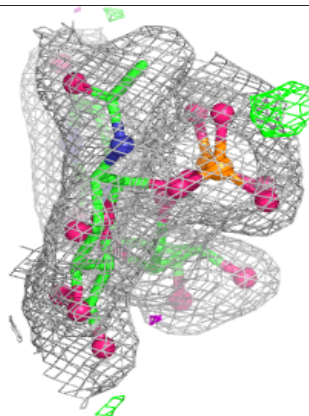
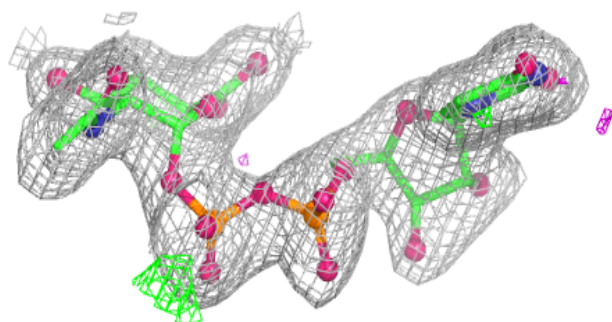
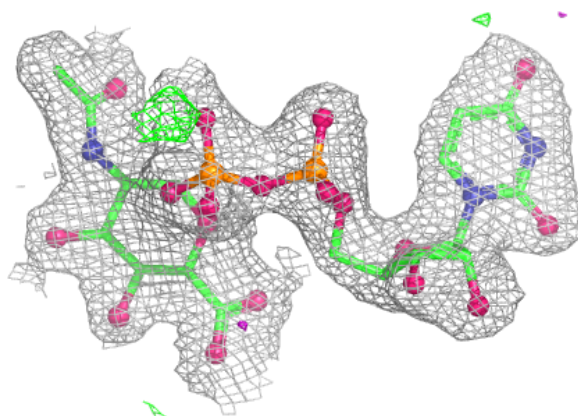
**Electron density around NAI E 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

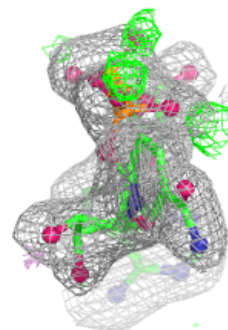
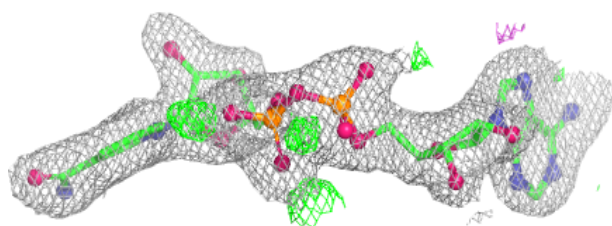
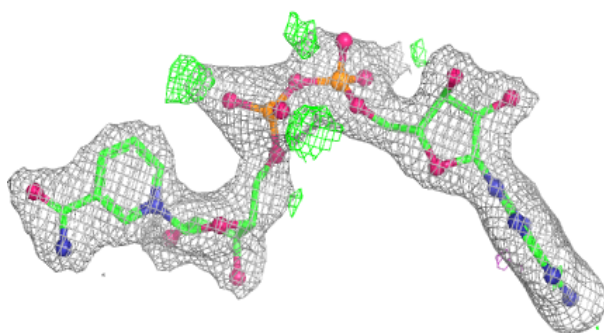


Electron density around HP7 C 550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

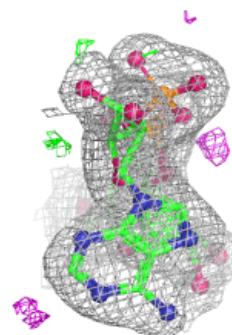
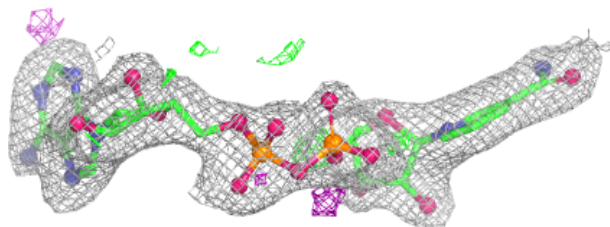
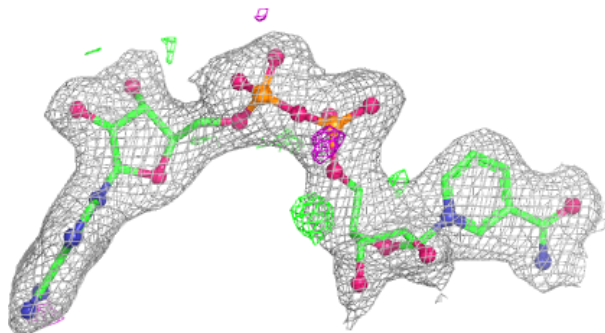
**Electron density around NAI K 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

