



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 03:04 AM UTC

PDB ID : 1HTQ / pdb_00001htq
Title : Multicopy crystallographic structure of a relaxed glutamine synthetase from Mycobacterium tuberculosis
Authors : Gill, H.S.; Pfluegl, G.M.; Eisenberg, D.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2001-01-01
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

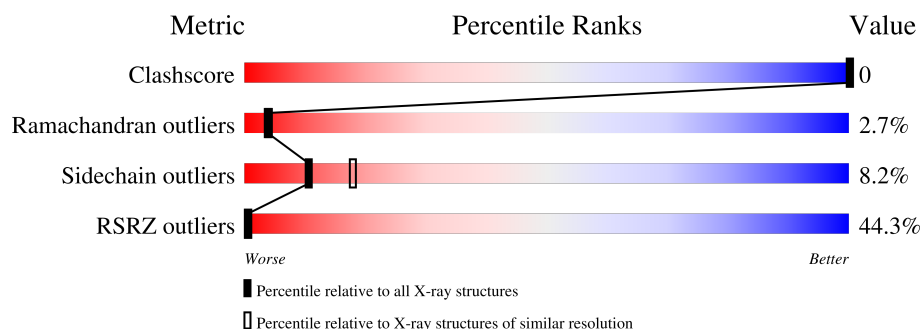
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	1-A	477	43% 89% 11%
1	1-B	477	42% 89% 11%
1	1-C	477	40% 89% 11%
1	1-D	477	45% 89% 11%
1	1-E	477	44% 89% 11%
1	1-F	477	48% 89% 11%

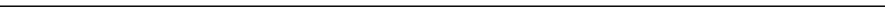
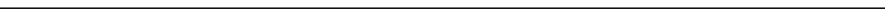
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Mol	Chain	Length	Quality of chain		
1	1-G	477	49%	89%	11%
1	1-H	477	43%	89%	11%
1	1-I	477	39%	89%	11%
1	1-J	477	41%	89%	11%
1	1-K	477	44%	89%	11%
1	1-L	477	53%	89%	11%
1	1-M	477	43%	89%	11%
1	1-N	477	44%	89%	11%
1	1-O	477	40%	89%	11%
1	1-P	477	48%	89%	11%
1	1-Q	477	45%	89%	11%
1	1-R	477	48%	89%	11%
1	1-S	477	48%	89%	11%
1	1-T	477	43%	89%	11%
1	1-U	477	43%	89%	11%
1	1-V	477	41%	89%	11%
1	1-W	477	43%	89%	11%
1	1-X	477	46%	89%	11%
1	10-A	477		89%	10%
1	10-B	477		89%	10%
1	10-C	477		89%	10%
1	10-D	477		89%	10%
1	10-E	477		89%	10%
1	10-F	477		89%	10%
1	10-G	477		89%	10%

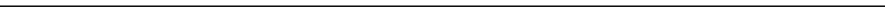
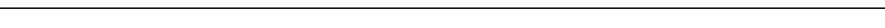
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Mol	Chain	Length	Quality of chain
1	10-H	477	 89% 10%
1	10-I	477	 89% 10%
1	10-J	477	 89% 10%
1	10-K	477	 89% 10%
1	10-L	477	 89% 10%
1	10-M	477	 89% 10%
1	10-N	477	 89% 10%
1	10-O	477	 89% 10%
1	10-P	477	 89% 10%
1	10-Q	477	 89% 10%
1	10-R	477	 89% 10%
1	10-S	477	 89% 10%
1	10-T	477	 89% 10%
1	10-U	477	 89% 10%
1	10-V	477	 89% 10%
1	10-W	477	 89% 10%
1	10-X	477	 89% 10%
1	2-A	477	 88% 11%
1	2-B	477	 88% 11%
1	2-C	477	 88% 11%
1	2-D	477	 88% 11%
1	2-E	477	 88% 11%
1	2-F	477	 88% 11%
1	2-G	477	 88% 11%
1	2-H	477	 88% 11%

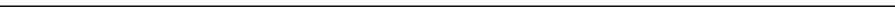
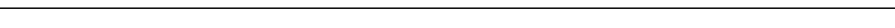
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Mol	Chain	Length	Quality of chain
1	2-I	477	 88% 11%
1	2-J	477	 88% 11%
1	2-K	477	 88% 11%
1	2-L	477	 88% 11%
1	2-M	477	 88% 11%
1	2-N	477	 88% 11%
1	2-O	477	 88% 11%
1	2-P	477	 88% 11%
1	2-Q	477	 88% 11%
1	2-R	477	 88% 11%
1	2-S	477	 88% 11%
1	2-T	477	 88% 11%
1	2-U	477	 88% 11%
1	2-V	477	 88% 11%
1	2-W	477	 88% 11%
1	2-X	477	 88% 11%
1	3-A	477	 90% 10%
1	3-B	477	 90% 10%
1	3-C	477	 90% 10%
1	3-D	477	 90% 10%
1	3-E	477	 90% 10%
1	3-F	477	 90% 10%
1	3-G	477	 90% 10%
1	3-H	477	 90% 10%
1	3-I	477	 90% 10%

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Mol	Chain	Length	Quality of chain	
1	3-J	477		90% 10%
1	3-K	477		90% 10%
1	3-L	477		90% 10%
1	3-M	477		90% 10%
1	3-N	477		90% 10%
1	3-O	477		90% 10%
1	3-P	477		90% 10%
1	3-Q	477		90% 10%
1	3-R	477		90% 10%
1	3-S	477		90% 10%
1	3-T	477		90% 10%
1	3-U	477		90% 10%
1	3-V	477		90% 10%
1	3-W	477		90% 10%
1	3-X	477		90% 10%
1	4-A	477		89% 11%
1	4-B	477		89% 11%
1	4-C	477		89% 11%
1	4-D	477		89% 11%
1	4-E	477		89% 11%
1	4-F	477		89% 11%
1	4-G	477		89% 11%
1	4-H	477		89% 11%
1	4-I	477		89% 11%
1	4-J	477		89% 11%

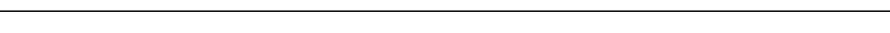
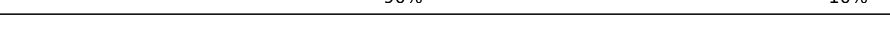
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Mol	Chain	Length	Quality of chain	
1	4-K	477		89% 11%
1	4-L	477		89% 11%
1	4-M	477		89% 11%
1	4-N	477		89% 11%
1	4-O	477		89% 11%
1	4-P	477		89% 11%
1	4-Q	477		89% 11%
1	4-R	477		89% 11%
1	4-S	477		89% 11%
1	4-T	477		89% 11%
1	4-U	477		89% 11%
1	4-V	477		89% 11%
1	4-W	477		89% 11%
1	4-X	477		89% 11%
1	5-A	477		90% 10%
1	5-B	477		90% 10%
1	5-C	477		90% 10%
1	5-D	477		90% 10%
1	5-E	477		90% 10%
1	5-F	477		90% 10%
1	5-G	477		90% 10%
1	5-H	477		90% 10%
1	5-I	477		90% 10%
1	5-J	477		90% 10%
1	5-K	477		90% 10%

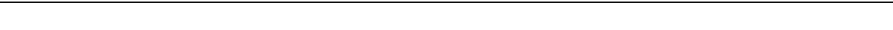
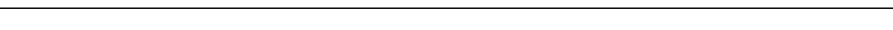
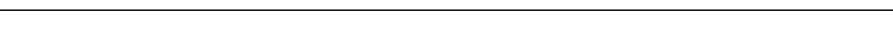
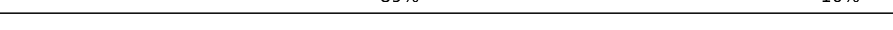
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Mol	Chain	Length	Quality of chain	
1	5-L	477		90% 10%
1	5-M	477		90% 10%
1	5-N	477		90% 10%
1	5-O	477		90% 10%
1	5-P	477		90% 10%
1	5-Q	477		90% 10%
1	5-R	477		90% 10%
1	5-S	477		90% 10%
1	5-T	477		90% 10%
1	5-U	477		90% 10%
1	5-V	477		90% 10%
1	5-W	477		90% 10%
1	5-X	477		90% 10%
1	6-A	477		89% 10%
1	6-B	477		90% 10%
1	6-C	477		89% 10%
1	6-D	477		90% 10%
1	6-E	477		90% 10%
1	6-F	477		89% 10%
1	6-G	477		89% 10%
1	6-H	477		90% 10%
1	6-I	477		89% 10%
1	6-J	477		89% 10%
1	6-K	477		89% 10%
1	6-L	477		89% 10%

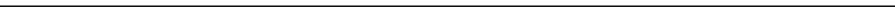
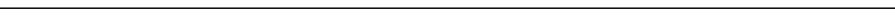
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Mol	Chain	Length	Quality of chain
1	6-M	477	 90% 10%
1	6-N	477	 89% 10%
1	6-O	477	 89% 10%
1	6-P	477	 90% 10%
1	6-Q	477	 89% 10%
1	6-R	477	 89% 10%
1	6-S	477	 90% 10%
1	6-T	477	 90% 10%
1	6-U	477	 89% 10%
1	6-V	477	 89% 10%
1	6-W	477	 89% 10%
1	6-X	477	 90% 10%
1	7-A	477	 89% 10% .
1	7-B	477	 89% 10% .
1	7-C	477	 89% 10% .
1	7-D	477	 89% 10% .
1	7-E	477	 89% 10% .
1	7-F	477	 89% 10% .
1	7-G	477	 89% 10% .
1	7-H	477	 89% 10% .
1	7-I	477	 89% 10% .
1	7-J	477	 89% 10% .
1	7-K	477	 89% 10% .
1	7-L	477	 89% 10% .
1	7-M	477	 89% 10% .

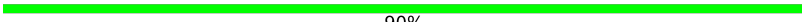
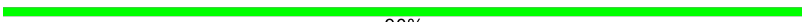
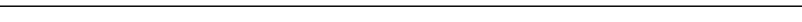
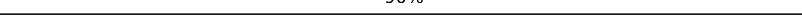
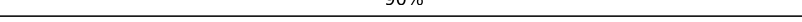
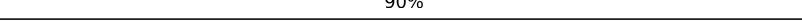
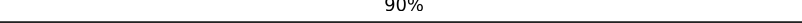
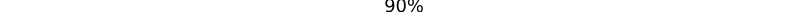
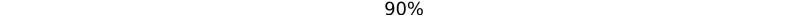
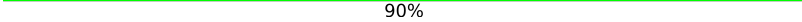
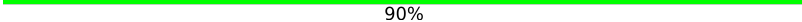
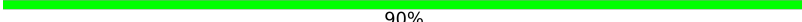
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Mol	Chain	Length	Quality of chain
1	7-N	477	 89% 10% .
1	7-O	477	 89% 10% .
1	7-P	477	 89% 10% .
1	7-Q	477	 89% 10% .
1	7-R	477	 89% 10% .
1	7-S	477	 89% 10% .
1	7-T	477	 89% 10% .
1	7-U	477	 89% 10% .
1	7-V	477	 89% 10% .
1	7-W	477	 89% 10% .
1	7-X	477	 89% 10% .
1	8-A	477	 90% 10%
1	8-B	477	 90% 10%
1	8-C	477	 90% 10%
1	8-D	477	 90% 10%
1	8-E	477	 90% 10%
1	8-F	477	 90% 10%
1	8-G	477	 90% 10%
1	8-H	477	 90% 10%
1	8-I	477	 90% 10%
1	8-J	477	 90% 10%
1	8-K	477	 90% 10%
1	8-L	477	 90% 10%
1	8-M	477	 90% 10%
1	8-N	477	 90% 10%

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Mol	Chain	Length	Quality of chain	
1	8-O	477		10%
1	8-P	477		10%
1	8-Q	477		10%
1	8-R	477		10%
1	8-S	477		10%
1	8-T	477		10%
1	8-U	477		10%
1	8-V	477		10%
1	8-W	477		10%
1	8-X	477		10%
1	9-A	477		10%
1	9-B	477		10%
1	9-C	477		10%
1	9-D	477		10%
1	9-E	477		10%
1	9-F	477		10%
1	9-G	477		10%
1	9-H	477		10%
1	9-I	477		10%
1	9-J	477		10%
1	9-K	477		10%
1	9-L	477		10%
1	9-M	477		10%
1	9-N	477		10%
1	9-O	477		10%

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Mol	Chain	Length	Quality of chain
1	9-P	477	 90% 10%
1	9-Q	477	 90% 10%
1	9-R	477	 90% 10%
1	9-S	477	 90% 10%
1	9-T	477	 90% 10%
1	9-U	477	 90% 10%
1	9-V	477	 90% 10%
1	9-W	477	 90% 10%
1	9-X	477	 90% 10%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MN	1-G	470	-	-	-	X
4	CIT	1-A	7476	-	X	-	-
4	CIT	1-B	7478	-	X	-	-
4	CIT	1-C	7480	-	X	-	-
4	CIT	1-D	7482	-	X	-	-
4	CIT	1-E	7484	-	X	-	-
4	CIT	1-F	7486	-	X	-	-
4	CIT	1-G	7488	-	X	-	-
4	CIT	1-H	7490	-	X	-	-
4	CIT	1-I	7492	-	X	-	-
4	CIT	1-J	7494	-	X	-	-
4	CIT	1-K	7496	-	X	-	-
4	CIT	1-L	7498	-	X	-	-
4	CIT	1-M	7500	-	X	-	-
4	CIT	1-N	7502	-	X	-	-
4	CIT	1-O	7504	-	X	-	-
4	CIT	1-P	7506	-	X	-	-
4	CIT	1-Q	7508	-	X	-	-
4	CIT	1-R	7510	-	X	-	-
4	CIT	1-S	7512	-	X	-	-
4	CIT	1-T	7514	-	X	-	-
4	CIT	1-U	7516	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CIT	1-V	7518	-	X	-	-
4	CIT	1-W	7520	-	X	-	-
4	CIT	1-X	7522	-	X	-	-
4	CIT	10-A	7476	-	X	-	-
4	CIT	10-B	7478	-	X	-	-
4	CIT	10-C	7480	-	X	-	-
4	CIT	10-D	7482	-	X	-	-
4	CIT	10-E	7484	-	X	-	-
4	CIT	10-F	7486	-	X	-	-
4	CIT	10-G	7488	-	X	-	-
4	CIT	10-H	7490	-	X	-	-
4	CIT	10-I	7492	-	X	-	-
4	CIT	10-J	7494	-	X	-	-
4	CIT	10-K	7496	-	X	-	-
4	CIT	10-L	7498	-	X	-	-
4	CIT	10-M	7500	-	X	-	-
4	CIT	10-N	7502	-	X	-	-
4	CIT	10-O	7504	-	X	-	-
4	CIT	10-P	7506	-	X	-	-
4	CIT	10-Q	7508	-	X	-	-
4	CIT	10-R	7510	-	X	-	-
4	CIT	10-S	7512	-	X	-	-
4	CIT	10-T	7514	-	X	-	-
4	CIT	10-U	7516	-	X	-	-
4	CIT	10-V	7518	-	X	-	-
4	CIT	10-W	7520	-	X	-	-
4	CIT	10-X	7522	-	X	-	-
4	CIT	2-A	7476	-	X	-	-
4	CIT	2-B	7478	-	X	-	-
4	CIT	2-C	7480	-	X	-	-
4	CIT	2-D	7482	-	X	-	-
4	CIT	2-E	7484	-	X	-	-
4	CIT	2-F	7486	-	X	-	-
4	CIT	2-G	7488	-	X	-	-
4	CIT	2-H	7490	-	X	-	-
4	CIT	2-I	7492	-	X	-	-
4	CIT	2-J	7494	-	X	-	-
4	CIT	2-K	7496	-	X	-	-
4	CIT	2-L	7498	-	X	-	-
4	CIT	2-M	7500	-	X	-	-
4	CIT	2-N	7502	-	X	-	-
4	CIT	2-O	7504	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CIT	2-P	7506	-	X	-	-
4	CIT	2-Q	7508	-	X	-	-
4	CIT	2-R	7510	-	X	-	-
4	CIT	2-S	7512	-	X	-	-
4	CIT	2-T	7514	-	X	-	-
4	CIT	2-U	7516	-	X	-	-
4	CIT	2-V	7518	-	X	-	-
4	CIT	2-W	7520	-	X	-	-
4	CIT	2-X	7522	-	X	-	-
4	CIT	3-A	7476	-	X	-	-
4	CIT	3-B	7478	-	X	-	-
4	CIT	3-C	7480	-	X	-	-
4	CIT	3-D	7482	-	X	-	-
4	CIT	3-E	7484	-	X	-	-
4	CIT	3-F	7486	-	X	-	-
4	CIT	3-G	7488	-	X	-	-
4	CIT	3-H	7490	-	X	-	-
4	CIT	3-I	7492	-	X	-	-
4	CIT	3-J	7494	-	X	-	-
4	CIT	3-K	7496	-	X	-	-
4	CIT	3-L	7498	-	X	-	-
4	CIT	3-M	7500	-	X	-	-
4	CIT	3-N	7502	-	X	-	-
4	CIT	3-O	7504	-	X	-	-
4	CIT	3-P	7506	-	X	-	-
4	CIT	3-Q	7508	-	X	-	-
4	CIT	3-R	7510	-	X	-	-
4	CIT	3-S	7512	-	X	-	-
4	CIT	3-T	7514	-	X	-	-
4	CIT	3-U	7516	-	X	-	-
4	CIT	3-V	7518	-	X	-	-
4	CIT	3-W	7520	-	X	-	-
4	CIT	3-X	7522	-	X	-	-
4	CIT	4-A	7476	-	X	-	-
4	CIT	4-B	7478	-	X	-	-
4	CIT	4-C	7480	-	X	-	-
4	CIT	4-D	7482	-	X	-	-
4	CIT	4-E	7484	-	X	-	-
4	CIT	4-F	7486	-	X	-	-
4	CIT	4-G	7488	-	X	-	-
4	CIT	4-H	7490	-	X	-	-
4	CIT	4-I	7492	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CIT	4-J	7494	-	X	-	-
4	CIT	4-K	7496	-	X	-	-
4	CIT	4-L	7498	-	X	-	-
4	CIT	4-M	7500	-	X	-	-
4	CIT	4-N	7502	-	X	-	-
4	CIT	4-O	7504	-	X	-	-
4	CIT	4-P	7506	-	X	-	-
4	CIT	4-Q	7508	-	X	-	-
4	CIT	4-R	7510	-	X	-	-
4	CIT	4-S	7512	-	X	-	-
4	CIT	4-T	7514	-	X	-	-
4	CIT	4-U	7516	-	X	-	-
4	CIT	4-V	7518	-	X	-	-
4	CIT	4-W	7520	-	X	-	-
4	CIT	4-X	7522	-	X	-	-
4	CIT	5-A	7476	-	X	-	-
4	CIT	5-B	7478	-	X	-	-
4	CIT	5-C	7480	-	X	-	-
4	CIT	5-D	7482	-	X	-	-
4	CIT	5-E	7484	-	X	-	-
4	CIT	5-F	7486	-	X	-	-
4	CIT	5-G	7488	-	X	-	-
4	CIT	5-H	7490	-	X	-	-
4	CIT	5-I	7492	-	X	-	-
4	CIT	5-J	7494	-	X	-	-
4	CIT	5-K	7496	-	X	-	-
4	CIT	5-L	7498	-	X	-	-
4	CIT	5-M	7500	-	X	-	-
4	CIT	5-N	7502	-	X	-	-
4	CIT	5-O	7504	-	X	-	-
4	CIT	5-P	7506	-	X	-	-
4	CIT	5-Q	7508	-	X	-	-
4	CIT	5-R	7510	-	X	-	-
4	CIT	5-S	7512	-	X	-	-
4	CIT	5-T	7514	-	X	-	-
4	CIT	5-U	7516	-	X	-	-
4	CIT	5-V	7518	-	X	-	-
4	CIT	5-W	7520	-	X	-	-
4	CIT	5-X	7522	-	X	-	-
4	CIT	6-A	7476	-	X	-	-
4	CIT	6-B	7478	-	X	-	-
4	CIT	6-C	7480	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CIT	6-D	7482	-	X	-	-
4	CIT	6-E	7484	-	X	-	-
4	CIT	6-F	7486	-	X	-	-
4	CIT	6-G	7488	-	X	-	-
4	CIT	6-H	7490	-	X	-	-
4	CIT	6-I	7492	-	X	-	-
4	CIT	6-J	7494	-	X	-	-
4	CIT	6-K	7496	-	X	-	-
4	CIT	6-L	7498	-	X	-	-
4	CIT	6-M	7500	-	X	-	-
4	CIT	6-N	7502	-	X	-	-
4	CIT	6-O	7504	-	X	-	-
4	CIT	6-P	7506	-	X	-	-
4	CIT	6-Q	7508	-	X	-	-
4	CIT	6-R	7510	-	X	-	-
4	CIT	6-S	7512	-	X	-	-
4	CIT	6-T	7514	-	X	-	-
4	CIT	6-U	7516	-	X	-	-
4	CIT	6-V	7518	-	X	-	-
4	CIT	6-W	7520	-	X	-	-
4	CIT	6-X	7522	-	X	-	-
4	CIT	7-A	7476	-	X	-	-
4	CIT	7-B	7478	-	X	-	-
4	CIT	7-C	7480	-	X	-	-
4	CIT	7-D	7482	-	X	-	-
4	CIT	7-E	7484	-	X	-	-
4	CIT	7-F	7486	-	X	-	-
4	CIT	7-G	7488	-	X	-	-
4	CIT	7-H	7490	-	X	-	-
4	CIT	7-I	7492	-	X	-	-
4	CIT	7-J	7494	-	X	-	-
4	CIT	7-K	7496	-	X	-	-
4	CIT	7-L	7498	-	X	-	-
4	CIT	7-M	7500	-	X	-	-
4	CIT	7-N	7502	-	X	-	-
4	CIT	7-O	7504	-	X	-	-
4	CIT	7-P	7506	-	X	-	-
4	CIT	7-Q	7508	-	X	-	-
4	CIT	7-R	7510	-	X	-	-
4	CIT	7-S	7512	-	X	-	-
4	CIT	7-T	7514	-	X	-	-
4	CIT	7-U	7516	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CIT	7-V	7518	-	X	-	-
4	CIT	7-W	7520	-	X	-	-
4	CIT	7-X	7522	-	X	-	-
4	CIT	8-A	7476	-	X	-	-
4	CIT	8-B	7478	-	X	-	-
4	CIT	8-C	7480	-	X	-	-
4	CIT	8-D	7482	-	X	-	-
4	CIT	8-E	7484	-	X	-	-
4	CIT	8-F	7486	-	X	-	-
4	CIT	8-G	7488	-	X	-	-
4	CIT	8-H	7490	-	X	-	-
4	CIT	8-I	7492	-	X	-	-
4	CIT	8-J	7494	-	X	-	-
4	CIT	8-K	7496	-	X	-	-
4	CIT	8-L	7498	-	X	-	-
4	CIT	8-M	7500	-	X	-	-
4	CIT	8-N	7502	-	X	-	-
4	CIT	8-O	7504	-	X	-	-
4	CIT	8-P	7506	-	X	-	-
4	CIT	8-Q	7508	-	X	-	-
4	CIT	8-R	7510	-	X	-	-
4	CIT	8-S	7512	-	X	-	-
4	CIT	8-T	7514	-	X	-	-
4	CIT	8-U	7516	-	X	-	-
4	CIT	8-V	7518	-	X	-	-
4	CIT	8-W	7520	-	X	-	-
4	CIT	8-X	7522	-	X	-	-
4	CIT	9-A	7476	-	X	-	-
4	CIT	9-B	7478	-	X	-	-
4	CIT	9-C	7480	-	X	-	-
4	CIT	9-D	7482	-	X	-	-
4	CIT	9-E	7484	-	X	-	-
4	CIT	9-F	7486	-	X	-	-
4	CIT	9-G	7488	-	X	-	-
4	CIT	9-H	7490	-	X	-	-
4	CIT	9-I	7492	-	X	-	-
4	CIT	9-J	7494	-	X	-	-
4	CIT	9-K	7496	-	X	-	-
4	CIT	9-L	7498	-	X	-	-
4	CIT	9-M	7500	-	X	-	-
4	CIT	9-N	7502	-	X	-	-
4	CIT	9-O	7504	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CIT	9-P	7506	-	X	-	-
4	CIT	9-Q	7508	-	X	-	-
4	CIT	9-R	7510	-	X	-	-
4	CIT	9-S	7512	-	X	-	-
4	CIT	9-T	7514	-	X	-	-
4	CIT	9-U	7516	-	X	-	-
4	CIT	9-V	7518	-	X	-	-
4	CIT	9-W	7520	-	X	-	-
4	CIT	9-X	7522	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 978720 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 glutamine synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-A	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	7-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-B	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-C	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-D	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	8-D	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-D	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-D	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-E	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	9-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-F	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-G	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	10-H	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-I	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-J	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-K	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-L	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	2-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-M	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-N	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	3-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-O	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-P	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	4-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-Q	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-R	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	5-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-S	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-T	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	6-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-U	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	7-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	8-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	9-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	10-V	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	1-W	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	2-W	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	3-W	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	4-W	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	5-W	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			
1	6-W	477	Total	C	N	O	S	0	0	0
			3778	2406	633	727	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	7-W	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-W	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-W	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-W	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	1-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	2-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	3-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	4-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	5-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	6-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	7-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	8-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	9-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0
1	10-X	477	Total 3778	C 2406	N 633	O 727	S 12	0	0	0