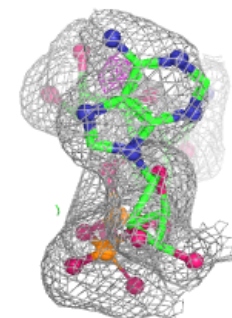
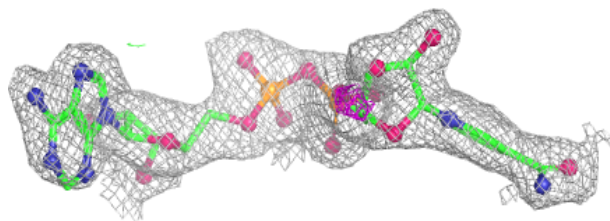
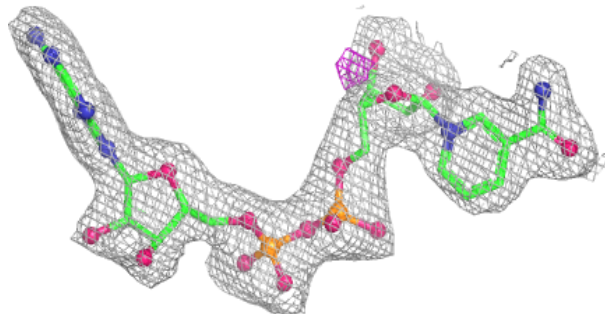


Electron density around NAI D 500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

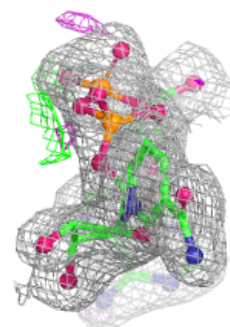
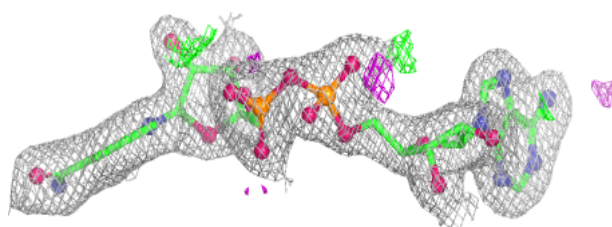
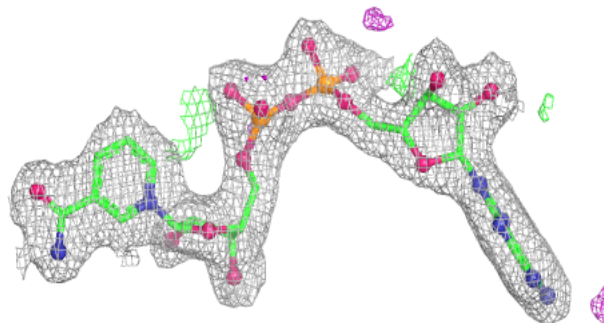
**Electron density around NAI J 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

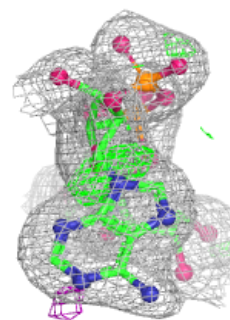
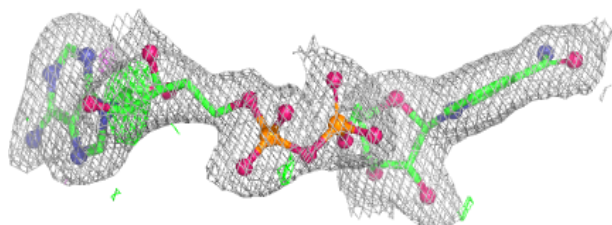
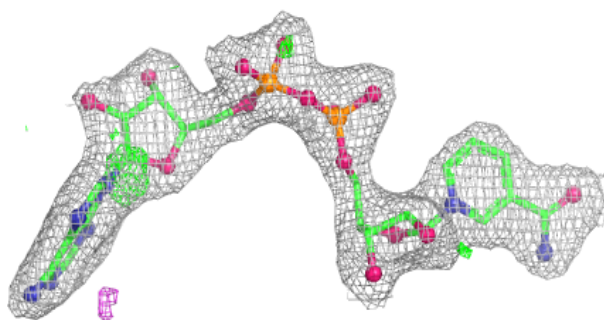


Electron density around NAI A 500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

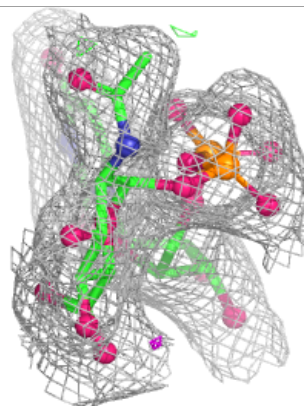
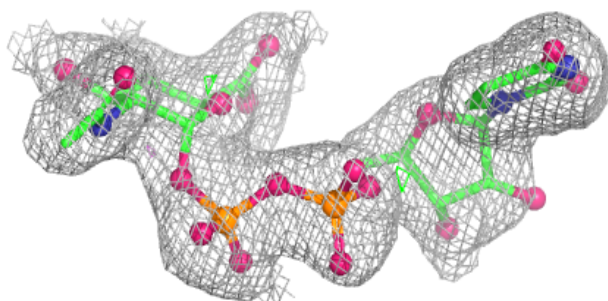
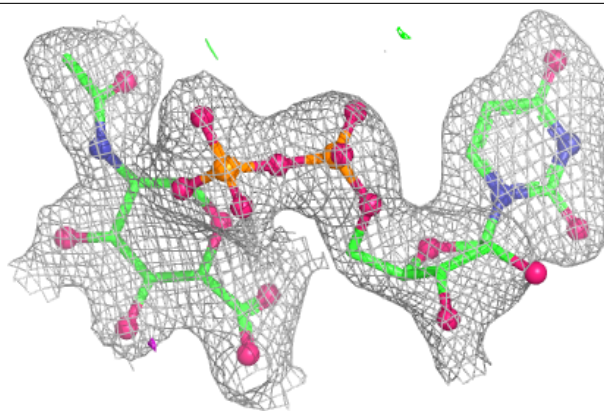
**Electron density around NAI C 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

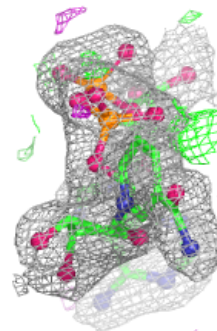
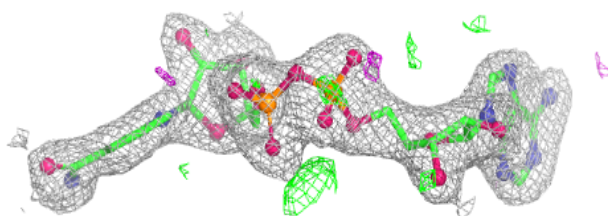
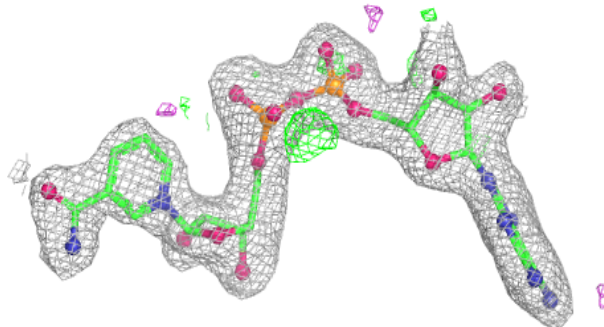


Electron density around HP7 G 550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