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	1-A	1	Total 1	Mn 1	0	0
2	2-A	1	Total 1	Mn 1	0	0
2	3-A	1	Total 1	Mn 1	0	0
2	4-A	1	Total 1	Mn 1	0	0
2	5-A	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	6-A	1	Total 1	Mn 1	0	0
2	7-A	1	Total 1	Mn 1	0	0
2	8-A	1	Total 1	Mn 1	0	0
2	9-A	1	Total 1	Mn 1	0	0
2	10-A	1	Total 1	Mn 1	0	0
2	1-B	1	Total 1	Mn 1	0	0
2	2-B	1	Total 1	Mn 1	0	0
2	3-B	1	Total 1	Mn 1	0	0
2	4-B	1	Total 1	Mn 1	0	0
2	5-B	1	Total 1	Mn 1	0	0
2	6-B	1	Total 1	Mn 1	0	0
2	7-B	1	Total 1	Mn 1	0	0
2	8-B	1	Total 1	Mn 1	0	0
2	9-B	1	Total 1	Mn 1	0	0
2	10-B	1	Total 1	Mn 1	0	0
2	1-C	1	Total 1	Mn 1	0	0
2	2-C	1	Total 1	Mn 1	0	0
2	3-C	1	Total 1	Mn 1	0	0
2	4-C	1	Total 1	Mn 1	0	0
2	5-C	1	Total 1	Mn 1	0	0
2	6-C	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	7-C	1	Total 1	Mn 1	0	0
2	8-C	1	Total 1	Mn 1	0	0
2	9-C	1	Total 1	Mn 1	0	0
2	10-C	1	Total 1	Mn 1	0	0
2	1-D	1	Total 1	Mn 1	0	0
2	2-D	1	Total 1	Mn 1	0	0
2	3-D	1	Total 1	Mn 1	0	0
2	4-D	1	Total 1	Mn 1	0	0
2	5-D	1	Total 1	Mn 1	0	0
2	6-D	1	Total 1	Mn 1	0	0
2	7-D	1	Total 1	Mn 1	0	0
2	8-D	1	Total 1	Mn 1	0	0
2	9-D	1	Total 1	Mn 1	0	0
2	10-D	1	Total 1	Mn 1	0	0
2	1-E	1	Total 1	Mn 1	0	0
2	2-E	1	Total 1	Mn 1	0	0
2	3-E	1	Total 1	Mn 1	0	0
2	4-E	1	Total 1	Mn 1	0	0
2	5-E	1	Total 1	Mn 1	0	0
2	6-E	1	Total 1	Mn 1	0	0
2	7-E	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	8-E	1	Total 1	Mn 1	0	0
2	9-E	1	Total 1	Mn 1	0	0
2	10-E	1	Total 1	Mn 1	0	0
2	1-F	1	Total 1	Mn 1	0	0
2	2-F	1	Total 1	Mn 1	0	0
2	3-F	1	Total 1	Mn 1	0	0
2	4-F	1	Total 1	Mn 1	0	0
2	5-F	1	Total 1	Mn 1	0	0
2	6-F	1	Total 1	Mn 1	0	0
2	7-F	1	Total 1	Mn 1	0	0
2	8-F	1	Total 1	Mn 1	0	0
2	9-F	1	Total 1	Mn 1	0	0
2	10-F	1	Total 1	Mn 1	0	0
2	1-G	1	Total 1	Mn 1	0	0
2	2-G	1	Total 1	Mn 1	0	0
2	3-G	1	Total 1	Mn 1	0	0
2	4-G	1	Total 1	Mn 1	0	0
2	5-G	1	Total 1	Mn 1	0	0
2	6-G	1	Total 1	Mn 1	0	0
2	7-G	1	Total 1	Mn 1	0	0
2	8-G	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	9-G	1	Total 1	Mn 1	0	0
2	10-G	1	Total 1	Mn 1	0	0
2	1-H	1	Total 1	Mn 1	0	0
2	2-H	1	Total 1	Mn 1	0	0
2	3-H	1	Total 1	Mn 1	0	0
2	4-H	1	Total 1	Mn 1	0	0
2	5-H	1	Total 1	Mn 1	0	0
2	6-H	1	Total 1	Mn 1	0	0
2	7-H	1	Total 1	Mn 1	0	0
2	8-H	1	Total 1	Mn 1	0	0
2	9-H	1	Total 1	Mn 1	0	0
2	10-H	1	Total 1	Mn 1	0	0
2	1-I	1	Total 1	Mn 1	0	0
2	2-I	1	Total 1	Mn 1	0	0
2	3-I	1	Total 1	Mn 1	0	0
2	4-I	1	Total 1	Mn 1	0	0
2	5-I	1	Total 1	Mn 1	0	0
2	6-I	1	Total 1	Mn 1	0	0
2	7-I	1	Total 1	Mn 1	0	0
2	8-I	1	Total 1	Mn 1	0	0
2	9-I	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	10-I	1	Total 1	Mn 1	0	0
2	1-J	1	Total 1	Mn 1	0	0
2	2-J	1	Total 1	Mn 1	0	0
2	3-J	1	Total 1	Mn 1	0	0
2	4-J	1	Total 1	Mn 1	0	0
2	5-J	1	Total 1	Mn 1	0	0
2	6-J	1	Total 1	Mn 1	0	0
2	7-J	1	Total 1	Mn 1	0	0
2	8-J	1	Total 1	Mn 1	0	0
2	9-J	1	Total 1	Mn 1	0	0
2	10-J	1	Total 1	Mn 1	0	0
2	1-K	1	Total 1	Mn 1	0	0
2	2-K	1	Total 1	Mn 1	0	0
2	3-K	1	Total 1	Mn 1	0	0
2	4-K	1	Total 1	Mn 1	0	0
2	5-K	1	Total 1	Mn 1	0	0
2	6-K	1	Total 1	Mn 1	0	0
2	7-K	1	Total 1	Mn 1	0	0
2	8-K	1	Total 1	Mn 1	0	0
2	9-K	1	Total 1	Mn 1	0	0
2	10-K	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	1-L	1	Total 1	Mn 1	0	0
2	2-L	1	Total 1	Mn 1	0	0
2	3-L	1	Total 1	Mn 1	0	0
2	4-L	1	Total 1	Mn 1	0	0
2	5-L	1	Total 1	Mn 1	0	0
2	6-L	1	Total 1	Mn 1	0	0
2	7-L	1	Total 1	Mn 1	0	0
2	8-L	1	Total 1	Mn 1	0	0
2	9-L	1	Total 1	Mn 1	0	0
2	10-L	1	Total 1	Mn 1	0	0
2	1-M	1	Total 1	Mn 1	0	0
2	2-M	1	Total 1	Mn 1	0	0
2	3-M	1	Total 1	Mn 1	0	0
2	4-M	1	Total 1	Mn 1	0	0
2	5-M	1	Total 1	Mn 1	0	0
2	6-M	1	Total 1	Mn 1	0	0
2	7-M	1	Total 1	Mn 1	0	0
2	8-M	1	Total 1	Mn 1	0	0
2	9-M	1	Total 1	Mn 1	0	0
2	10-M	1	Total 1	Mn 1	0	0
2	1-N	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	2-N	1	Total 1	Mn 1	0	0
2	3-N	1	Total 1	Mn 1	0	0
2	4-N	1	Total 1	Mn 1	0	0
2	5-N	1	Total 1	Mn 1	0	0
2	6-N	1	Total 1	Mn 1	0	0
2	7-N	1	Total 1	Mn 1	0	0
2	8-N	1	Total 1	Mn 1	0	0
2	9-N	1	Total 1	Mn 1	0	0
2	10-N	1	Total 1	Mn 1	0	0
2	1-O	1	Total 1	Mn 1	0	0
2	2-O	1	Total 1	Mn 1	0	0
2	3-O	1	Total 1	Mn 1	0	0
2	4-O	1	Total 1	Mn 1	0	0
2	5-O	1	Total 1	Mn 1	0	0
2	6-O	1	Total 1	Mn 1	0	0
2	7-O	1	Total 1	Mn 1	0	0
2	8-O	1	Total 1	Mn 1	0	0
2	9-O	1	Total 1	Mn 1	0	0
2	10-O	1	Total 1	Mn 1	0	0
2	1-P	1	Total 1	Mn 1	0	0
2	2-P	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	3-P	1	Total 1	Mn 1	0	0
2	4-P	1	Total 1	Mn 1	0	0
2	5-P	1	Total 1	Mn 1	0	0
2	6-P	1	Total 1	Mn 1	0	0
2	7-P	1	Total 1	Mn 1	0	0
2	8-P	1	Total 1	Mn 1	0	0
2	9-P	1	Total 1	Mn 1	0	0
2	10-P	1	Total 1	Mn 1	0	0
2	1-Q	1	Total 1	Mn 1	0	0
2	2-Q	1	Total 1	Mn 1	0	0
2	3-Q	1	Total 1	Mn 1	0	0
2	4-Q	1	Total 1	Mn 1	0	0
2	5-Q	1	Total 1	Mn 1	0	0
2	6-Q	1	Total 1	Mn 1	0	0
2	7-Q	1	Total 1	Mn 1	0	0
2	8-Q	1	Total 1	Mn 1	0	0
2	9-Q	1	Total 1	Mn 1	0	0
2	10-Q	1	Total 1	Mn 1	0	0
2	1-R	1	Total 1	Mn 1	0	0
2	2-R	1	Total 1	Mn 1	0	0
2	3-R	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	4-R	1	Total 1	Mn 1	0	0
2	5-R	1	Total 1	Mn 1	0	0
2	6-R	1	Total 1	Mn 1	0	0
2	7-R	1	Total 1	Mn 1	0	0
2	8-R	1	Total 1	Mn 1	0	0
2	9-R	1	Total 1	Mn 1	0	0
2	10-R	1	Total 1	Mn 1	0	0
2	1-S	1	Total 1	Mn 1	0	0
2	2-S	1	Total 1	Mn 1	0	0
2	3-S	1	Total 1	Mn 1	0	0
2	4-S	1	Total 1	Mn 1	0	0
2	5-S	1	Total 1	Mn 1	0	0
2	6-S	1	Total 1	Mn 1	0	0
2	7-S	1	Total 1	Mn 1	0	0
2	8-S	1	Total 1	Mn 1	0	0
2	9-S	1	Total 1	Mn 1	0	0
2	10-S	1	Total 1	Mn 1	0	0
2	1-T	1	Total 1	Mn 1	0	0
2	2-T	1	Total 1	Mn 1	0	0
2	3-T	1	Total 1	Mn 1	0	0
2	4-T	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	5-T	1	Total 1	Mn 1	0	0
2	6-T	1	Total 1	Mn 1	0	0
2	7-T	1	Total 1	Mn 1	0	0
2	8-T	1	Total 1	Mn 1	0	0
2	9-T	1	Total 1	Mn 1	0	0
2	10-T	1	Total 1	Mn 1	0	0
2	1-U	1	Total 1	Mn 1	0	0
2	2-U	1	Total 1	Mn 1	0	0
2	3-U	1	Total 1	Mn 1	0	0
2	4-U	1	Total 1	Mn 1	0	0
2	5-U	1	Total 1	Mn 1	0	0
2	6-U	1	Total 1	Mn 1	0	0
2	7-U	1	Total 1	Mn 1	0	0
2	8-U	1	Total 1	Mn 1	0	0
2	9-U	1	Total 1	Mn 1	0	0
2	10-U	1	Total 1	Mn 1	0	0
2	1-V	1	Total 1	Mn 1	0	0
2	2-V	1	Total 1	Mn 1	0	0
2	3-V	1	Total 1	Mn 1	0	0
2	4-V	1	Total 1	Mn 1	0	0
2	5-V	1	Total 1	Mn 1	0	0

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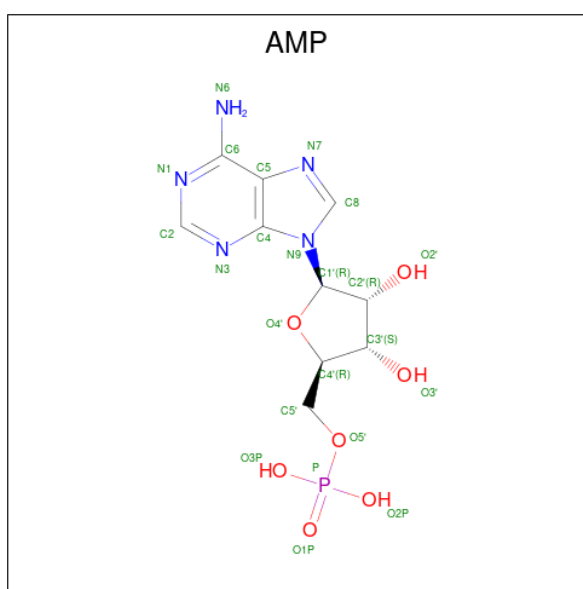
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	6-V	1	Total 1	Mn 1	0	0
2	7-V	1	Total 1	Mn 1	0	0
2	8-V	1	Total 1	Mn 1	0	0
2	9-V	1	Total 1	Mn 1	0	0
2	10-V	1	Total 1	Mn 1	0	0
2	1-W	1	Total 1	Mn 1	0	0
2	2-W	1	Total 1	Mn 1	0	0
2	3-W	1	Total 1	Mn 1	0	0
2	4-W	1	Total 1	Mn 1	0	0
2	5-W	1	Total 1	Mn 1	0	0
2	6-W	1	Total 1	Mn 1	0	0
2	7-W	1	Total 1	Mn 1	0	0
2	8-W	1	Total 1	Mn 1	0	0
2	9-W	1	Total 1	Mn 1	0	0
2	10-W	1	Total 1	Mn 1	0	0
2	1-X	1	Total 1	Mn 1	0	0
2	2-X	1	Total 1	Mn 1	0	0
2	3-X	1	Total 1	Mn 1	0	0
2	4-X	1	Total 1	Mn 1	0	0
2	5-X	1	Total 1	Mn 1	0	0
2	6-X	1	Total 1	Mn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	7-X	1	Total	Mn	0	0
			1	1		
2	8-X	1	Total	Mn	0	0
			1	1		
2	9-X	1	Total	Mn	0	0
			1	1		
2	10-X	1	Total	Mn	0	0
			1	1		

- Molecule 3 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	1-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	2-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	3-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	4-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	5-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	6-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	7-A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	8-A	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-A	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-A	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-B	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-C	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	9-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-C	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-D	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-E	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	10-E	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-F	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-G	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-G	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	1-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-H	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-I	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-J	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	2-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-J	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-K	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-L	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	3-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-L	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-M	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-N	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	4-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-N	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-O	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-P	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	5-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-P	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-Q	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-R	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	6-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-R	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-S	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-T	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	7-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-T	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-U	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-V	1	Total 23	C 10	N 5	O 7	P 1	0	0

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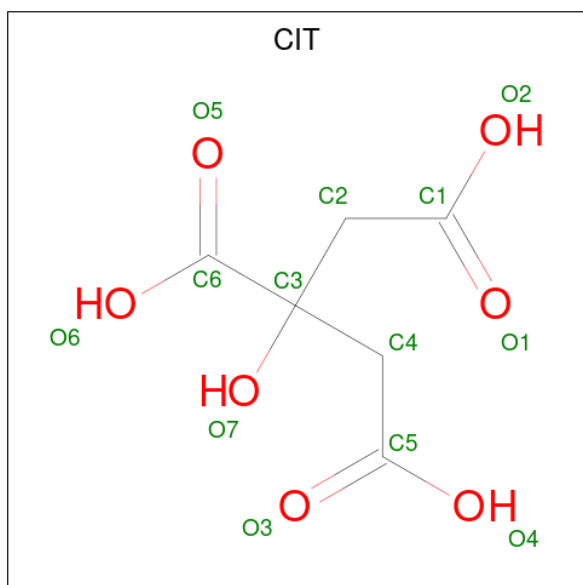
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	8-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-V	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	9-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	10-W	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	1-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	2-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	3-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	4-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	5-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	6-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	7-X	1	Total 23	C 10	N 5	O 7	P 1	0	0
3	8-X	1	Total 23	C 10	N 5	O 7	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	9-X	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	10-X	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	1-A	1	Total	C	O	0	0
			13	6	7		
4	2-A	1	Total	C	O	0	0
			13	6	7		
4	3-A	1	Total	C	O	0	0
			13	6	7		
4	4-A	1	Total	C	O	0	0
			13	6	7		
4	5-A	1	Total	C	O	0	0
			13	6	7		
4	6-A	1	Total	C	O	0	0
			13	6	7		
4	7-A	1	Total	C	O	0	0
			13	6	7		
4	8-A	1	Total	C	O	0	0
			13	6	7		
4	9-A	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	10-A	1	Total	C	O	0	0
			13	6	7		
4	1-B	1	Total	C	O	0	0
			13	6	7		
4	2-B	1	Total	C	O	0	0
			13	6	7		
4	3-B	1	Total	C	O	0	0
			13	6	7		
4	4-B	1	Total	C	O	0	0
			13	6	7		
4	5-B	1	Total	C	O	0	0
			13	6	7		
4	6-B	1	Total	C	O	0	0
			13	6	7		
4	7-B	1	Total	C	O	0	0
			13	6	7		
4	8-B	1	Total	C	O	0	0
			13	6	7		
4	9-B	1	Total	C	O	0	0
			13	6	7		
4	10-B	1	Total	C	O	0	0
			13	6	7		
4	1-C	1	Total	C	O	0	0
			13	6	7		
4	2-C	1	Total	C	O	0	0
			13	6	7		
4	3-C	1	Total	C	O	0	0
			13	6	7		
4	4-C	1	Total	C	O	0	0
			13	6	7		
4	5-C	1	Total	C	O	0	0
			13	6	7		
4	6-C	1	Total	C	O	0	0
			13	6	7		
4	7-C	1	Total	C	O	0	0
			13	6	7		
4	8-C	1	Total	C	O	0	0
			13	6	7		
4	9-C	1	Total	C	O	0	0
			13	6	7		
4	10-C	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	1-D	1	Total	C	O	0	0
			13	6	7		
4	2-D	1	Total	C	O	0	0
			13	6	7		
4	3-D	1	Total	C	O	0	0
			13	6	7		
4	4-D	1	Total	C	O	0	0
			13	6	7		
4	5-D	1	Total	C	O	0	0
			13	6	7		
4	6-D	1	Total	C	O	0	0
			13	6	7		
4	7-D	1	Total	C	O	0	0
			13	6	7		
4	8-D	1	Total	C	O	0	0
			13	6	7		
4	9-D	1	Total	C	O	0	0
			13	6	7		
4	10-D	1	Total	C	O	0	0
			13	6	7		
4	1-E	1	Total	C	O	0	0
			13	6	7		
4	2-E	1	Total	C	O	0	0
			13	6	7		
4	3-E	1	Total	C	O	0	0
			13	6	7		
4	4-E	1	Total	C	O	0	0
			13	6	7		
4	5-E	1	Total	C	O	0	0
			13	6	7		
4	6-E	1	Total	C	O	0	0
			13	6	7		
4	7-E	1	Total	C	O	0	0
			13	6	7		
4	8-E	1	Total	C	O	0	0
			13	6	7		
4	9-E	1	Total	C	O	0	0
			13	6	7		
4	10-E	1	Total	C	O	0	0
			13	6	7		
4	1-F	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	2-F	1	Total	C	O	0	0
			13	6	7		
4	3-F	1	Total	C	O	0	0
			13	6	7		
4	4-F	1	Total	C	O	0	0
			13	6	7		
4	5-F	1	Total	C	O	0	0
			13	6	7		
4	6-F	1	Total	C	O	0	0
			13	6	7		
4	7-F	1	Total	C	O	0	0
			13	6	7		
4	8-F	1	Total	C	O	0	0
			13	6	7		
4	9-F	1	Total	C	O	0	0
			13	6	7		
4	10-F	1	Total	C	O	0	0
			13	6	7		
4	1-G	1	Total	C	O	0	0
			13	6	7		
4	2-G	1	Total	C	O	0	0
			13	6	7		
4	3-G	1	Total	C	O	0	0
			13	6	7		
4	4-G	1	Total	C	O	0	0
			13	6	7		
4	5-G	1	Total	C	O	0	0
			13	6	7		
4	6-G	1	Total	C	O	0	0
			13	6	7		
4	7-G	1	Total	C	O	0	0
			13	6	7		
4	8-G	1	Total	C	O	0	0
			13	6	7		
4	9-G	1	Total	C	O	0	0
			13	6	7		
4	10-G	1	Total	C	O	0	0
			13	6	7		
4	1-H	1	Total	C	O	0	0
			13	6	7		
4	2-H	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	3-H	1	Total	C	O	0	0
			13	6	7		
4	4-H	1	Total	C	O	0	0
			13	6	7		
4	5-H	1	Total	C	O	0	0
			13	6	7		
4	6-H	1	Total	C	O	0	0
			13	6	7		
4	7-H	1	Total	C	O	0	0
			13	6	7		
4	8-H	1	Total	C	O	0	0
			13	6	7		
4	9-H	1	Total	C	O	0	0
			13	6	7		
4	10-H	1	Total	C	O	0	0
			13	6	7		
4	1-I	1	Total	C	O	0	0
			13	6	7		
4	2-I	1	Total	C	O	0	0
			13	6	7		
4	3-I	1	Total	C	O	0	0
			13	6	7		
4	4-I	1	Total	C	O	0	0
			13	6	7		
4	5-I	1	Total	C	O	0	0
			13	6	7		
4	6-I	1	Total	C	O	0	0
			13	6	7		
4	7-I	1	Total	C	O	0	0
			13	6	7		
4	8-I	1	Total	C	O	0	0
			13	6	7		
4	9-I	1	Total	C	O	0	0
			13	6	7		
4	10-I	1	Total	C	O	0	0
			13	6	7		
4	1-J	1	Total	C	O	0	0
			13	6	7		
4	2-J	1	Total	C	O	0	0
			13	6	7		
4	3-J	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	4-J	1	Total	C	O	0	0
			13	6	7		
4	5-J	1	Total	C	O	0	0
			13	6	7		
4	6-J	1	Total	C	O	0	0
			13	6	7		
4	7-J	1	Total	C	O	0	0
			13	6	7		
4	8-J	1	Total	C	O	0	0
			13	6	7		
4	9-J	1	Total	C	O	0	0
			13	6	7		
4	10-J	1	Total	C	O	0	0
			13	6	7		
4	1-K	1	Total	C	O	0	0
			13	6	7		
4	2-K	1	Total	C	O	0	0
			13	6	7		
4	3-K	1	Total	C	O	0	0
			13	6	7		
4	4-K	1	Total	C	O	0	0
			13	6	7		
4	5-K	1	Total	C	O	0	0
			13	6	7		
4	6-K	1	Total	C	O	0	0
			13	6	7		
4	7-K	1	Total	C	O	0	0
			13	6	7		
4	8-K	1	Total	C	O	0	0
			13	6	7		
4	9-K	1	Total	C	O	0	0
			13	6	7		
4	10-K	1	Total	C	O	0	0
			13	6	7		
4	1-L	1	Total	C	O	0	0
			13	6	7		
4	2-L	1	Total	C	O	0	0
			13	6	7		
4	3-L	1	Total	C	O	0	0
			13	6	7		
4	4-L	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	5-L	1	Total	C	O	0	0
			13	6	7		
4	6-L	1	Total	C	O	0	0
			13	6	7		
4	7-L	1	Total	C	O	0	0
			13	6	7		
4	8-L	1	Total	C	O	0	0
			13	6	7		
4	9-L	1	Total	C	O	0	0
			13	6	7		
4	10-L	1	Total	C	O	0	0
			13	6	7		
4	1-M	1	Total	C	O	0	0
			13	6	7		
4	2-M	1	Total	C	O	0	0
			13	6	7		
4	3-M	1	Total	C	O	0	0
			13	6	7		
4	4-M	1	Total	C	O	0	0
			13	6	7		
4	5-M	1	Total	C	O	0	0
			13	6	7		
4	6-M	1	Total	C	O	0	0
			13	6	7		
4	7-M	1	Total	C	O	0	0
			13	6	7		
4	8-M	1	Total	C	O	0	0
			13	6	7		
4	9-M	1	Total	C	O	0	0
			13	6	7		
4	10-M	1	Total	C	O	0	0
			13	6	7		
4	1-N	1	Total	C	O	0	0
			13	6	7		
4	2-N	1	Total	C	O	0	0
			13	6	7		
4	3-N	1	Total	C	O	0	0
			13	6	7		
4	4-N	1	Total	C	O	0	0
			13	6	7		
4	5-N	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	6-N	1	Total	C	O	0	0
			13	6	7		
4	7-N	1	Total	C	O	0	0
			13	6	7		
4	8-N	1	Total	C	O	0	0
			13	6	7		
4	9-N	1	Total	C	O	0	0
			13	6	7		
4	10-N	1	Total	C	O	0	0
			13	6	7		
4	1-O	1	Total	C	O	0	0
			13	6	7		
4	2-O	1	Total	C	O	0	0
			13	6	7		
4	3-O	1	Total	C	O	0	0
			13	6	7		
4	4-O	1	Total	C	O	0	0
			13	6	7		
4	5-O	1	Total	C	O	0	0
			13	6	7		
4	6-O	1	Total	C	O	0	0
			13	6	7		
4	7-O	1	Total	C	O	0	0
			13	6	7		
4	8-O	1	Total	C	O	0	0
			13	6	7		
4	9-O	1	Total	C	O	0	0
			13	6	7		
4	10-O	1	Total	C	O	0	0
			13	6	7		
4	1-P	1	Total	C	O	0	0
			13	6	7		
4	2-P	1	Total	C	O	0	0
			13	6	7		
4	3-P	1	Total	C	O	0	0
			13	6	7		
4	4-P	1	Total	C	O	0	0
			13	6	7		
4	5-P	1	Total	C	O	0	0
			13	6	7		
4	6-P	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	7-P	1	Total	C	O	0	0
			13	6	7		
4	8-P	1	Total	C	O	0	0
			13	6	7		
4	9-P	1	Total	C	O	0	0
			13	6	7		
4	10-P	1	Total	C	O	0	0
			13	6	7		
4	1-Q	1	Total	C	O	0	0
			13	6	7		
4	2-Q	1	Total	C	O	0	0
			13	6	7		
4	3-Q	1	Total	C	O	0	0
			13	6	7		
4	4-Q	1	Total	C	O	0	0
			13	6	7		
4	5-Q	1	Total	C	O	0	0
			13	6	7		
4	6-Q	1	Total	C	O	0	0
			13	6	7		
4	7-Q	1	Total	C	O	0	0
			13	6	7		
4	8-Q	1	Total	C	O	0	0
			13	6	7		
4	9-Q	1	Total	C	O	0	0
			13	6	7		
4	10-Q	1	Total	C	O	0	0
			13	6	7		
4	1-R	1	Total	C	O	0	0
			13	6	7		
4	2-R	1	Total	C	O	0	0
			13	6	7		
4	3-R	1	Total	C	O	0	0
			13	6	7		
4	4-R	1	Total	C	O	0	0
			13	6	7		
4	5-R	1	Total	C	O	0	0
			13	6	7		
4	6-R	1	Total	C	O	0	0
			13	6	7		
4	7-R	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	8-R	1	Total	C	O	0	0
			13	6	7		
4	9-R	1	Total	C	O	0	0
			13	6	7		
4	10-R	1	Total	C	O	0	0
			13	6	7		
4	1-S	1	Total	C	O	0	0
			13	6	7		
4	2-S	1	Total	C	O	0	0
			13	6	7		
4	3-S	1	Total	C	O	0	0
			13	6	7		
4	4-S	1	Total	C	O	0	0
			13	6	7		
4	5-S	1	Total	C	O	0	0
			13	6	7		
4	6-S	1	Total	C	O	0	0
			13	6	7		
4	7-S	1	Total	C	O	0	0
			13	6	7		
4	8-S	1	Total	C	O	0	0
			13	6	7		
4	9-S	1	Total	C	O	0	0
			13	6	7		
4	10-S	1	Total	C	O	0	0
			13	6	7		
4	1-T	1	Total	C	O	0	0
			13	6	7		
4	2-T	1	Total	C	O	0	0
			13	6	7		
4	3-T	1	Total	C	O	0	0
			13	6	7		
4	4-T	1	Total	C	O	0	0
			13	6	7		
4	5-T	1	Total	C	O	0	0
			13	6	7		
4	6-T	1	Total	C	O	0	0
			13	6	7		
4	7-T	1	Total	C	O	0	0
			13	6	7		
4	8-T	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	9-T	1	Total	C	O	0	0
			13	6	7		
4	10-T	1	Total	C	O	0	0
			13	6	7		
4	1-U	1	Total	C	O	0	0
			13	6	7		
4	2-U	1	Total	C	O	0	0
			13	6	7		
4	3-U	1	Total	C	O	0	0
			13	6	7		
4	4-U	1	Total	C	O	0	0
			13	6	7		
4	5-U	1	Total	C	O	0	0
			13	6	7		
4	6-U	1	Total	C	O	0	0
			13	6	7		
4	7-U	1	Total	C	O	0	0
			13	6	7		
4	8-U	1	Total	C	O	0	0
			13	6	7		
4	9-U	1	Total	C	O	0	0
			13	6	7		
4	10-U	1	Total	C	O	0	0
			13	6	7		
4	1-V	1	Total	C	O	0	0
			13	6	7		
4	2-V	1	Total	C	O	0	0
			13	6	7		
4	3-V	1	Total	C	O	0	0
			13	6	7		
4	4-V	1	Total	C	O	0	0
			13	6	7		
4	5-V	1	Total	C	O	0	0
			13	6	7		
4	6-V	1	Total	C	O	0	0
			13	6	7		
4	7-V	1	Total	C	O	0	0
			13	6	7		
4	8-V	1	Total	C	O	0	0
			13	6	7		
4	9-V	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	10-V	1	Total	C	O	0	0
			13	6	7		
4	1-W	1	Total	C	O	0	0
			13	6	7		
4	2-W	1	Total	C	O	0	0
			13	6	7		
4	3-W	1	Total	C	O	0	0
			13	6	7		
4	4-W	1	Total	C	O	0	0
			13	6	7		
4	5-W	1	Total	C	O	0	0
			13	6	7		
4	6-W	1	Total	C	O	0	0
			13	6	7		
4	7-W	1	Total	C	O	0	0
			13	6	7		
4	8-W	1	Total	C	O	0	0
			13	6	7		
4	9-W	1	Total	C	O	0	0
			13	6	7		
4	10-W	1	Total	C	O	0	0
			13	6	7		
4	1-X	1	Total	C	O	0	0
			13	6	7		
4	2-X	1	Total	C	O	0	0
			13	6	7		
4	3-X	1	Total	C	O	0	0
			13	6	7		
4	4-X	1	Total	C	O	0	0
			13	6	7		
4	5-X	1	Total	C	O	0	0
			13	6	7		
4	6-X	1	Total	C	O	0	0
			13	6	7		
4	7-X	1	Total	C	O	0	0
			13	6	7		
4	8-X	1	Total	C	O	0	0
			13	6	7		
4	9-X	1	Total	C	O	0	0
			13	6	7		
4	10-X	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	1-A	261	Total O 261 261	0	0
5	2-A	262	Total O 262 262	0	0
5	3-A	261	Total O 261 261	0	0
5	4-A	263	Total O 263 263	0	0
5	5-A	261	Total O 261 261	0	0
5	6-A	257	Total O 257 257	0	0
5	7-A	265	Total O 265 265	0	0
5	8-A	259	Total O 259 259	0	0
5	9-A	265	Total O 265 265	0	0
5	10-A	262	Total O 262 262	0	0
5	1-B	264	Total O 264 264	0	0
5	2-B	261	Total O 261 261	0	0
5	3-B	263	Total O 263 263	0	0
5	4-B	262	Total O 262 262	0	0
5	5-B	261	Total O 261 261	0	0
5	6-B	265	Total O 265 265	0	0
5	7-B	264	Total O 264 264	0	0
5	8-B	264	Total O 264 264	0	0
5	9-B	258	Total O 258 258	0	0
5	10-B	263	Total O 263 263	0	0
5	1-C	261	Total O 261 261	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	2-C	264	Total 264	O 264	0	0
5	3-C	265	Total 265	O 265	0	0
5	4-C	261	Total 261	O 261	0	0
5	5-C	263	Total 263	O 263	0	0
5	6-C	262	Total 262	O 262	0	0
5	7-C	262	Total 262	O 262	0	0
5	8-C	263	Total 263	O 263	0	0
5	9-C	261	Total 261	O 261	0	0
5	10-C	262	Total 262	O 262	0	0
5	1-D	260	Total 260	O 260	0	0
5	2-D	269	Total 269	O 269	0	0
5	3-D	260	Total 260	O 260	0	0
5	4-D	263	Total 263	O 263	0	0
5	5-D	262	Total 262	O 262	0	0
5	6-D	265	Total 265	O 265	0	0
5	7-D	261	Total 261	O 261	0	0
5	8-D	265	Total 265	O 265	0	0
5	9-D	266	Total 266	O 266	0	0
5	10-D	262	Total 262	O 262	0	0
5	1-E	261	Total 261	O 261	0	0
5	2-E	254	Total 254	O 254	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	3-E	257	Total 257	O 257	0	0
5	4-E	263	Total 263	O 263	0	0
5	5-E	259	Total 259	O 259	0	0
5	6-E	262	Total 262	O 262	0	0
5	7-E	265	Total 265	O 265	0	0
5	8-E	257	Total 257	O 257	0	0
5	9-E	262	Total 262	O 262	0	0
5	10-E	257	Total 257	O 257	0	0
5	1-F	262	Total 262	O 262	0	0
5	2-F	263	Total 263	O 263	0	0
5	3-F	272	Total 272	O 272	0	0
5	4-F	264	Total 264	O 264	0	0
5	5-F	266	Total 266	O 266	0	0
5	6-F	263	Total 263	O 263	0	0
5	7-F	262	Total 262	O 262	0	0
5	8-F	268	Total 268	O 268	0	0
5	9-F	262	Total 262	O 262	0	0
5	10-F	261	Total 261	O 261	0	0
5	1-G	265	Total 265	O 265	0	0
5	2-G	262	Total 262	O 262	0	0
5	3-G	257	Total 257	O 257	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	4-G	261	Total 261	O 261	0	0
5	5-G	263	Total 263	O 263	0	0
5	6-G	267	Total 267	O 267	0	0
5	7-G	259	Total 259	O 259	0	0
5	8-G	265	Total 265	O 265	0	0
5	9-G	263	Total 263	O 263	0	0
5	10-G	264	Total 264	O 264	0	0
5	1-H	262	Total 262	O 262	0	0
5	2-H	263	Total 263	O 263	0	0
5	3-H	261	Total 261	O 261	0	0
5	4-H	266	Total 266	O 266	0	0
5	5-H	270	Total 270	O 270	0	0
5	6-H	263	Total 263	O 263	0	0
5	7-H	262	Total 262	O 262	0	0
5	8-H	261	Total 261	O 261	0	0
5	9-H	268	Total 268	O 268	0	0
5	10-H	264	Total 264	O 264	0	0
5	1-I	265	Total 265	O 265	0	0
5	2-I	265	Total 265	O 265	0	0
5	3-I	266	Total 266	O 266	0	0
5	4-I	263	Total 263	O 263	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	5-I	260	Total 260	O 260	0	0
5	6-I	263	Total 263	O 263	0	0
5	7-I	261	Total 261	O 261	0	0
5	8-I	265	Total 265	O 265	0	0
5	9-I	262	Total 262	O 262	0	0
5	10-I	263	Total 263	O 263	0	0
5	1-J	262	Total 262	O 262	0	0
5	2-J	258	Total 258	O 258	0	0
5	3-J	260	Total 260	O 260	0	0
5	4-J	260	Total 260	O 260	0	0
5	5-J	263	Total 263	O 263	0	0
5	6-J	259	Total 259	O 259	0	0
5	7-J	266	Total 266	O 266	0	0
5	8-J	263	Total 263	O 263	0	0
5	9-J	260	Total 260	O 260	0	0
5	10-J	264	Total 264	O 264	0	0
5	1-K	272	Total 272	O 272	0	0
5	2-K	271	Total 271	O 271	0	0
5	3-K	268	Total 268	O 268	0	0
5	4-K	267	Total 267	O 267	0	0
5	5-K	268	Total 268	O 268	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	6-K	270	Total 270	O 270	0	0
5	7-K	263	Total 263	O 263	0	0
5	8-K	264	Total 264	O 264	0	0
5	9-K	269	Total 269	O 269	0	0
5	10-K	271	Total 271	O 271	0	0
5	1-L	261	Total 261	O 261	0	0
5	2-L	264	Total 264	O 264	0	0
5	3-L	266	Total 266	O 266	0	0
5	4-L	263	Total 263	O 263	0	0
5	5-L	260	Total 260	O 260	0	0
5	6-L	260	Total 260	O 260	0	0
5	7-L	266	Total 266	O 266	0	0
5	8-L	262	Total 262	O 262	0	0
5	9-L	260	Total 260	O 260	0	0
5	10-L	263	Total 263	O 263	0	0
5	1-M	261	Total 261	O 261	0	0
5	2-M	264	Total 264	O 264	0	0
5	3-M	259	Total 259	O 259	0	0
5	4-M	264	Total 264	O 264	0	0
5	5-M	264	Total 264	O 264	0	0
5	6-M	262	Total 262	O 262	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	7-M	260	Total 260	O 260	0	0
5	8-M	260	Total 260	O 260	0	0
5	9-M	265	Total 265	O 265	0	0
5	10-M	263	Total 263	O 263	0	0
5	1-N	263	Total 263	O 263	0	0
5	2-N	261	Total 261	O 261	0	0
5	3-N	263	Total 263	O 263	0	0
5	4-N	263	Total 263	O 263	0	0
5	5-N	265	Total 265	O 265	0	0
5	6-N	260	Total 260	O 260	0	0
5	7-N	266	Total 266	O 266	0	0
5	8-N	263	Total 263	O 263	0	0
5	9-N	261	Total 261	O 261	0	0
5	10-N	259	Total 259	O 259	0	0
5	1-O	263	Total 263	O 263	0	0
5	2-O	267	Total 267	O 267	0	0
5	3-O	265	Total 265	O 265	0	0
5	4-O	263	Total 263	O 263	0	0
5	5-O	267	Total 267	O 267	0	0
5	6-O	265	Total 265	O 265	0	0
5	7-O	262	Total 262	O 262	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	8-O	265	Total 265	O 265	0	0
5	9-O	263	Total 263	O 263	0	0
5	10-O	263	Total 263	O 263	0	0
5	1-P	261	Total 261	O 261	0	0
5	2-P	264	Total 264	O 264	0	0
5	3-P	260	Total 260	O 260	0	0
5	4-P	259	Total 259	O 259	0	0
5	5-P	262	Total 262	O 262	0	0
5	6-P	262	Total 262	O 262	0	0
5	7-P	261	Total 261	O 261	0	0
5	8-P	263	Total 263	O 263	0	0
5	9-P	265	Total 265	O 265	0	0
5	10-P	264	Total 264	O 264	0	0
5	1-Q	260	Total 260	O 260	0	0
5	2-Q	257	Total 257	O 257	0	0
5	3-Q	259	Total 259	O 259	0	0
5	4-Q	264	Total 264	O 264	0	0
5	5-Q	261	Total 261	O 261	0	0
5	6-Q	260	Total 260	O 260	0	0
5	7-Q	264	Total 264	O 264	0	0
5	8-Q	257	Total 257	O 257	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	9-Q	263	Total O 263 263	0	0
5	10-Q	257	Total O 257 257	0	0
5	1-R	261	Total O 261 261	0	0
5	2-R	265	Total O 265 265	0	0
5	3-R	268	Total O 268 268	0	0
5	4-R	263	Total O 263 263	0	0
5	5-R	265	Total O 265 265	0	0
5	6-R	266	Total O 266 266	0	0
5	7-R	264	Total O 264 264	0	0
5	8-R	265	Total O 265 265	0	0
5	9-R	264	Total O 264 264	0	0
5	10-R	262	Total O 262 262	0	0
5	1-S	265	Total O 265 265	0	0
5	2-S	259	Total O 259 259	0	0
5	3-S	264	Total O 264 264	0	0
5	4-S	260	Total O 260 260	0	0
5	5-S	263	Total O 263 263	0	0
5	6-S	266	Total O 266 266	0	0
5	7-S	263	Total O 263 263	0	0
5	8-S	269	Total O 269 269	0	0
5	9-S	259	Total O 259 259	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	10-S	266	Total 266	O 266	0	0
5	1-T	261	Total 261	O 261	0	0
5	2-T	259	Total 259	O 259	0	0
5	3-T	262	Total 262	O 262	0	0
5	4-T	262	Total 262	O 262	0	0
5	5-T	258	Total 258	O 258	0	0
5	6-T	257	Total 257	O 257	0	0
5	7-T	263	Total 263	O 263	0	0
5	8-T	259	Total 259	O 259	0	0
5	9-T	265	Total 265	O 265	0	0
5	10-T	262	Total 262	O 262	0	0
5	1-U	263	Total 263	O 263	0	0
5	2-U	267	Total 267	O 267	0	0
5	3-U	267	Total 267	O 267	0	0
5	4-U	264	Total 264	O 264	0	0
5	5-U	263	Total 263	O 263	0	0
5	6-U	265	Total 265	O 265	0	0
5	7-U	262	Total 262	O 262	0	0
5	8-U	263	Total 263	O 263	0	0
5	9-U	265	Total 265	O 265	0	0
5	10-U	264	Total 264	O 264	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1-V	265	Total 265	O 265	0	0
5	2-V	260	Total 260	O 260	0	0
5	3-V	258	Total 258	O 258	0	0
5	4-V	266	Total 266	O 266	0	0
5	5-V	261	Total 261	O 261	0	0
5	6-V	265	Total 265	O 265	0	0
5	7-V	265	Total 265	O 265	0	0
5	8-V	264	Total 264	O 264	0	0
5	9-V	259	Total 259	O 259	0	0
5	10-V	265	Total 265	O 265	0	0
5	1-W	269	Total 269	O 269	0	0
5	2-W	266	Total 266	O 266	0	0
5	3-W	266	Total 266	O 266	0	0
5	4-W	263	Total 263	O 263	0	0
5	5-W	262	Total 262	O 262	0	0
5	6-W	264	Total 264	O 264	0	0
5	7-W	265	Total 265	O 265	0	0
5	8-W	263	Total 263	O 263	0	0
5	9-W	261	Total 261	O 261	0	0
5	10-W	265	Total 265	O 265	0	0
5	1-X	264	Total 264	O 264	0	0