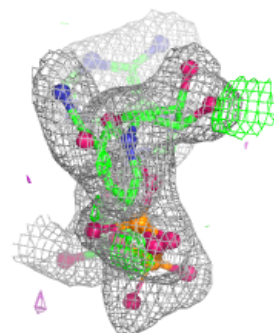
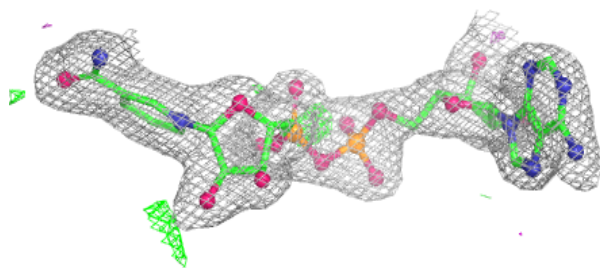
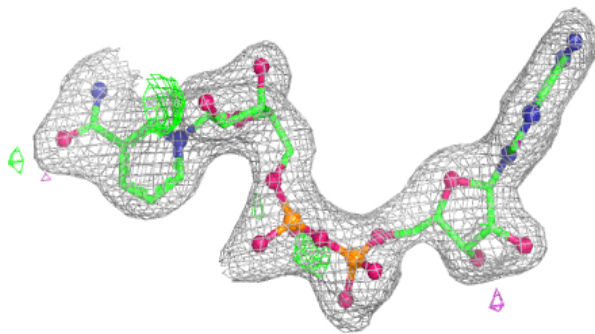
**Electron density around NAI M 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

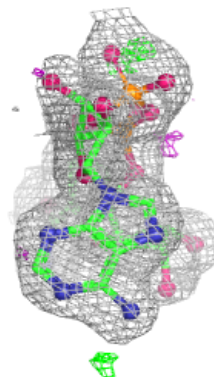
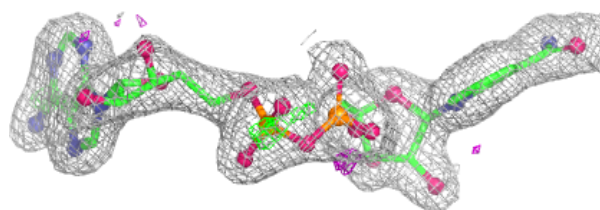
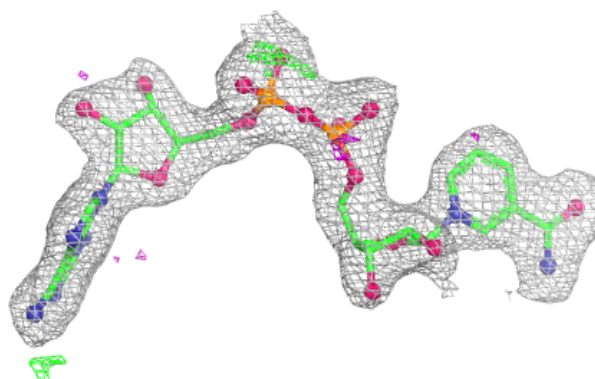


Electron density around NAI F 500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

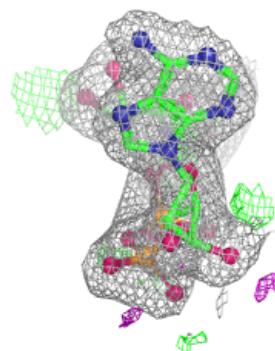
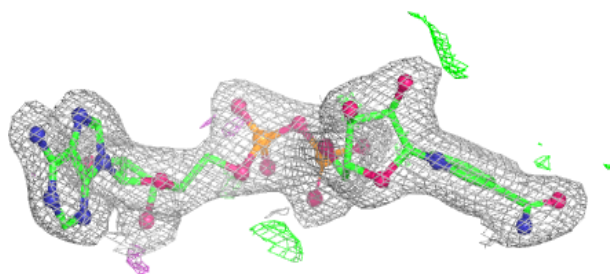
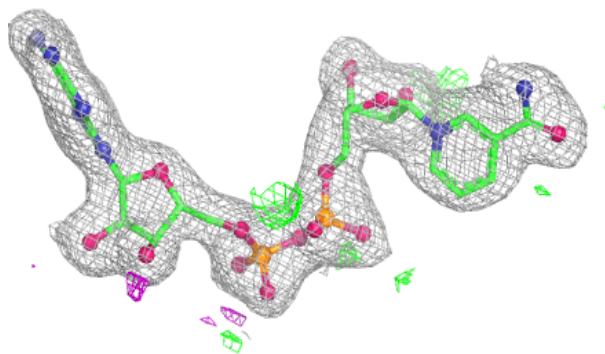
**Electron density around NAI G 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