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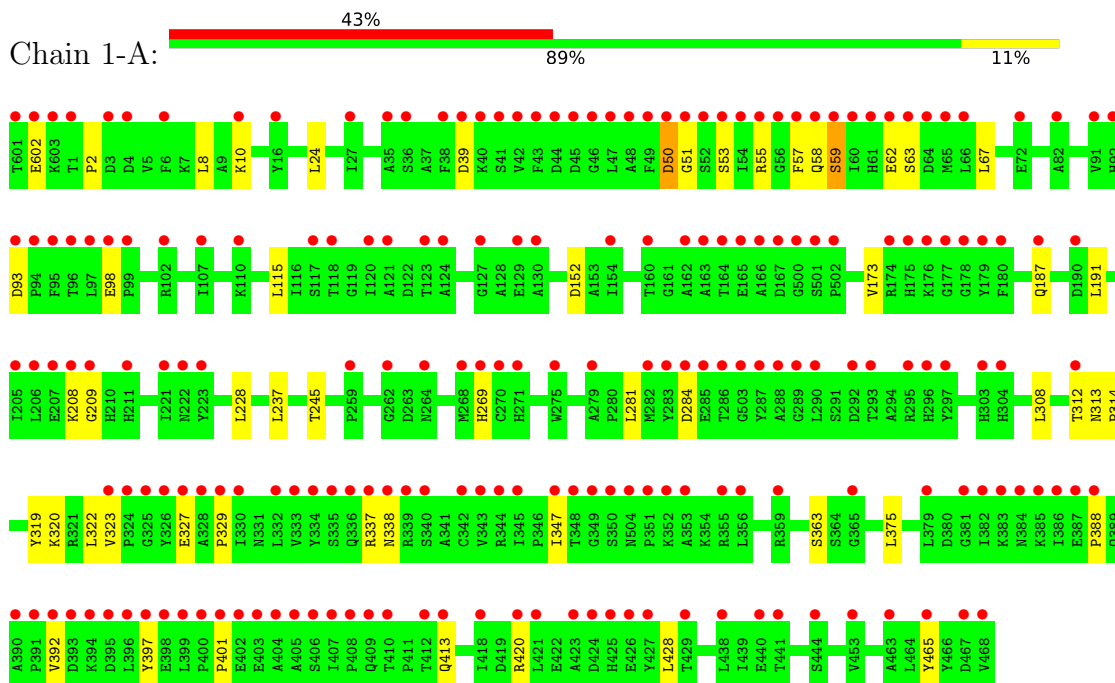
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	2-X	267	Total	O	0	0
			267	267		
5	3-X	265	Total	O	0	0
			265	265		
5	4-X	265	Total	O	0	0
			265	265		
5	5-X	265	Total	O	0	0
			265	265		
5	6-X	264	Total	O	0	0
			264	264		
5	7-X	261	Total	O	0	0
			261	261		
5	8-X	265	Total	O	0	0
			265	265		
5	9-X	266	Total	O	0	0
			266	266		
5	10-X	266	Total	O	0	0
			266	266		

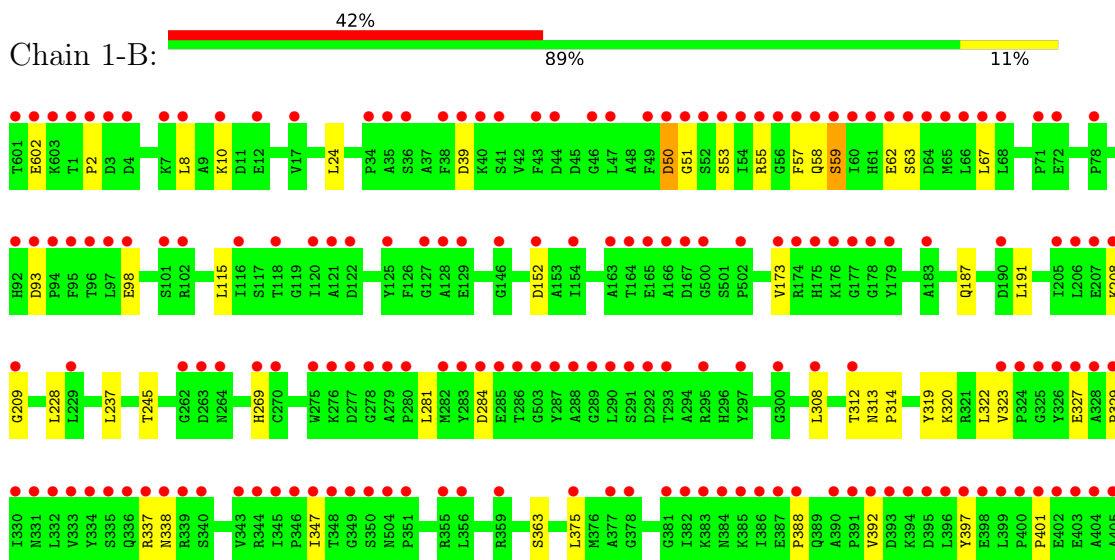
3 Residue-property plots

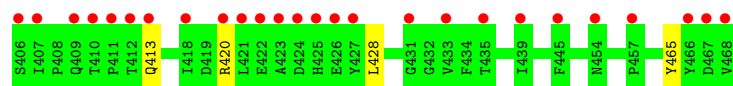
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: glutamine synthetase

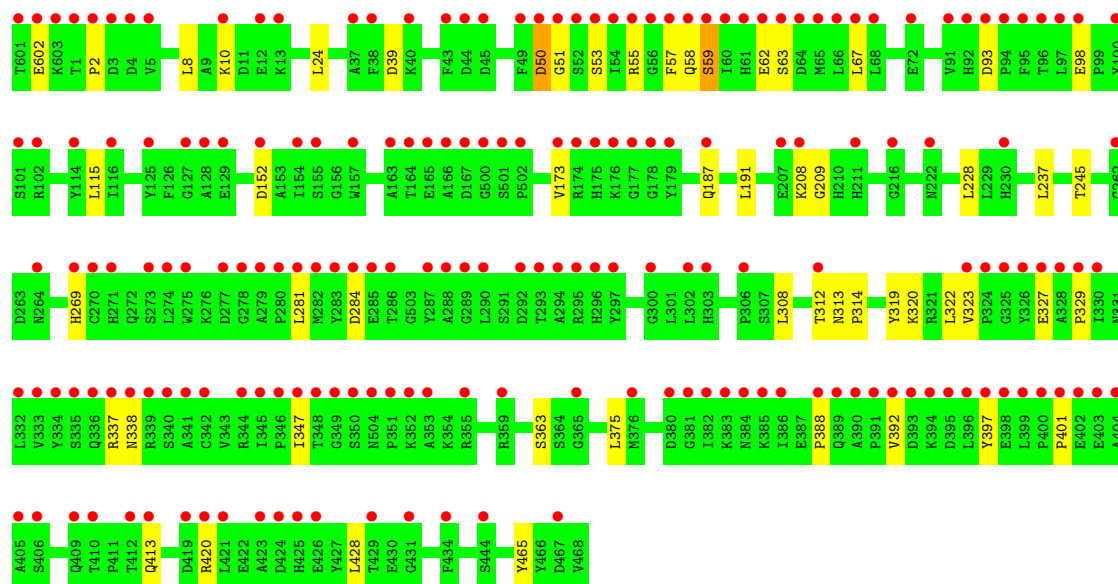
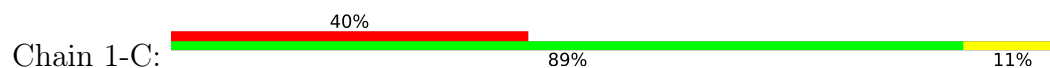


- Molecule 1: glutamine synthetase

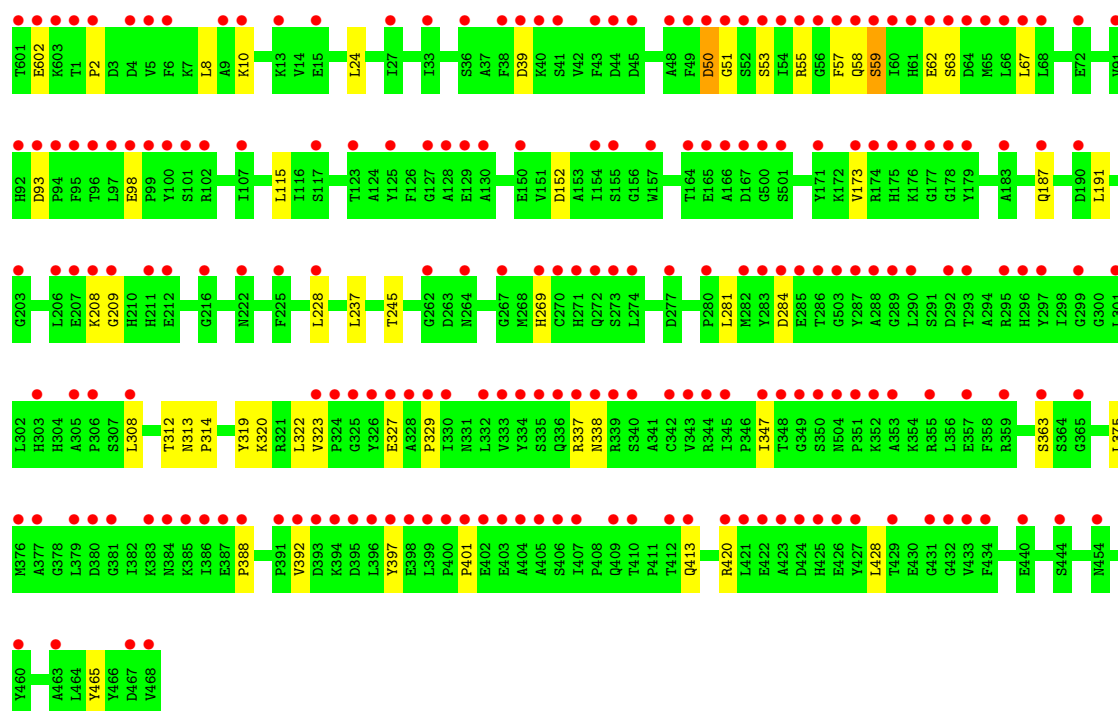




• Molecule 1: glutamine synthetase

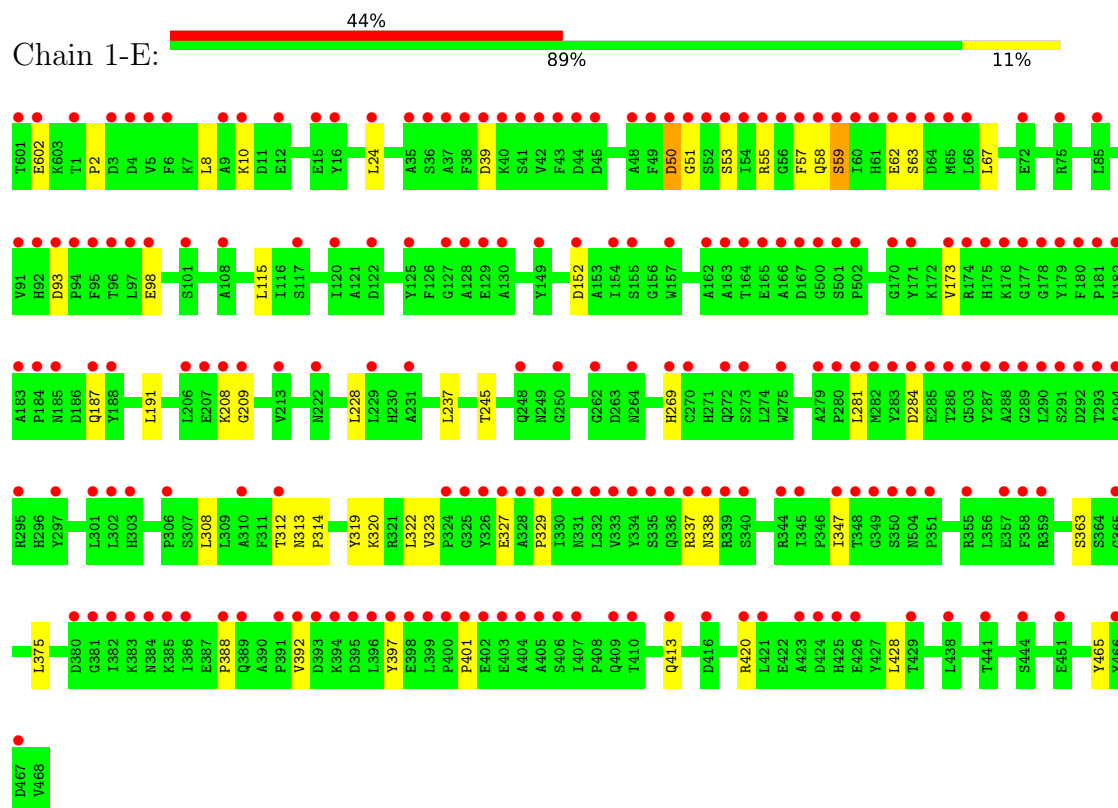


• Molecule 1: glutamine synthetase



- Molecule 1: glutamine synthetase

Chain 1-E:



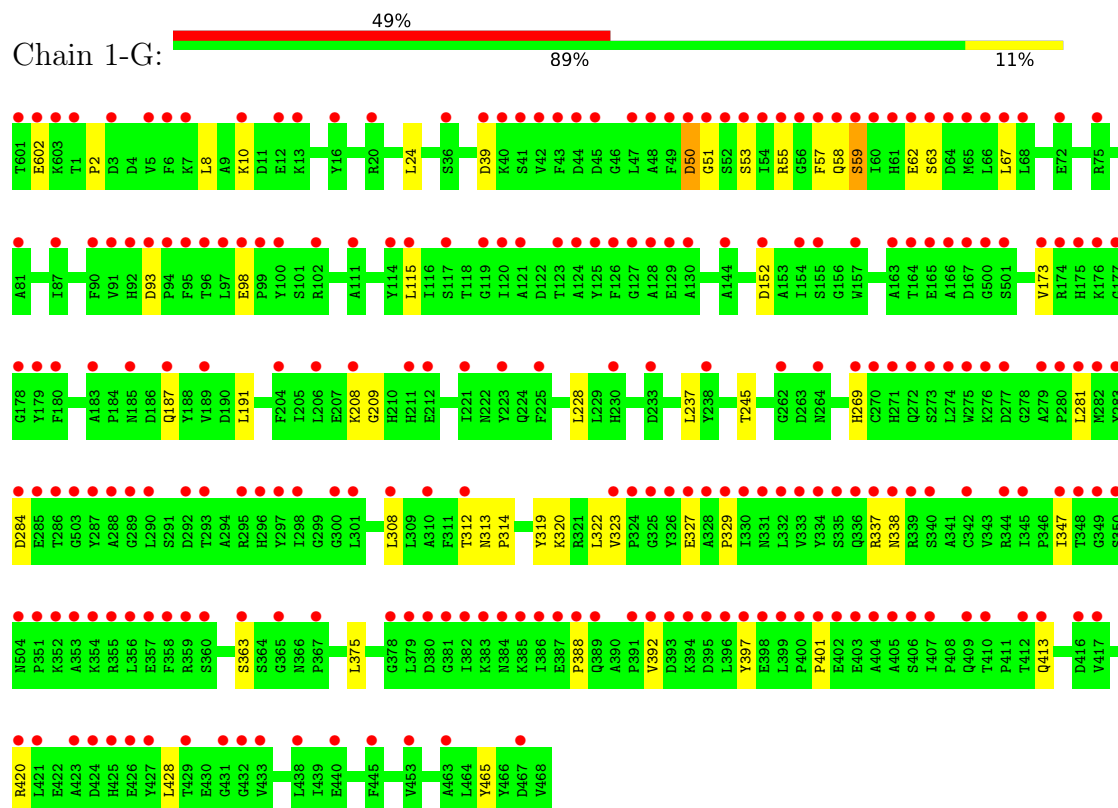
- Molecule 1: glutamine synthetase

Chain 1-F:



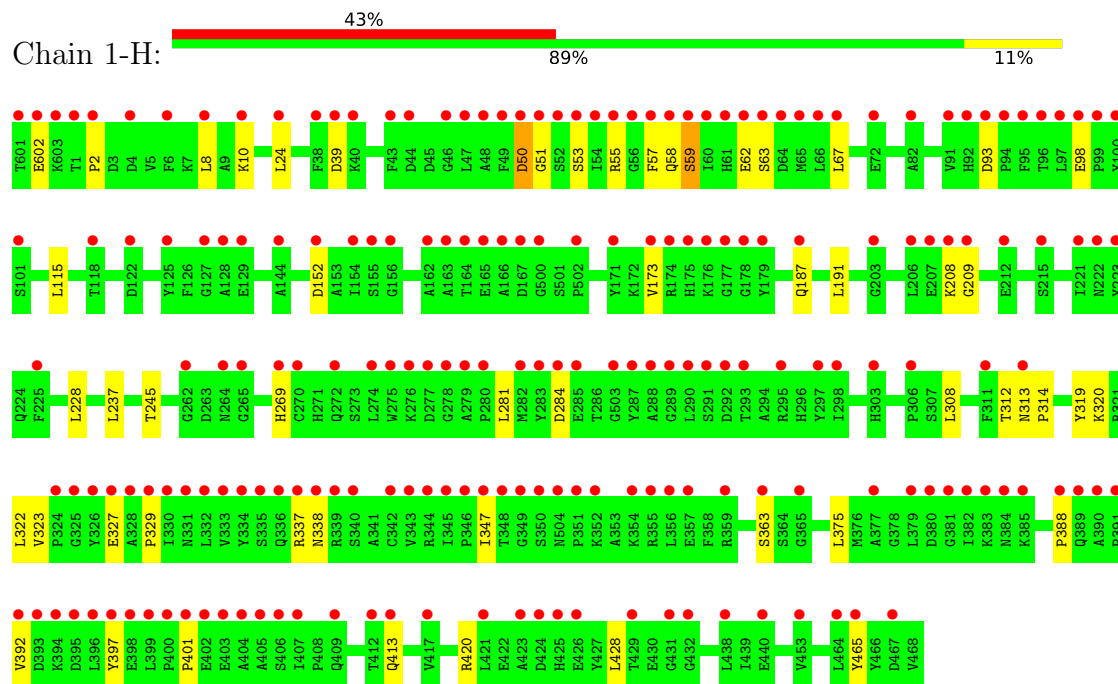
- Molecule 1: glutamine synthetase

Chain 1-G:



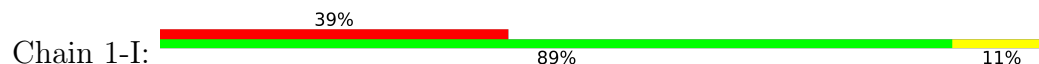
- Molecule 1: glutamine synthetase

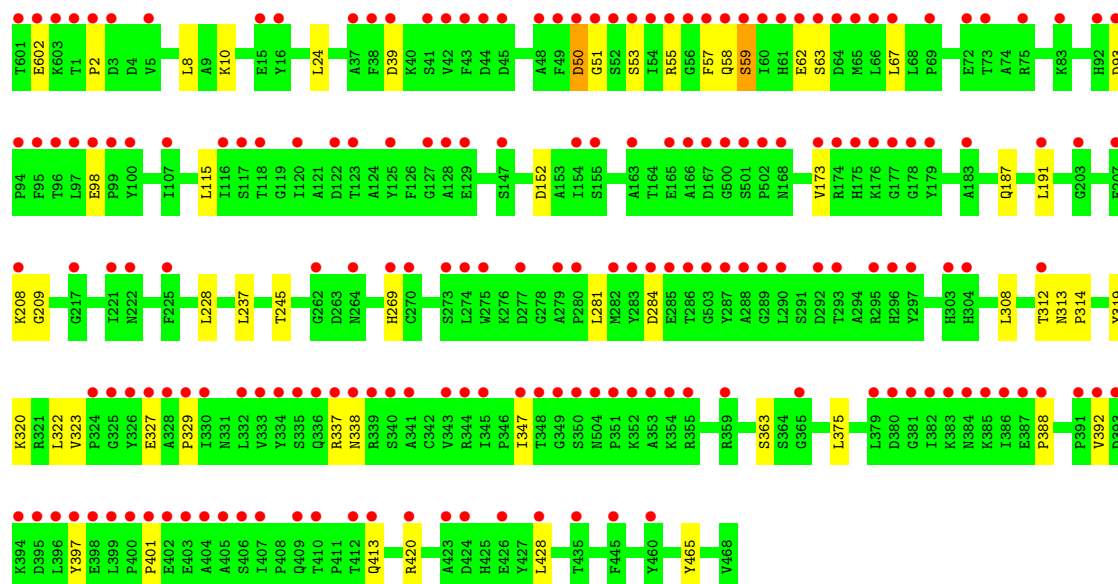
Chain 1-H:



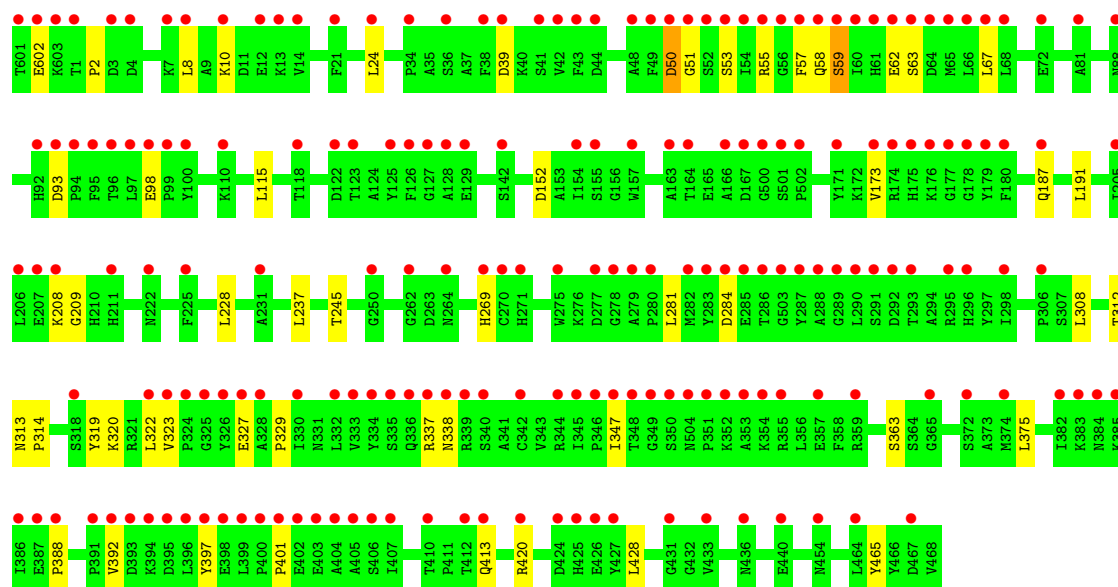
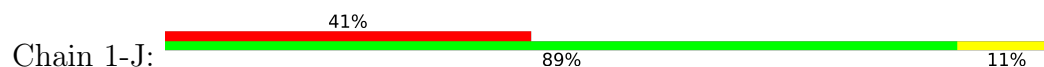
- Molecule 1: glutamine synthetase

Chain 1-I:

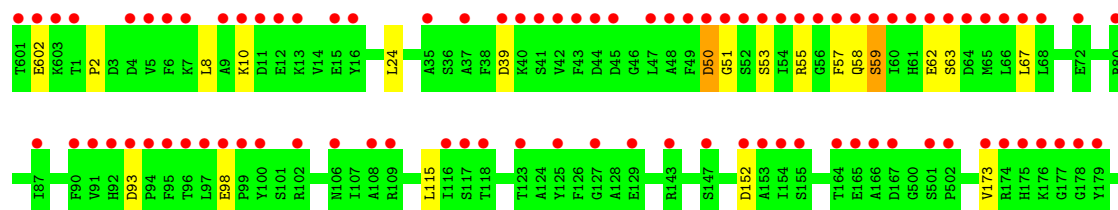
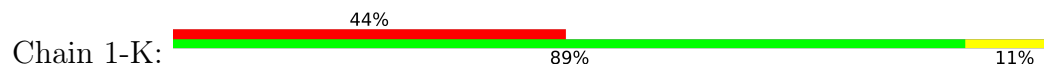


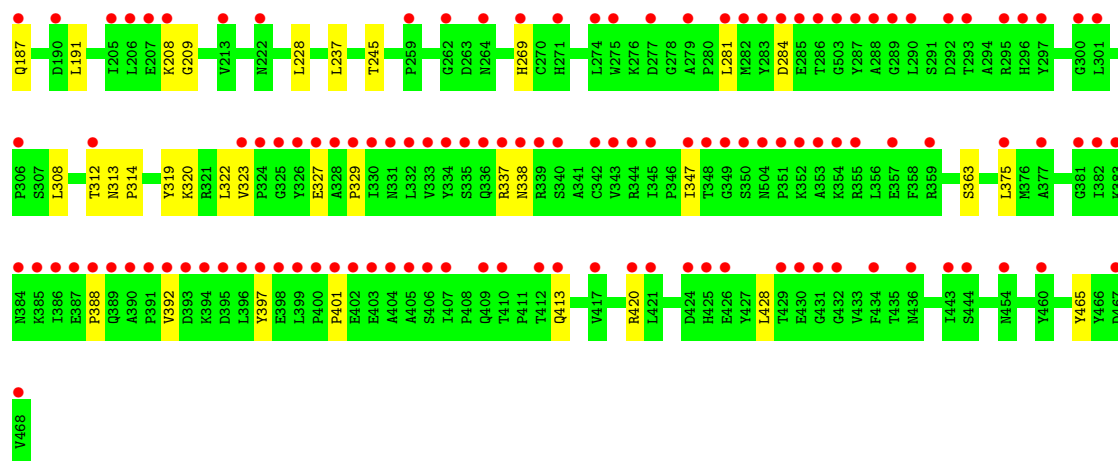


• Molecule 1: glutamine synthetase

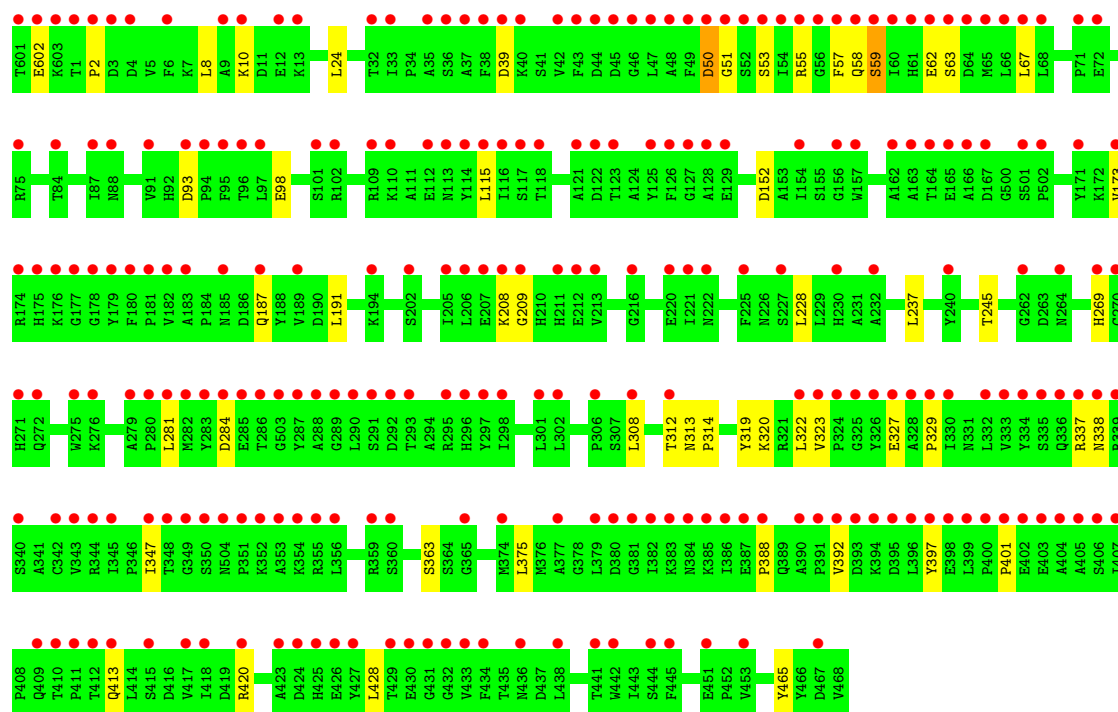
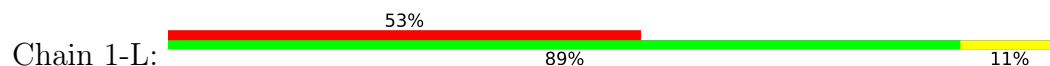


• Molecule 1: glutamine synthetase

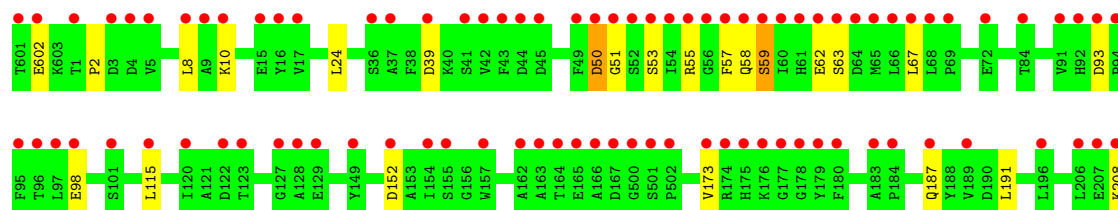


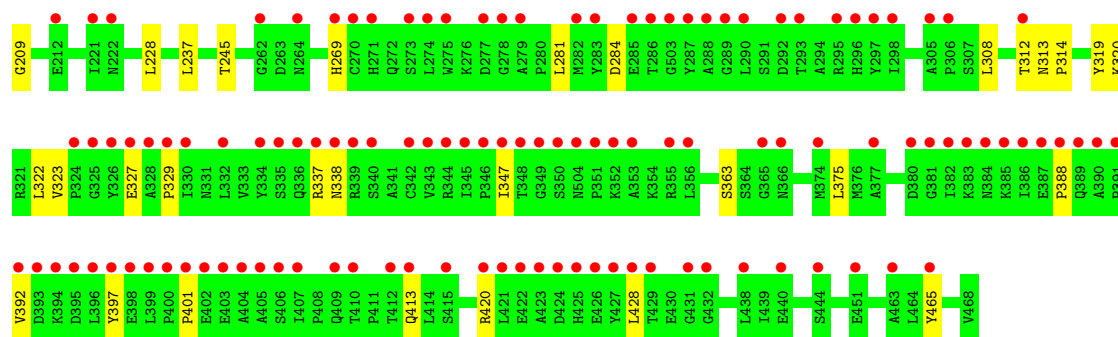


- Molecule 1: glutamine synthetase

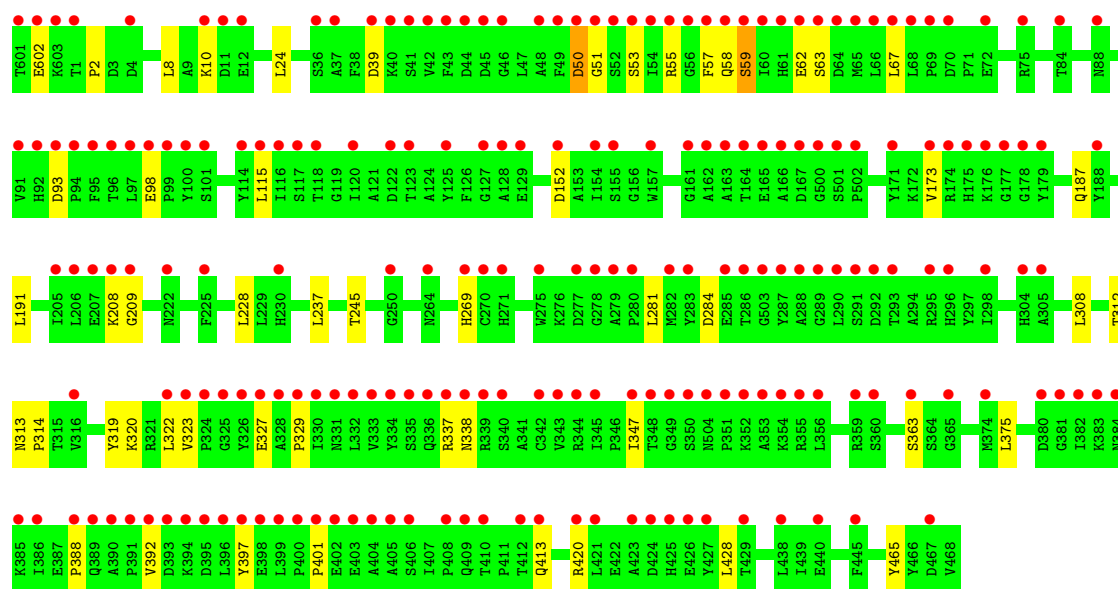


- Molecule 1: glutamine synthetase

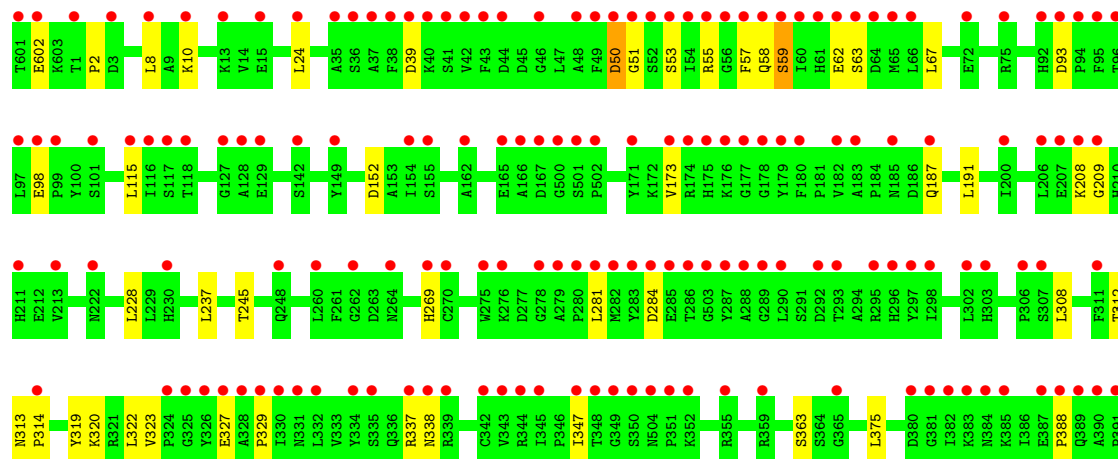
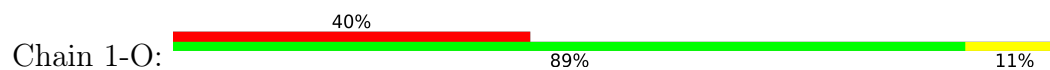




• Molecule 1: glutamine synthetase

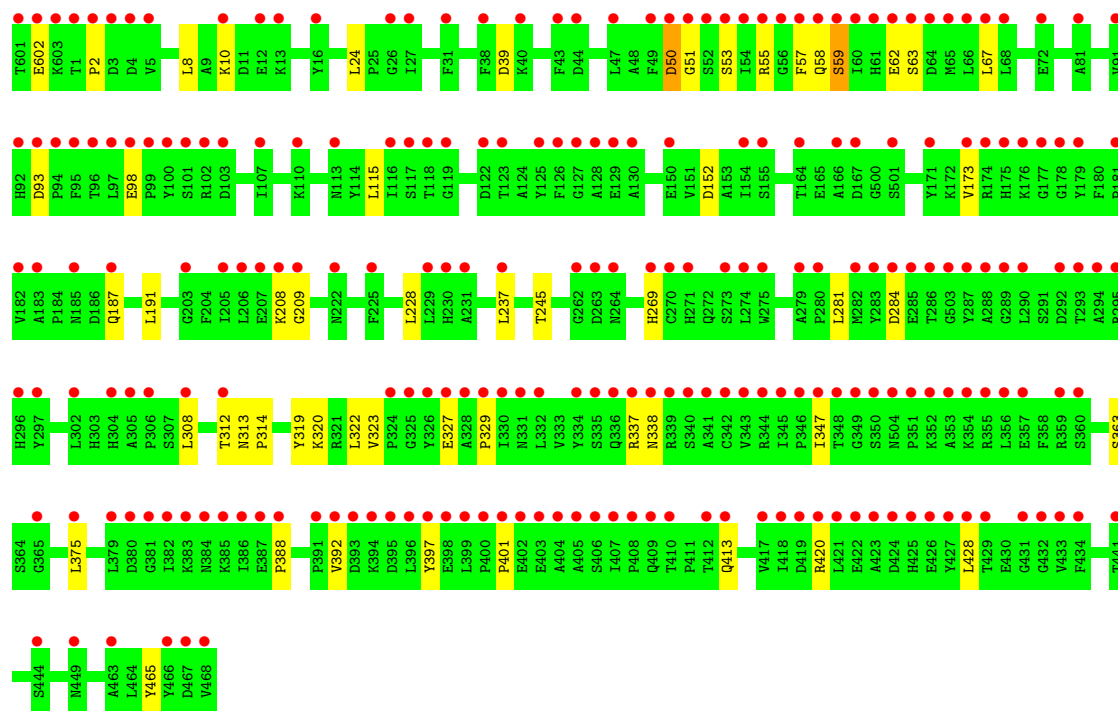
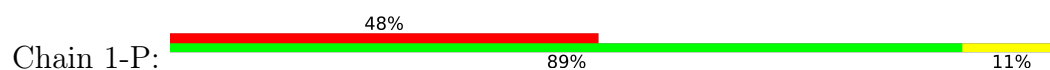


• Molecule 1: glutamine synthetase

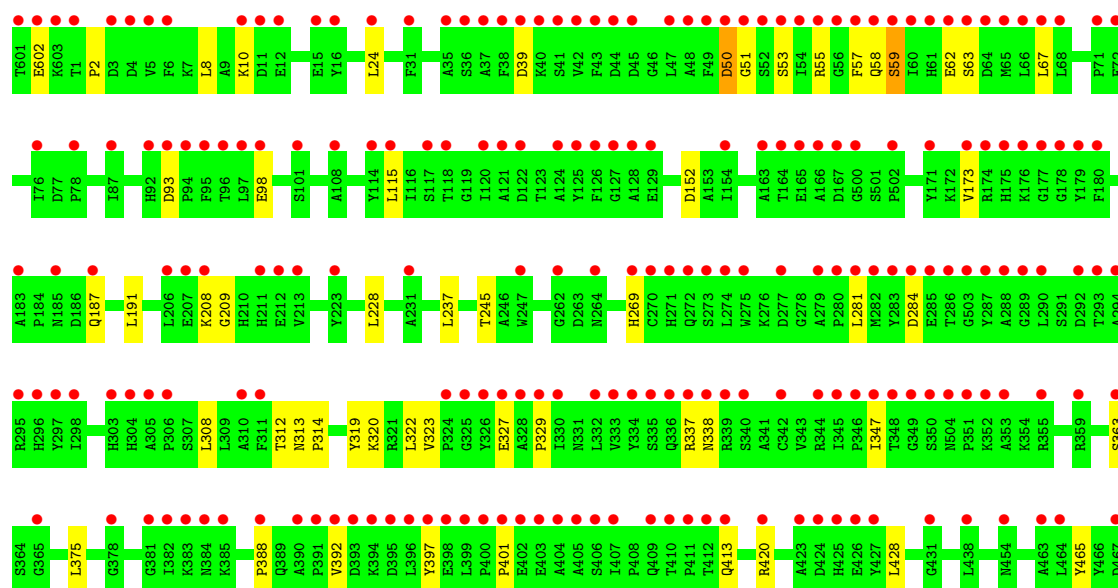




• Molecule 1: glutamine synthetase

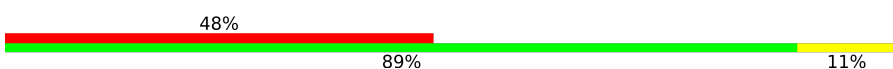


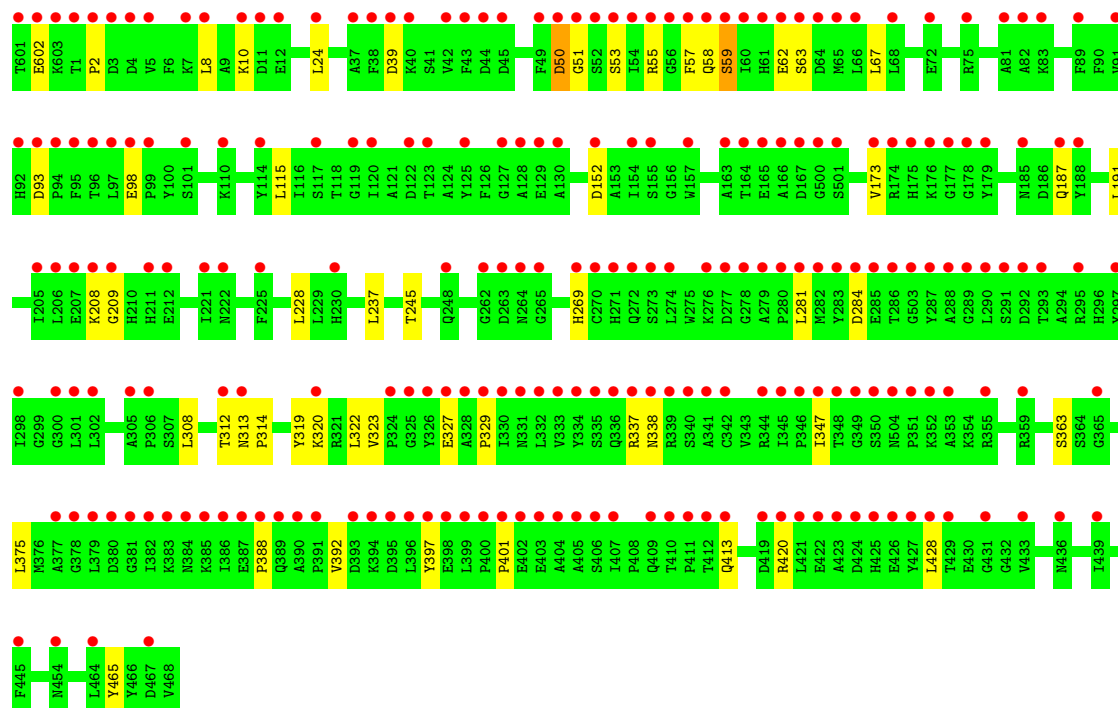
• Molecule 1: glutamine synthetase



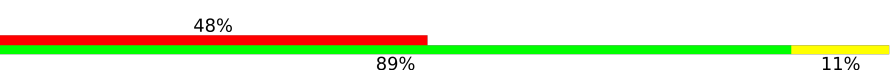
V468

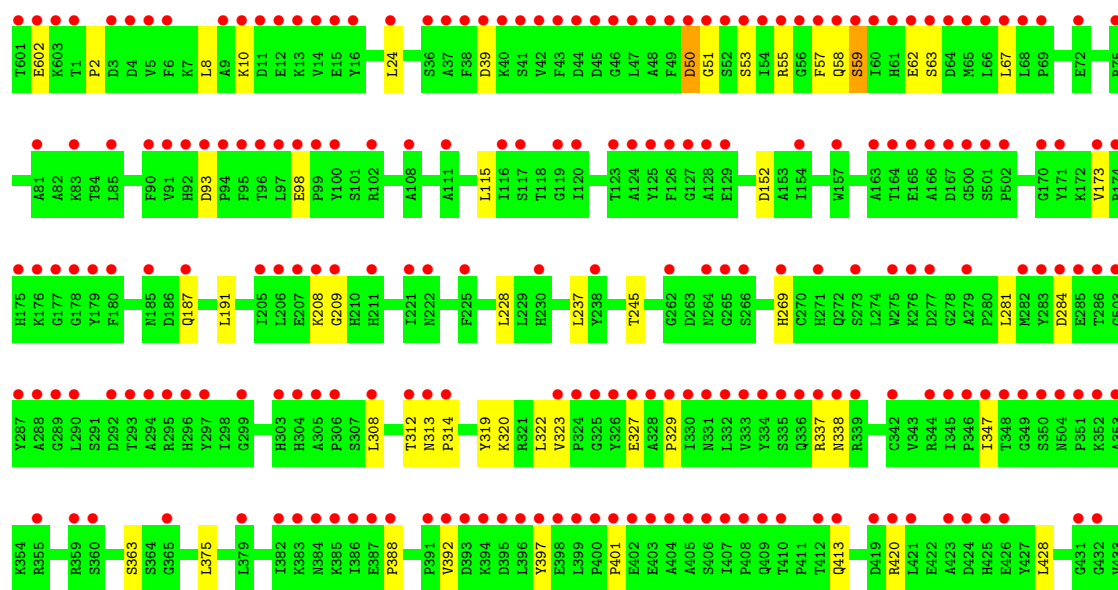
- Molecule 1: glutamine synthetase

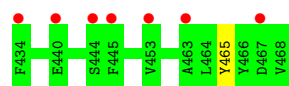
Chain 1-R: 