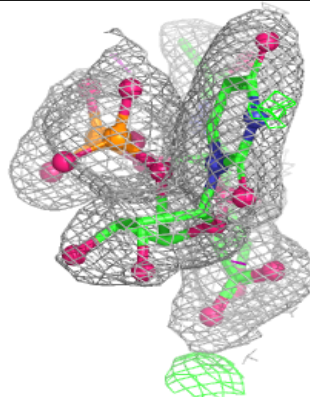
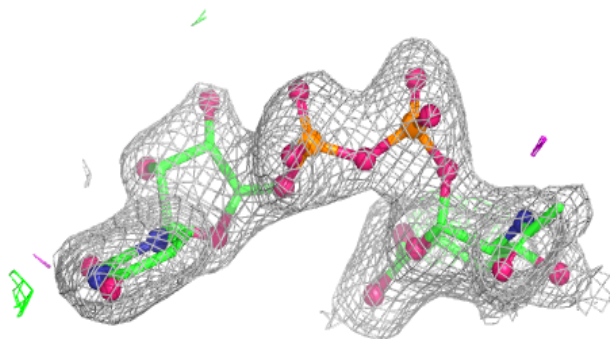
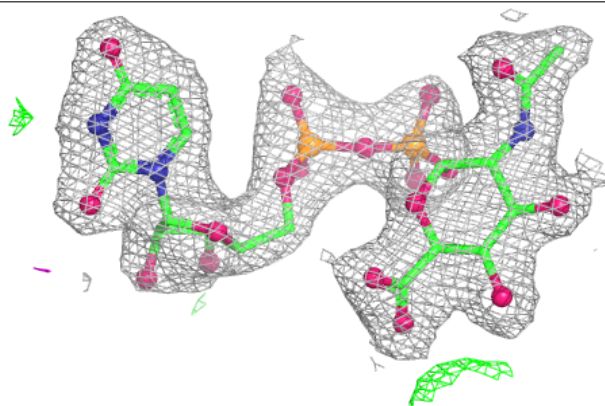


Electron density around NAI P 500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

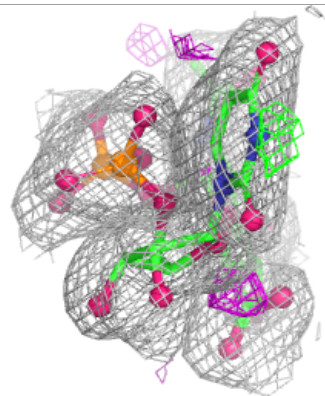
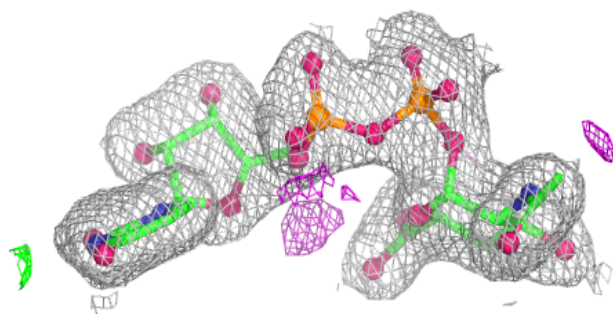
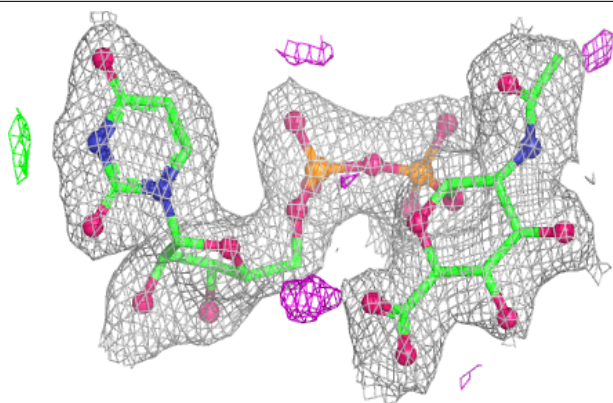
**Electron density around HP7 A 550:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