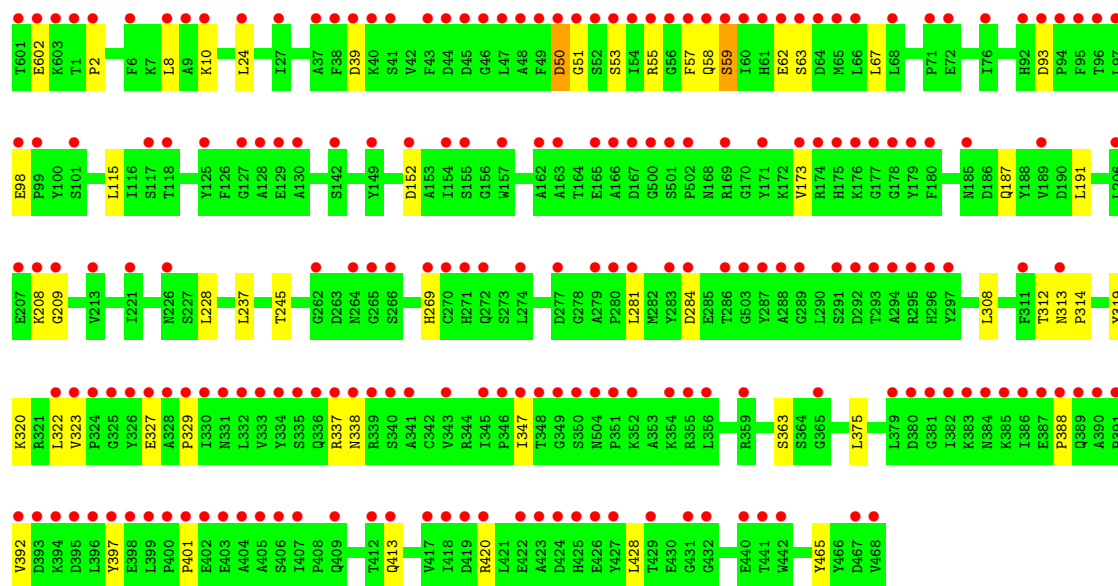
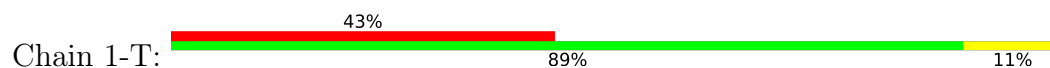
- Molecule 1: glutamine synthetase

Chain 1-S: 

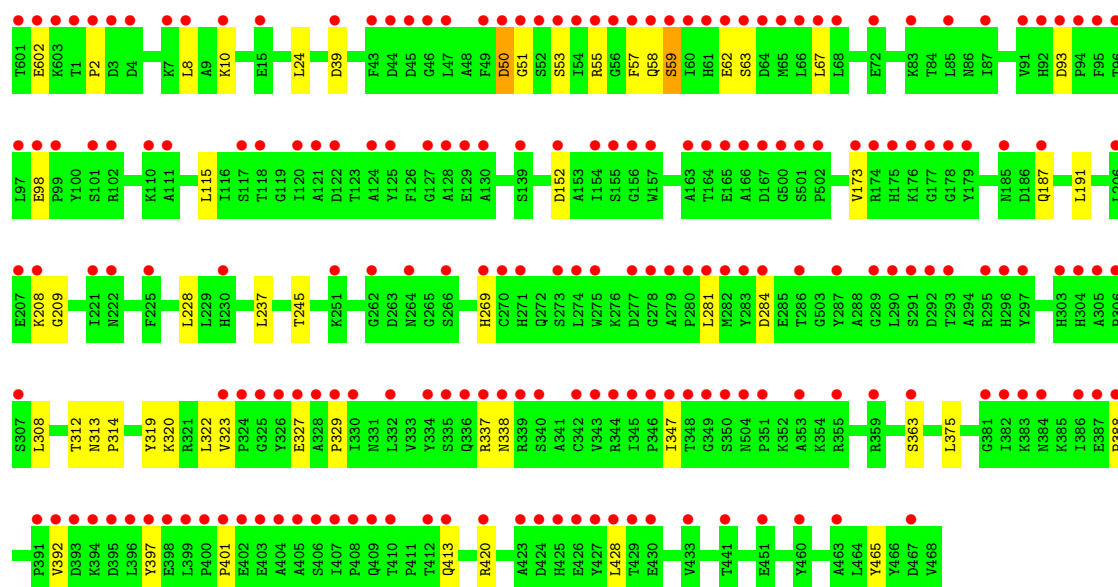
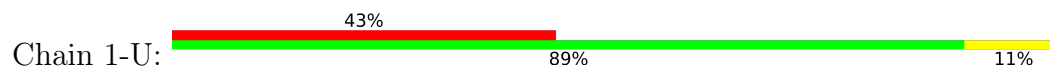




- Molecule 1: glutamine synthetase

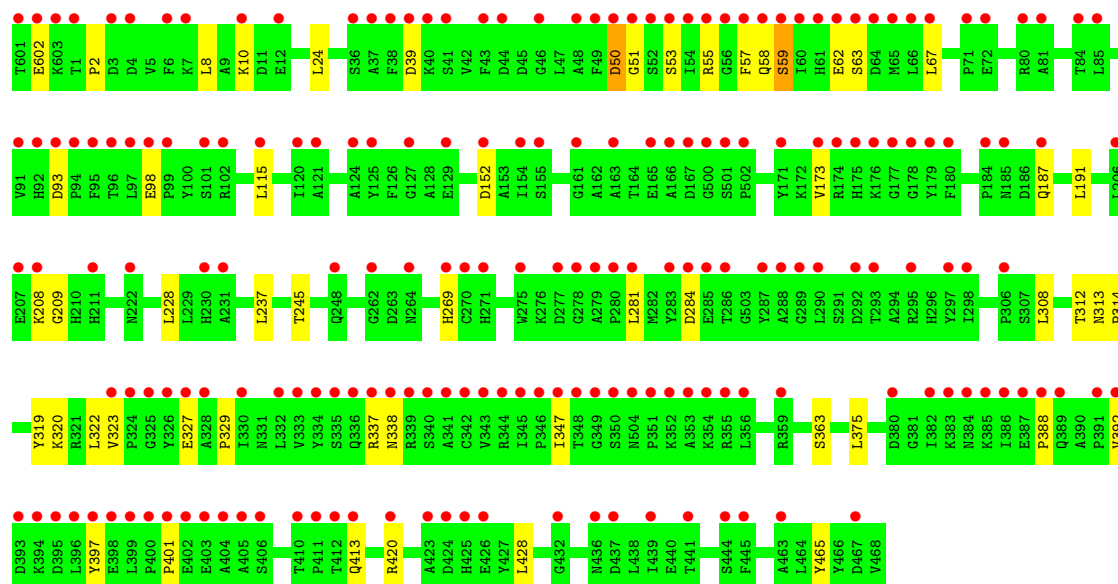


- Molecule 1: glutamine synthetase

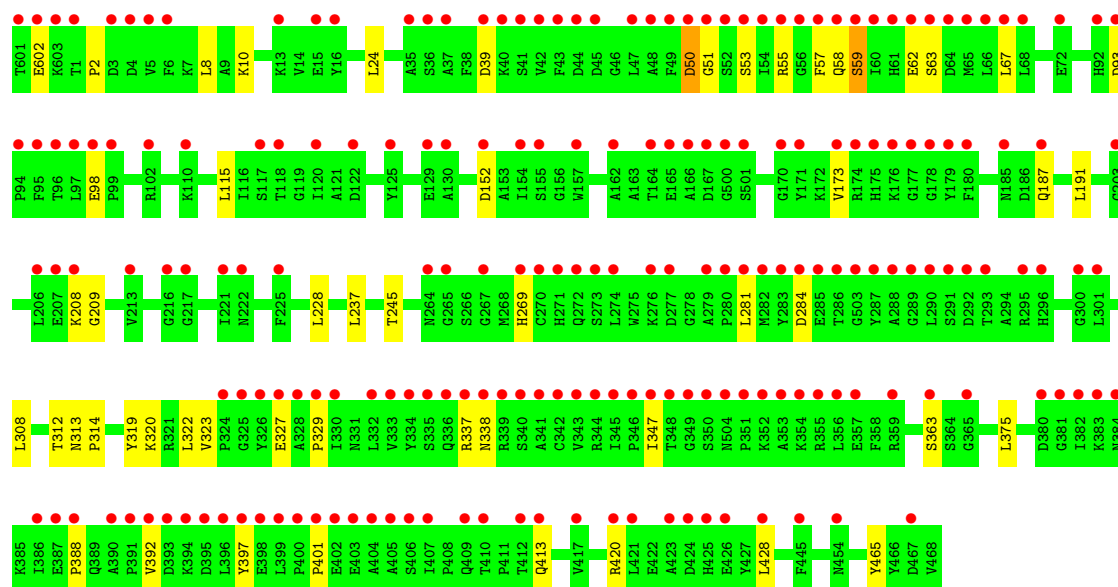
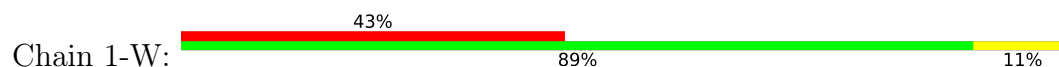


- Molecule 1: glutamine synthetase

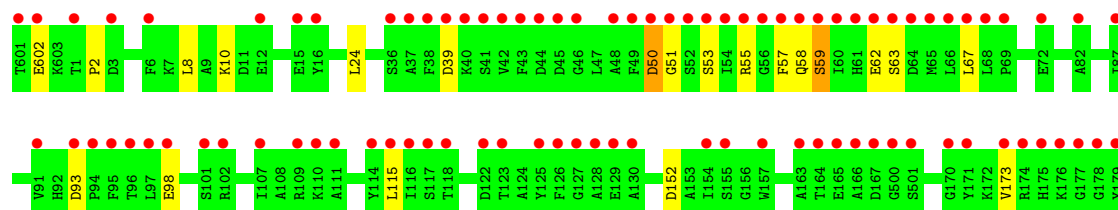
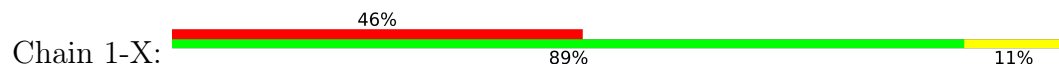


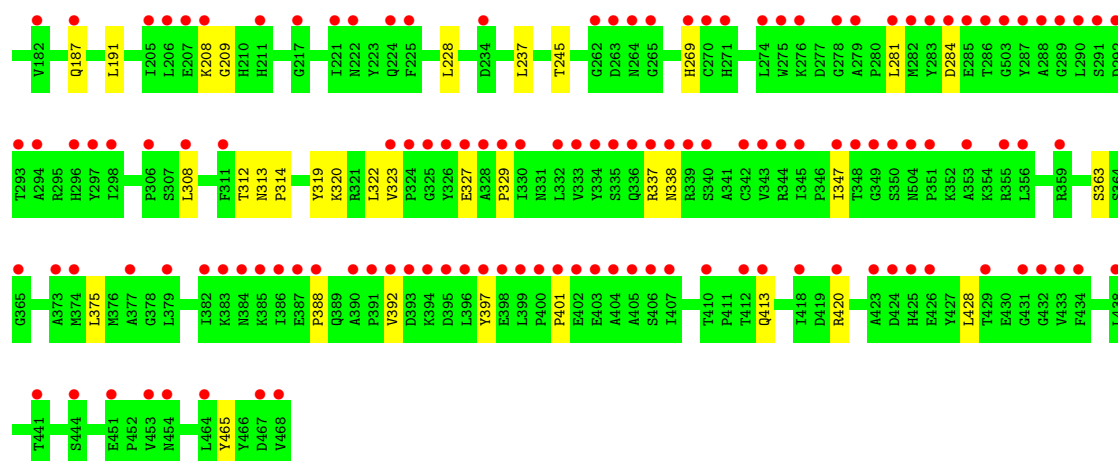


• Molecule 1: glutamine synthetase



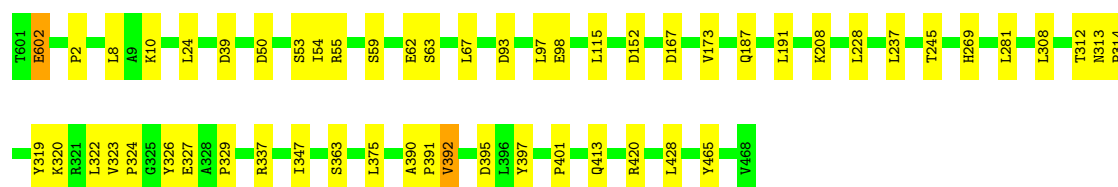
• Molecule 1: glutamine synthetase





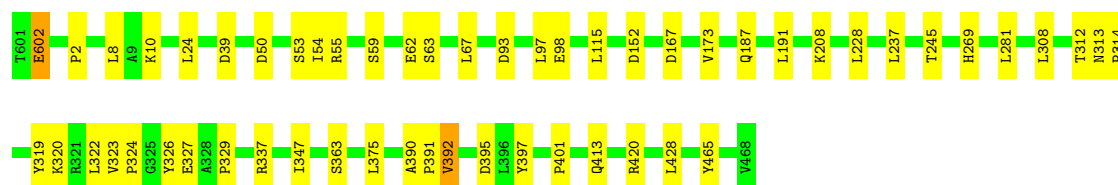
- Molecule 1: glutamine synthetase

Chain 2-A: 88% 11%



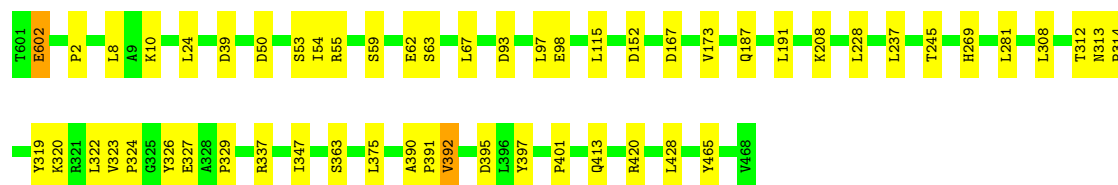
- Molecule 1: glutamine synthetase

Chain 2-B: 88% 11%



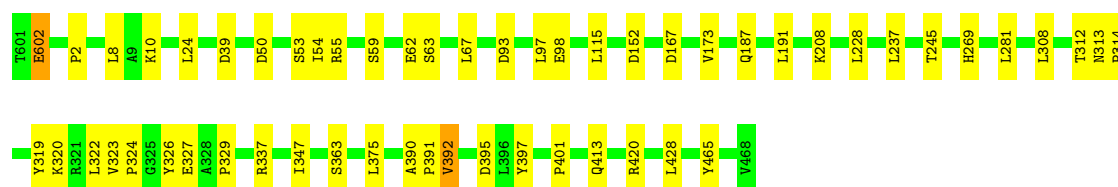
- Molecule 1: glutamine synthetase

Chain 2-C: 88% 11%



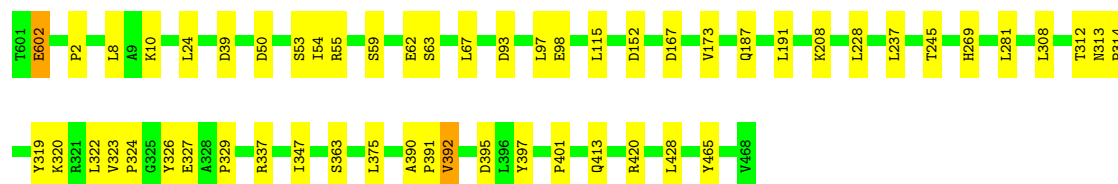
- Molecule 1: glutamine synthetase

Chain 2-D: 88% 11%



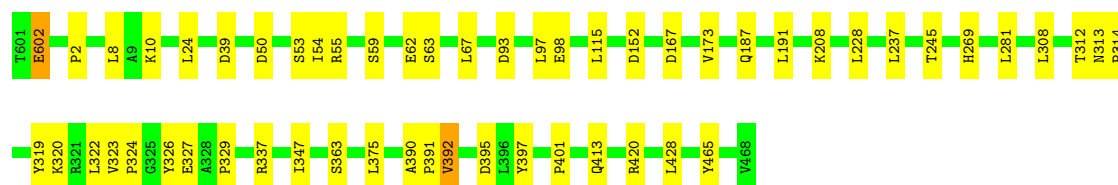
- Molecule 1: glutamine synthetase

Chain 2-E: 88% 11%



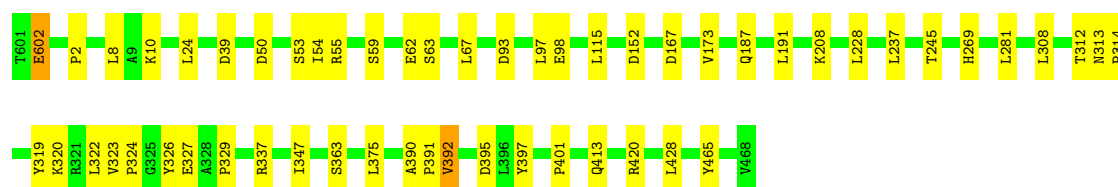
- Molecule 1: glutamine synthetase

Chain 2-F: 88% 11%



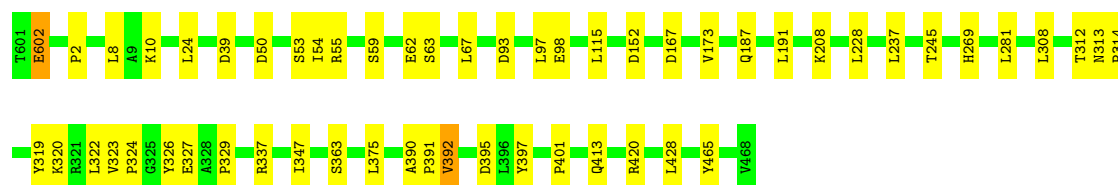
- Molecule 1: glutamine synthetase

Chain 2-G: 88% 11%



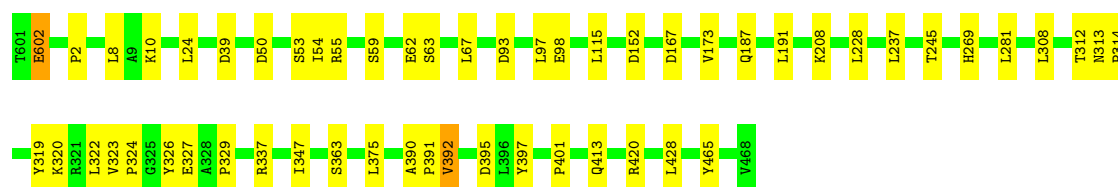
- Molecule 1: glutamine synthetase

Chain 2-H: 88% 11%



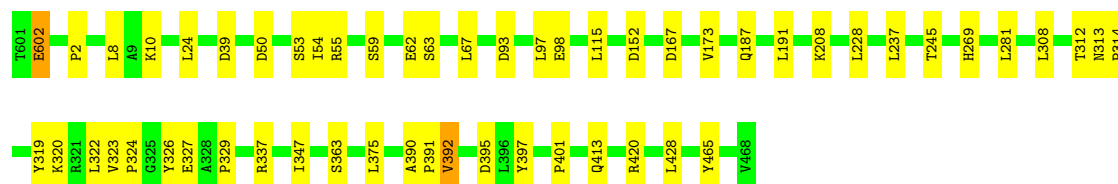
- Molecule 1: glutamine synthetase

Chain 2-I: 88% 11%



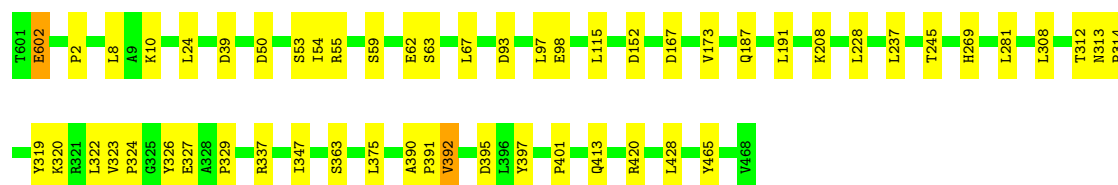
- Molecule 1: glutamine synthetase

Chain 2-J: 88% 11%



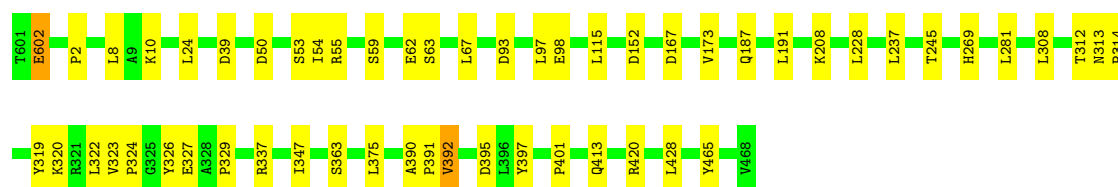
- Molecule 1: glutamine synthetase

Chain 2-K: 88% 11%



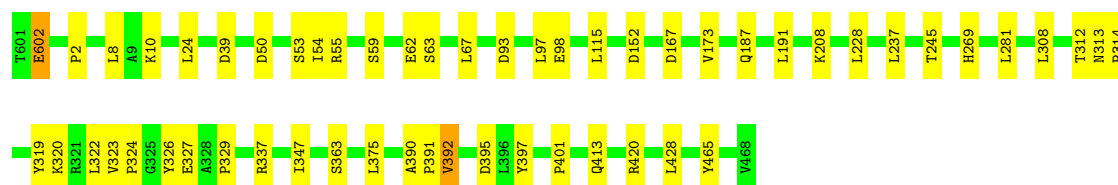
- Molecule 1: glutamine synthetase

Chain 2-L: 88% 11%



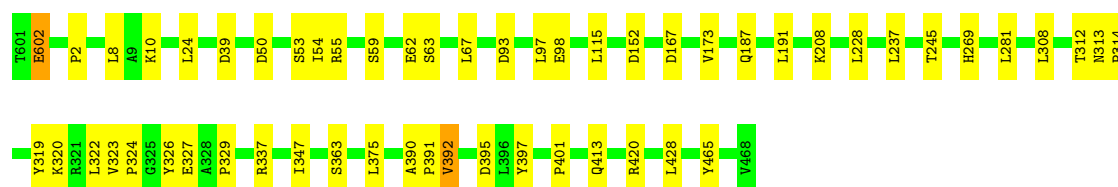
- Molecule 1: glutamine synthetase

Chain 2-M: 88% 11%



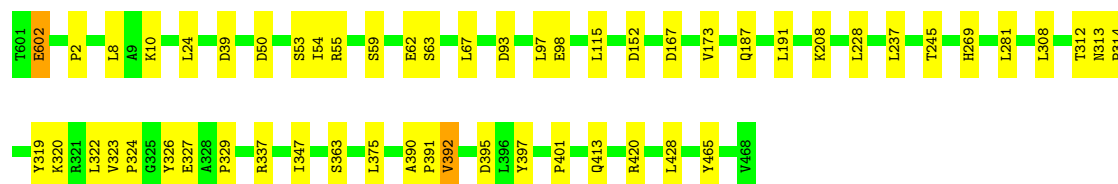
- Molecule 1: glutamine synthetase

Chain 2-N: 88% 11%



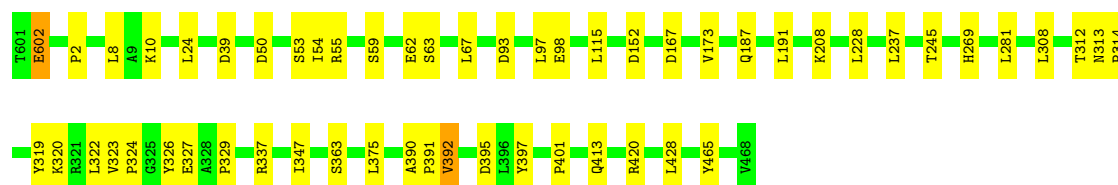
- Molecule 1: glutamine synthetase

Chain 2-O: 88% 11%



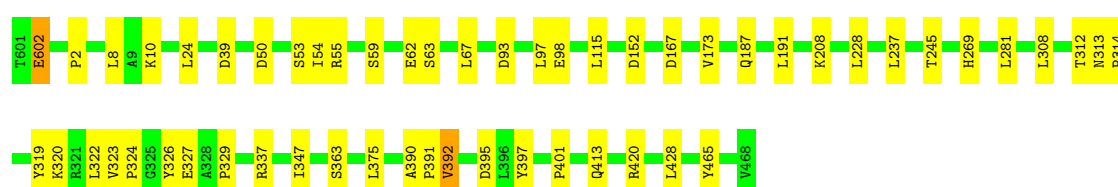
- Molecule 1: glutamine synthetase

Chain 2-P: 88% 11%



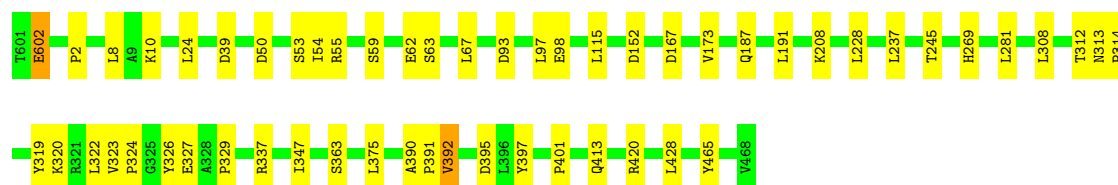
- Molecule 1: glutamine synthetase

Chain 2-Q: 88% 11%



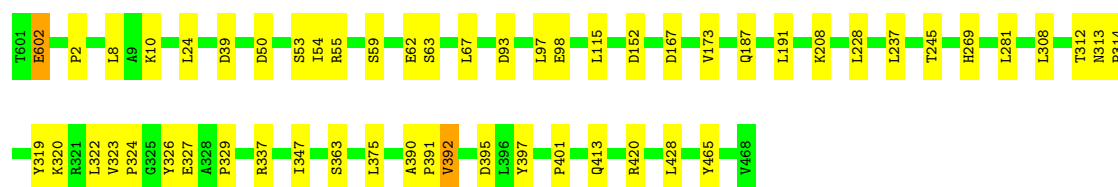
- Molecule 1: glutamine synthetase

Chain 2-R: 88% 11%



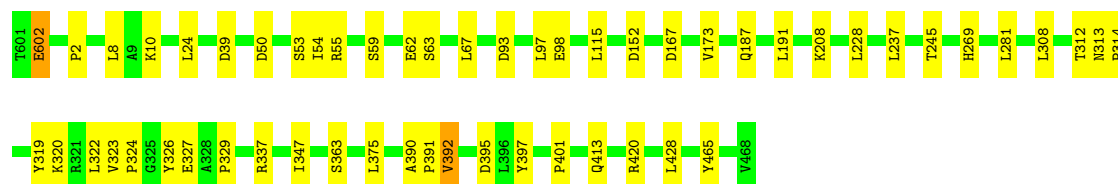
- Molecule 1: glutamine synthetase

Chain 2-S: 88% 11%



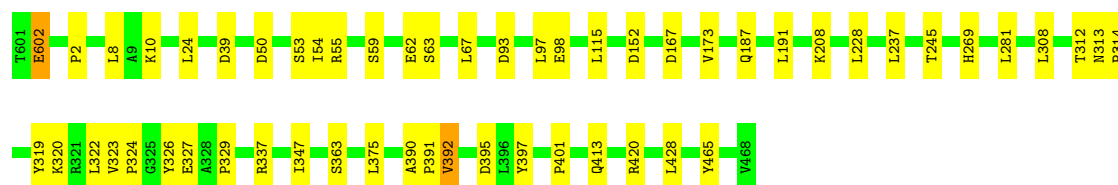
- Molecule 1: glutamine synthetase

Chain 2-T: 88% 11%



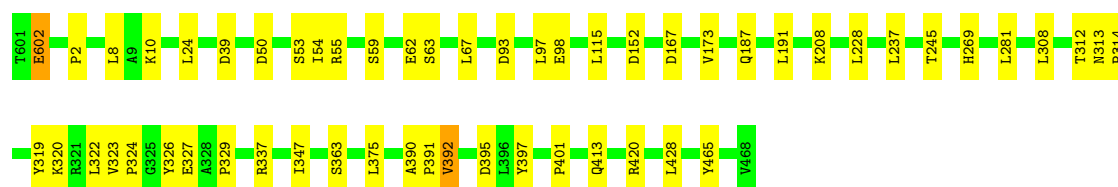
- Molecule 1: glutamine synthetase

Chain 2-U: 88% 11%



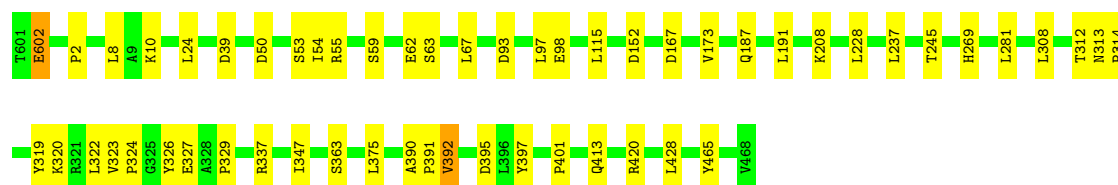
- Molecule 1: glutamine synthetase

Chain 2-V: 88% 11%



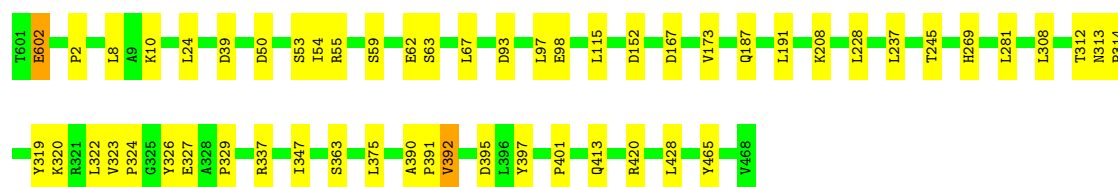
- Molecule 1: glutamine synthetase

Chain 2-W: 88% 11%



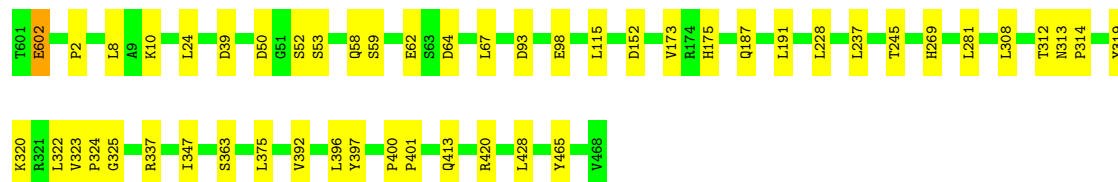
- Molecule 1: glutamine synthetase

Chain 2-X: 88% 11%



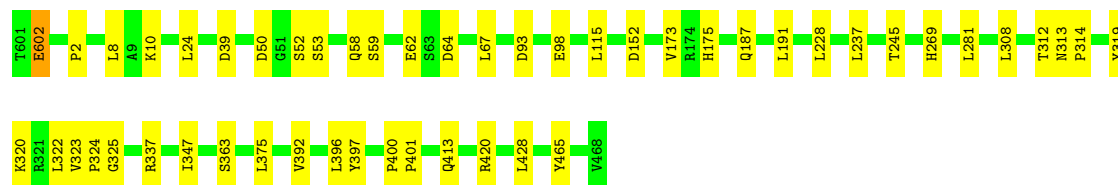
- Molecule 1: glutamine synthetase

Chain 3-A: 90% 10%



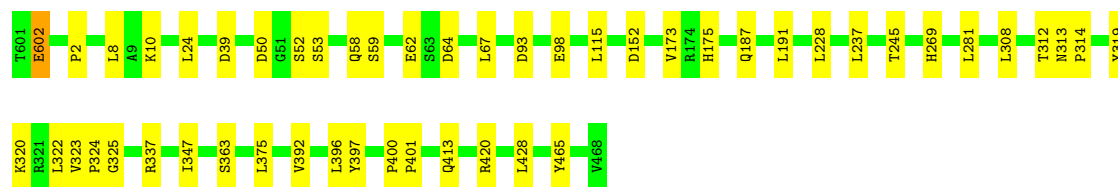
- Molecule 1: glutamine synthetase

Chain 3-B: 90% 10%



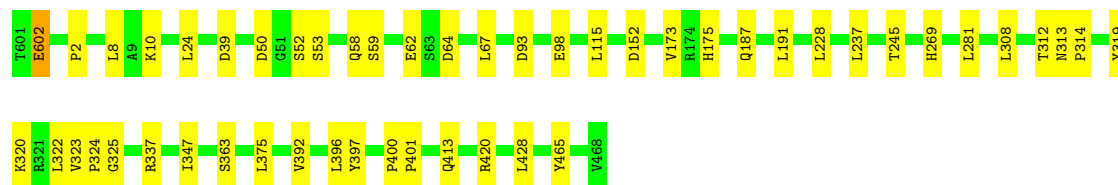
- Molecule 1: glutamine synthetase

Chain 3-C: 90% 10%



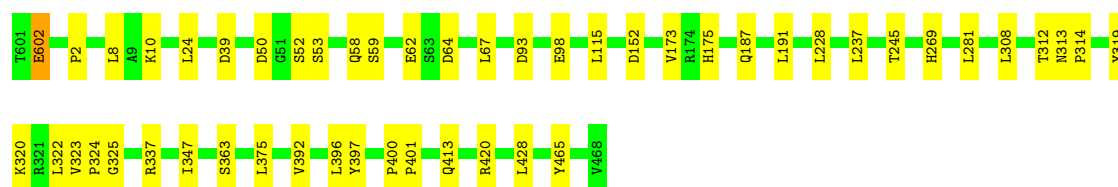
- Molecule 1: glutamine synthetase

Chain 3-D: 90% 10%



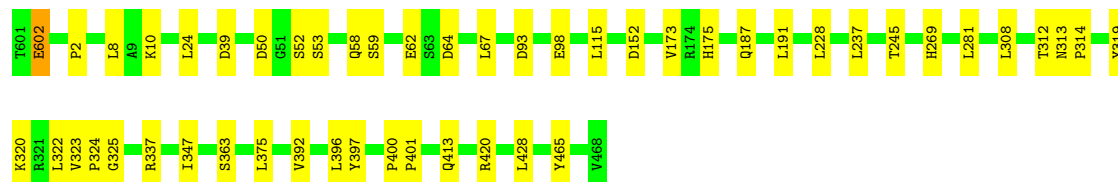
- Molecule 1: glutamine synthetase

Chain 3-E: 90% 10%



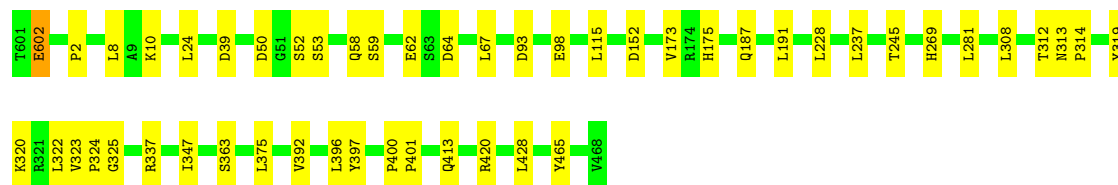
- Molecule 1: glutamine synthetase

Chain 3-F: 90% 10%



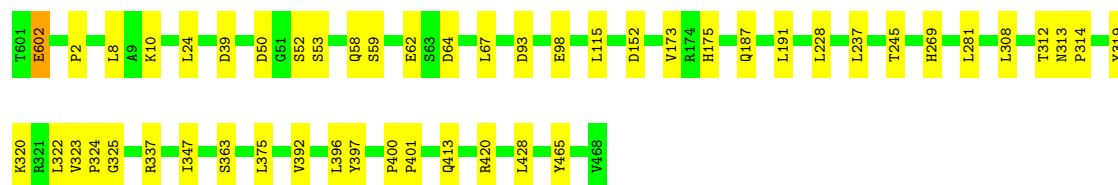
- Molecule 1: glutamine synthetase

Chain 3-G: 90% 10%



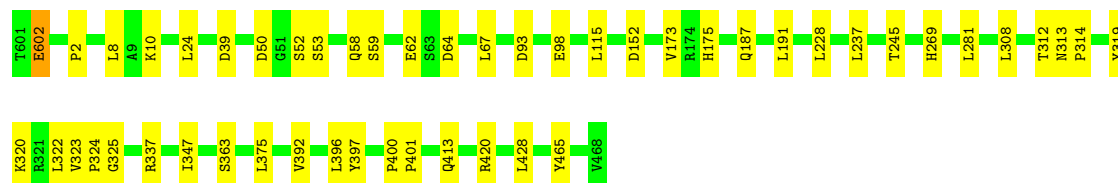
- Molecule 1: glutamine synthetase

Chain 3-H: 90% 10%



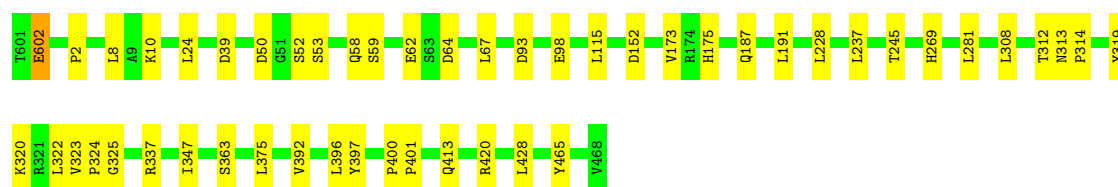
- Molecule 1: glutamine synthetase

Chain 3-I: 90% 10%



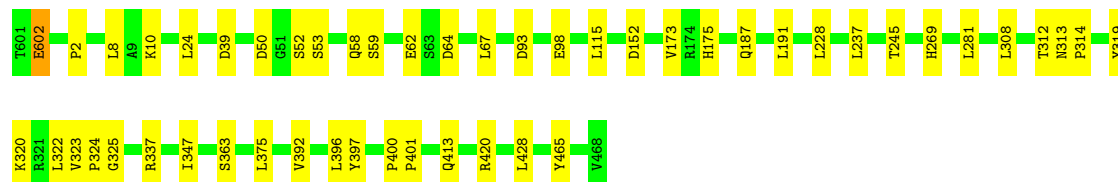
- Molecule 1: glutamine synthetase

Chain 3-J: 90% 10%



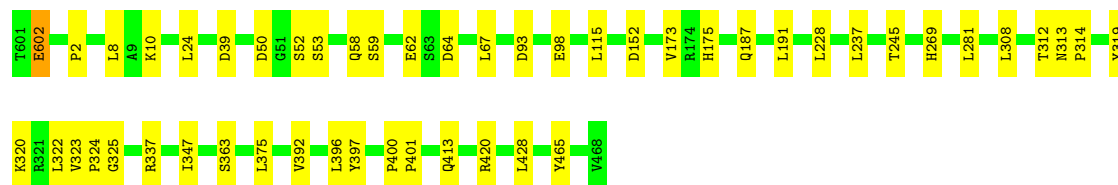
- Molecule 1: glutamine synthetase

Chain 3-K:  90% 10%



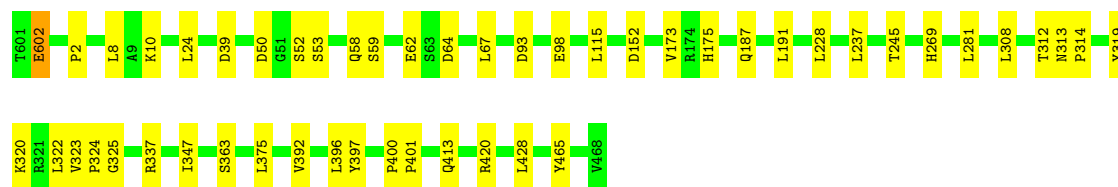
- Molecule 1: glutamine synthetase

Chain 3-L:  90% 10%