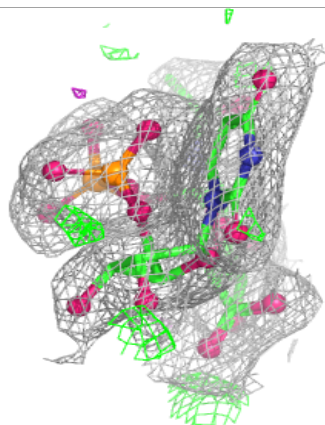
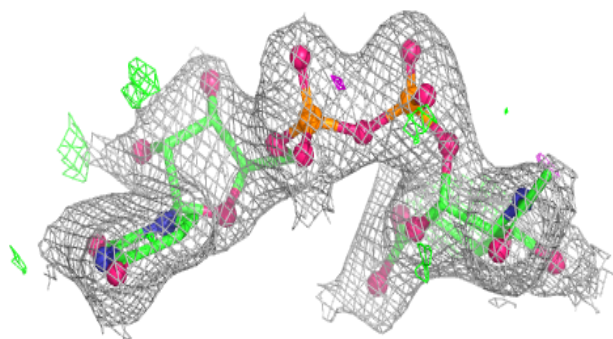
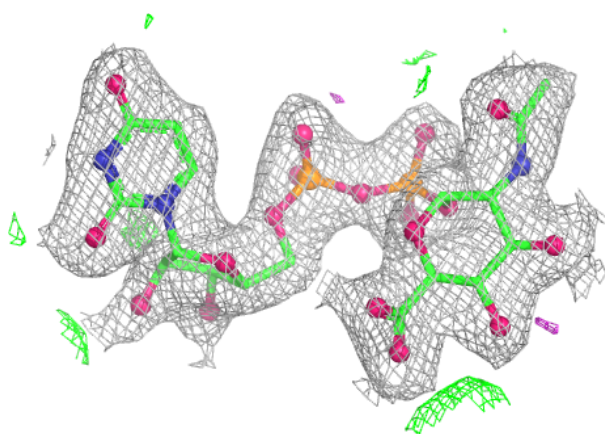


Electron density around HP7 M 550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

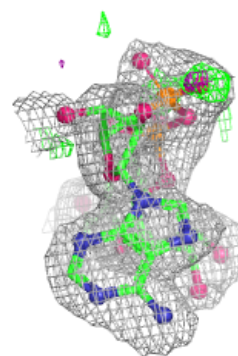
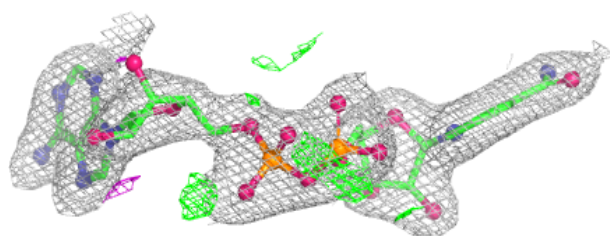
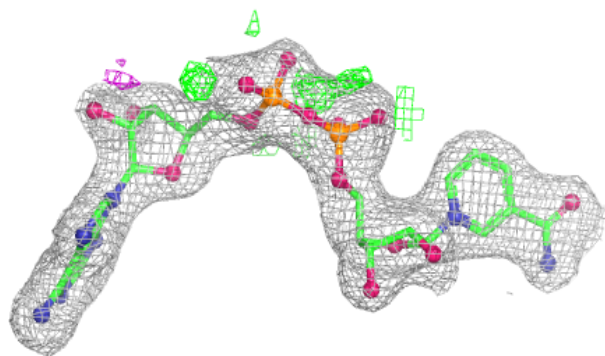
**Electron density around HP7 N 550:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

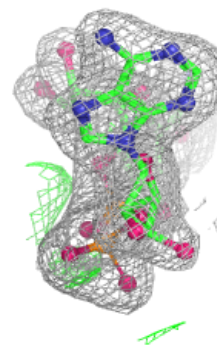
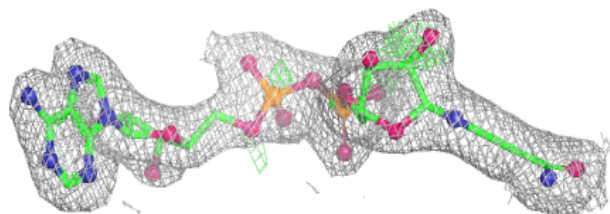
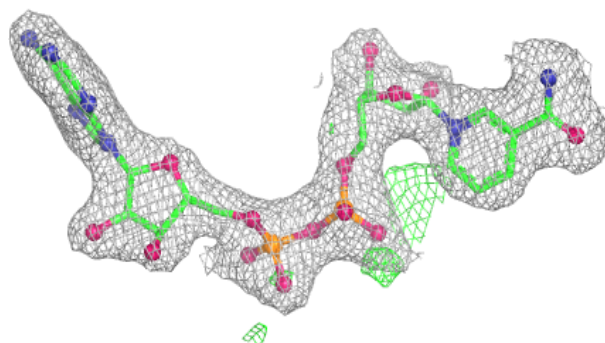


Electron density around NAI H 500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around NAI I 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.