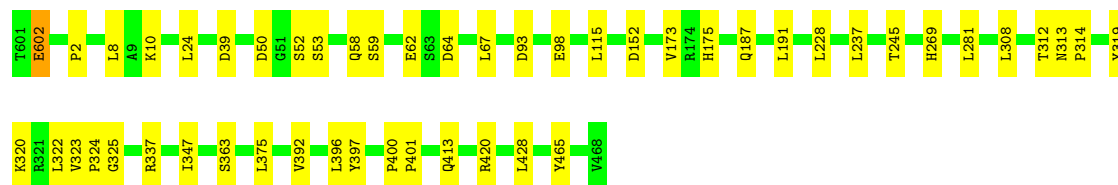
- Molecule 1: glutamine synthetase

Chain 3-M:  90% 10%



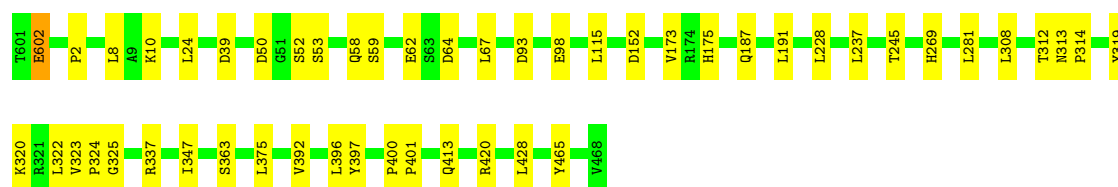
- Molecule 1: glutamine synthetase

Chain 3-N:  90% 10%



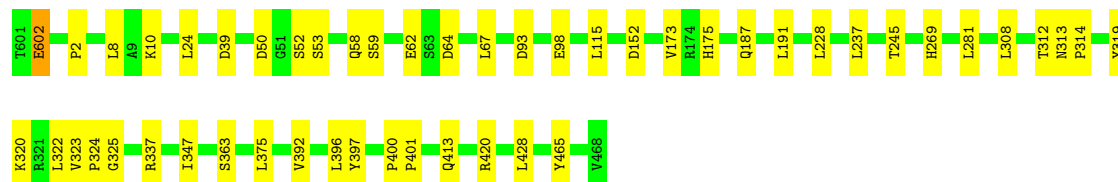
- Molecule 1: glutamine synthetase

Chain 3-O:  90% 10%



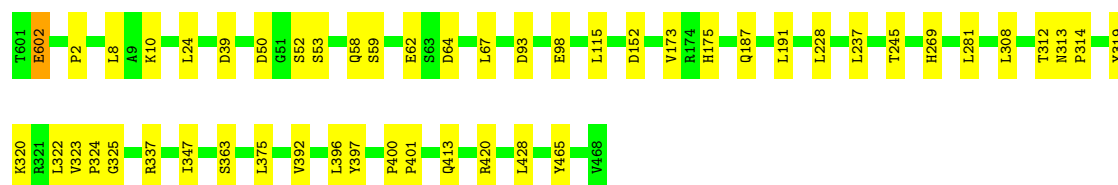
- Molecule 1: glutamine synthetase

Chain 3-P: 90% 10%



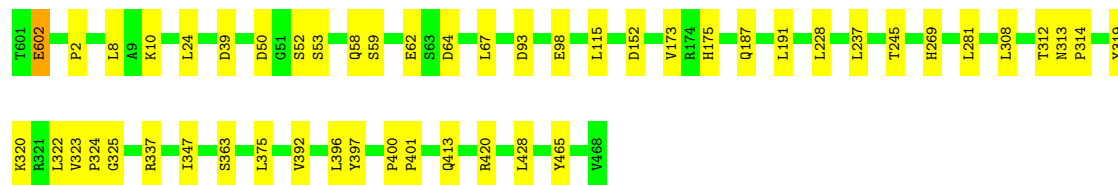
- Molecule 1: glutamine synthetase

Chain 3-Q: 90% 10%



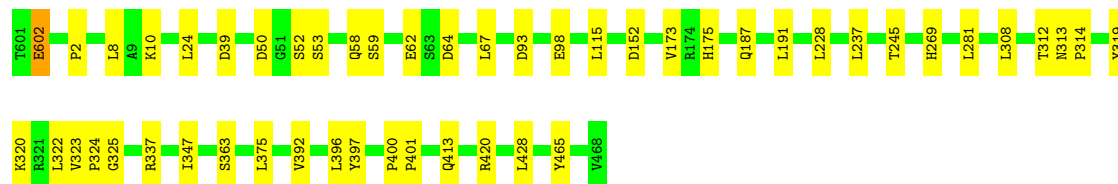
- Molecule 1: glutamine synthetase

Chain 3-R: 90% 10%



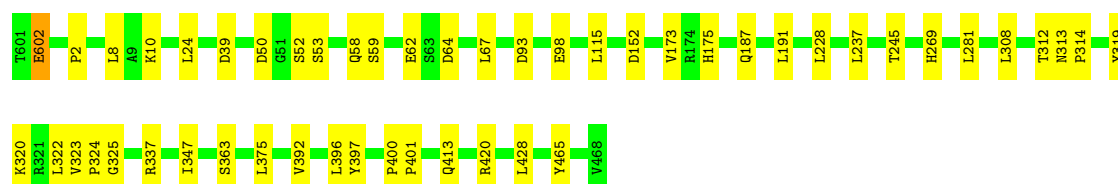
- Molecule 1: glutamine synthetase

Chain 3-S: 90% 10%



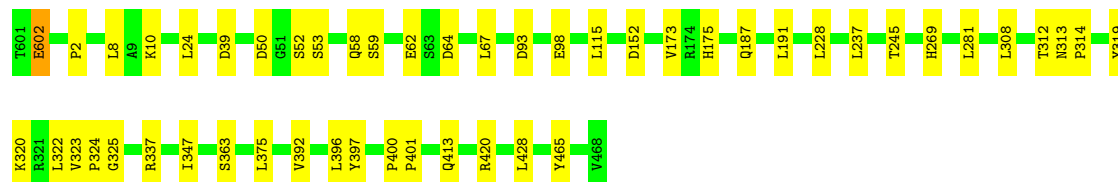
- Molecule 1: glutamine synthetase

Chain 3-T: 90% 10%



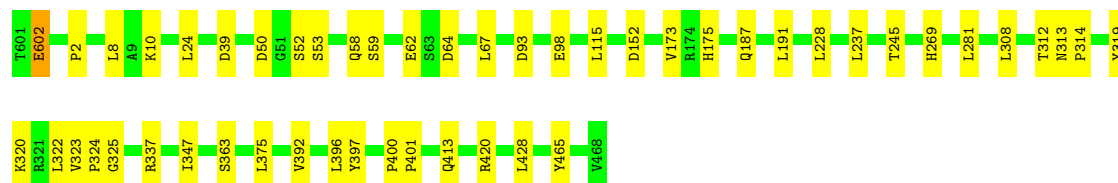
- Molecule 1: glutamine synthetase

Chain 3-U: 90% 10%



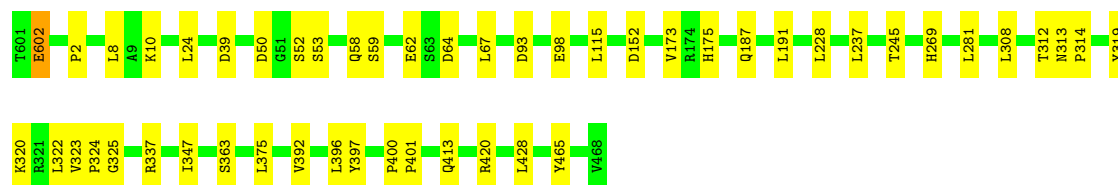
- Molecule 1: glutamine synthetase

Chain 3-V: 90% 10%



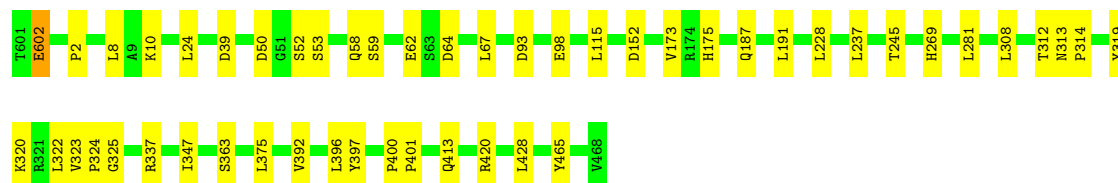
- Molecule 1: glutamine synthetase

Chain 3-W: 90% 10%



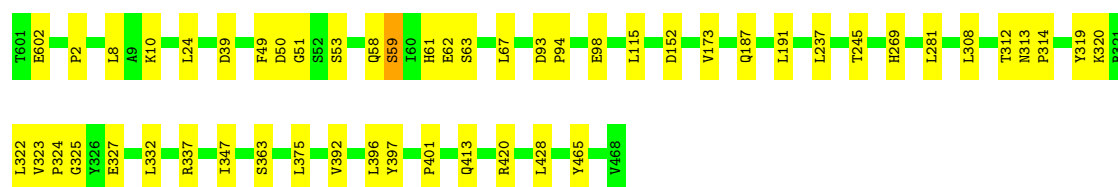
- Molecule 1: glutamine synthetase

Chain 3-X: 90% 10%



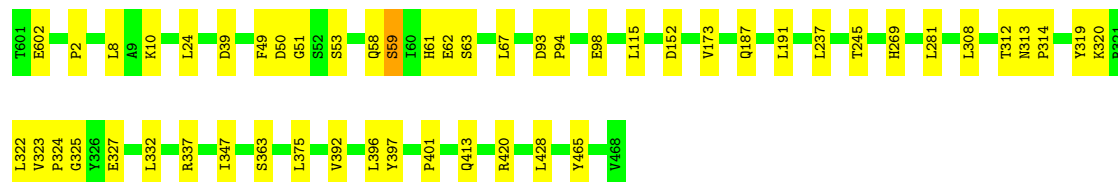
- Molecule 1: glutamine synthetase

Chain 4-A: 89% 11%



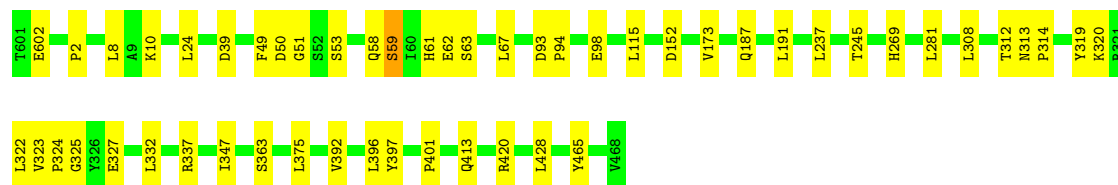
- Molecule 1: glutamine synthetase

Chain 4-B: 89% 11%



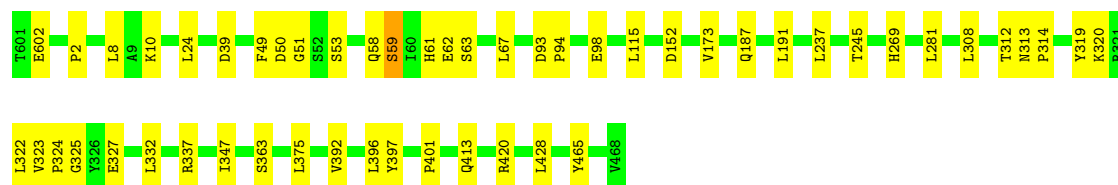
- Molecule 1: glutamine synthetase

Chain 4-C: 89% 11%



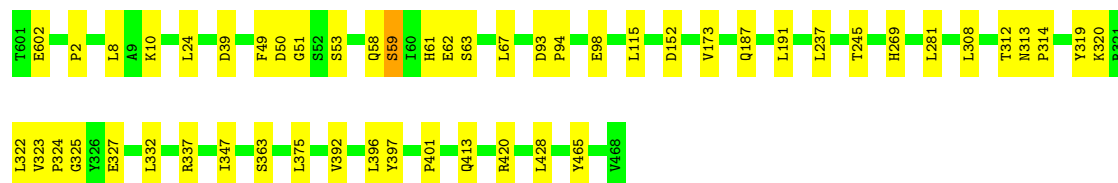
- Molecule 1: glutamine synthetase

Chain 4-D: 89% 11%



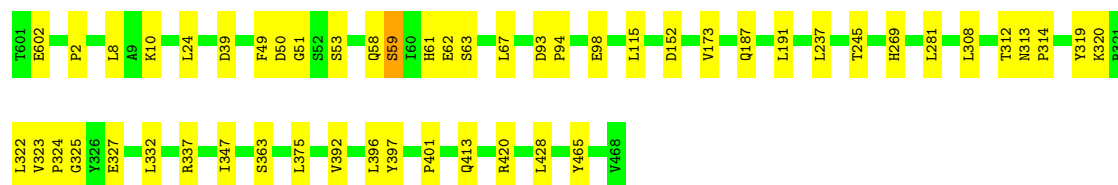
- Molecule 1: glutamine synthetase

Chain 4-E: 89% 11%



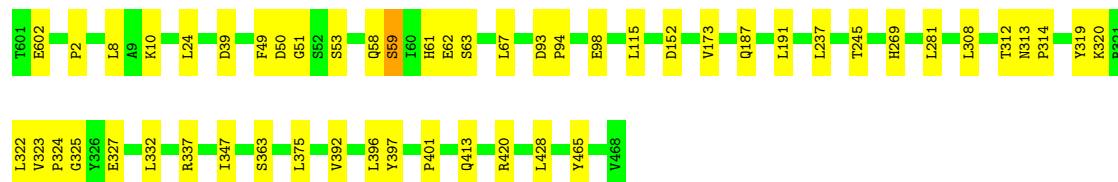
- Molecule 1: glutamine synthetase

Chain 4-F: 89% 11%



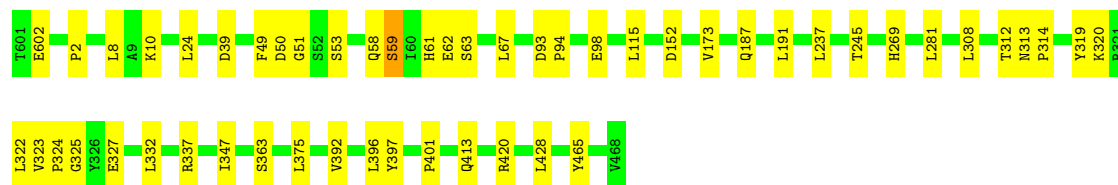
- Molecule 1: glutamine synthetase

Chain 4-G: 89% 11%



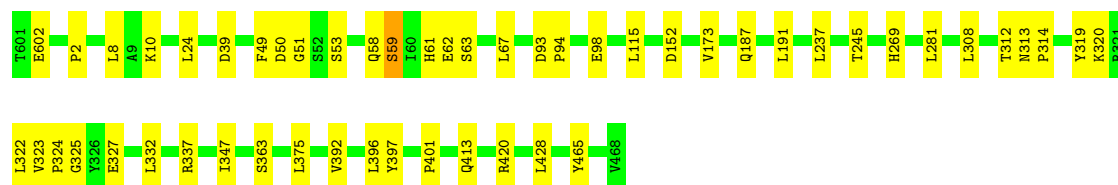
- Molecule 1: glutamine synthetase

Chain 4-H: 89% 11%



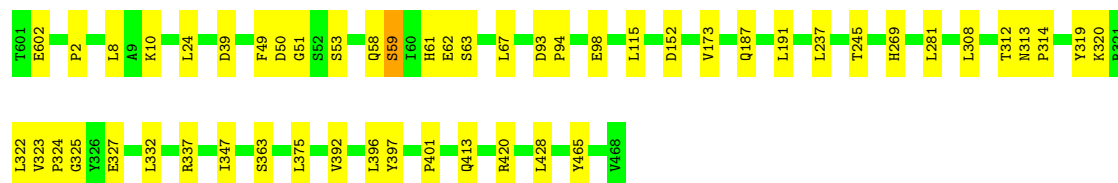
- Molecule 1: glutamine synthetase

Chain 4-I: 89% 11%



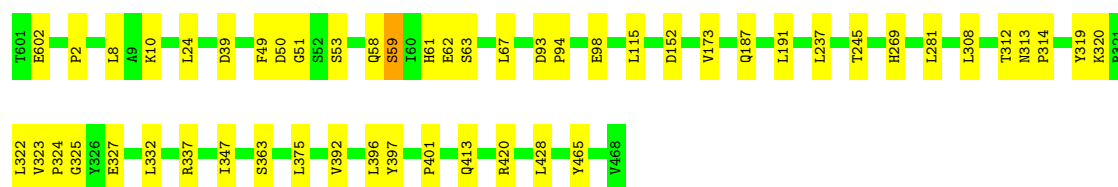
- Molecule 1: glutamine synthetase

Chain 4-J: 89% 11%



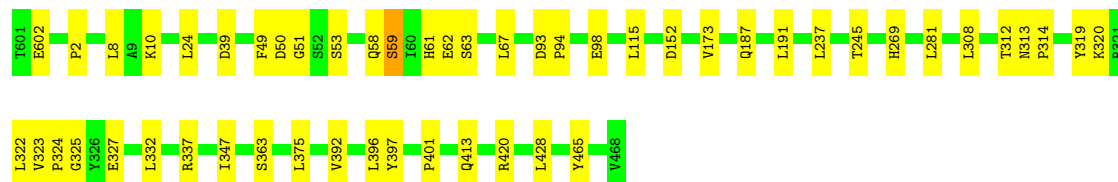
- Molecule 1: glutamine synthetase

Chain 4-K: 89% 11%



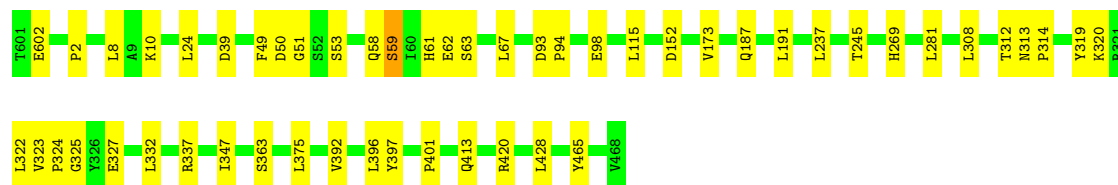
- Molecule 1: glutamine synthetase

Chain 4-L: 89% 11%



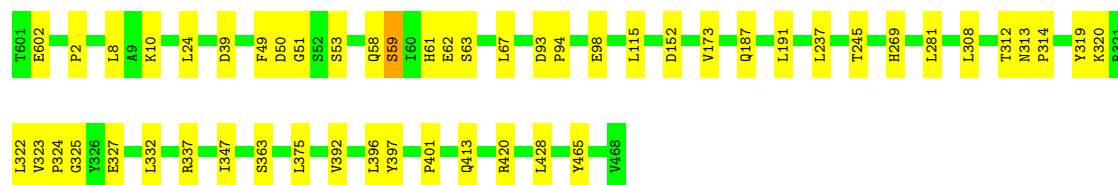
- Molecule 1: glutamine synthetase

Chain 4-M: 89% 11%



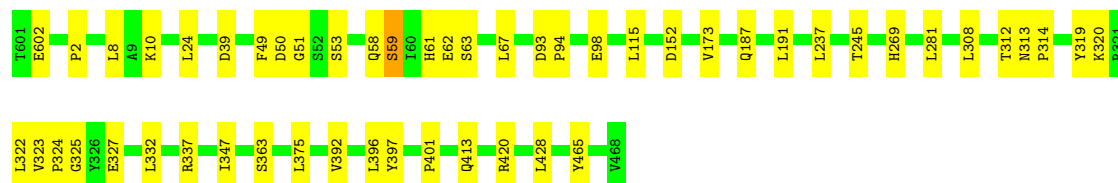
- Molecule 1: glutamine synthetase

Chain 4-N: 89% 11%



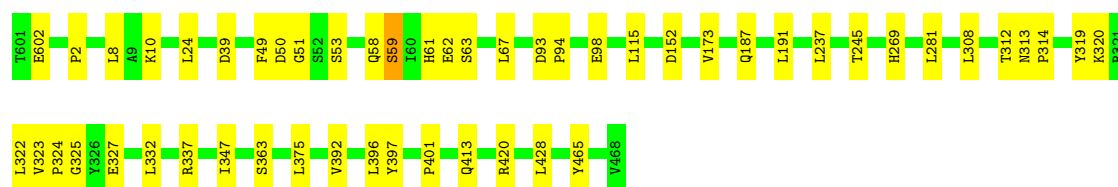
- Molecule 1: glutamine synthetase

Chain 4-O: 89% 11%



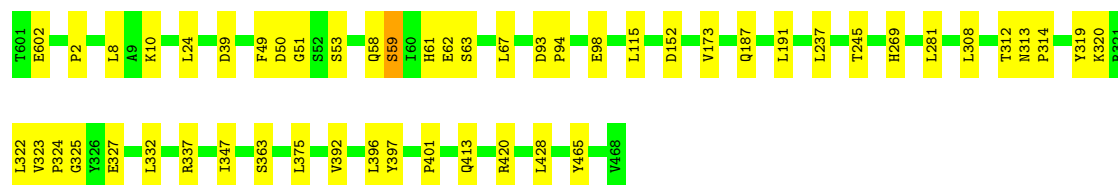
- Molecule 1: glutamine synthetase

Chain 4-P: 89% 11%



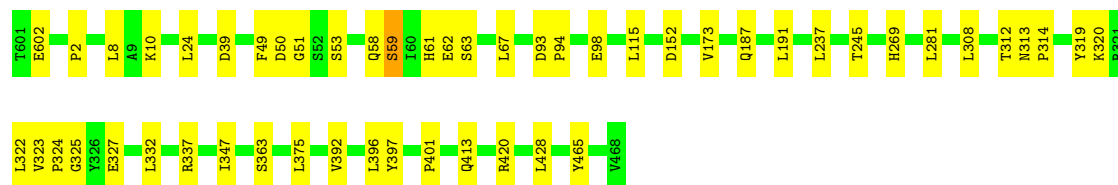
- Molecule 1: glutamine synthetase

Chain 4-Q: 89% 11%



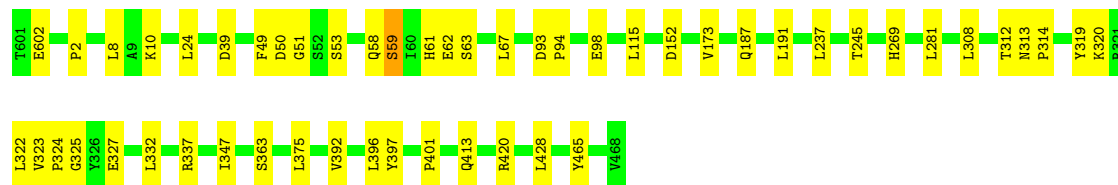
- Molecule 1: glutamine synthetase

Chain 4-R: 89% 11%



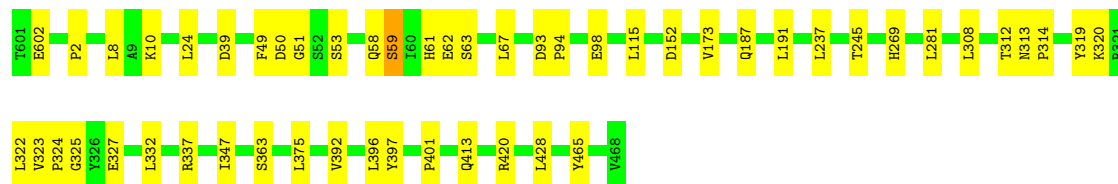
- Molecule 1: glutamine synthetase

Chain 4-S: 89% 11%



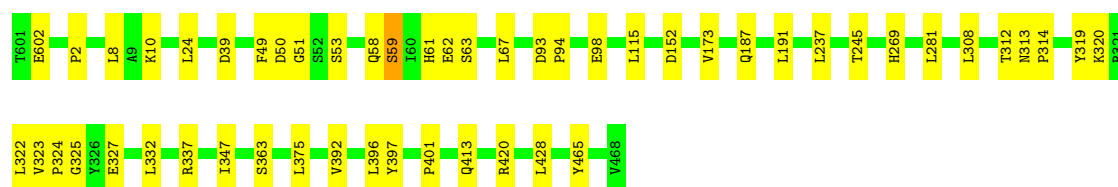
- Molecule 1: glutamine synthetase

Chain 4-T: 89% 11%



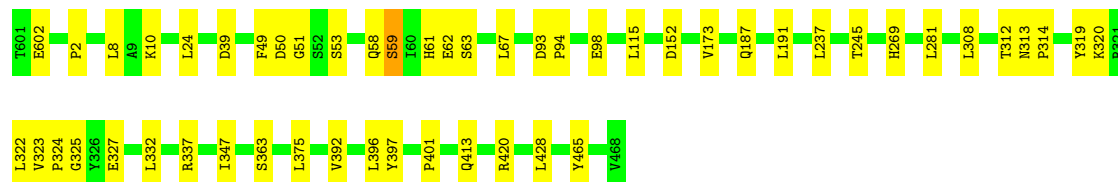
- Molecule 1: glutamine synthetase

Chain 4-U: 89% 11%



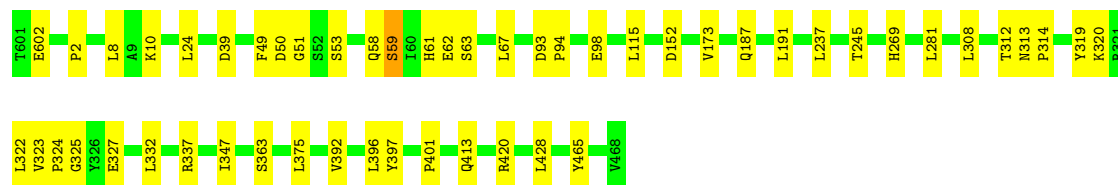
- Molecule 1: glutamine synthetase

Chain 4-V:  89% 11%



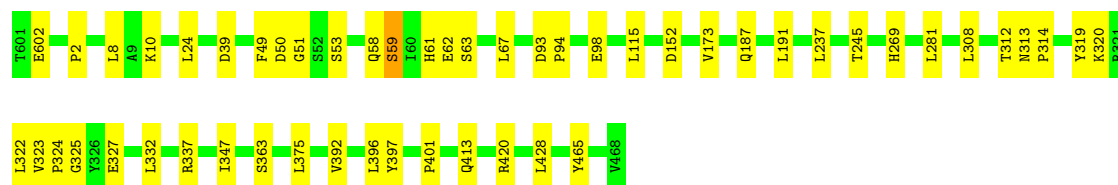
- Molecule 1: glutamine synthetase

Chain 4-W:  89% 11%



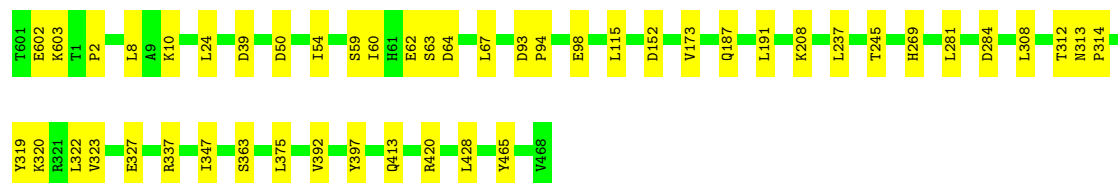
- Molecule 1: glutamine synthetase

Chain 4-X:  89% 11%



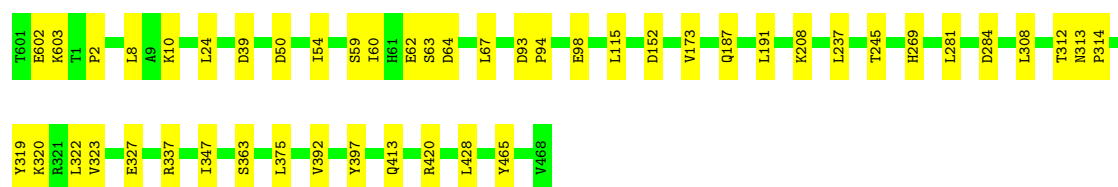
- Molecule 1: glutamine synthetase

Chain 5-A:  90% 10%



- Molecule 1: glutamine synthetase

Chain 5-B:  90% 10%



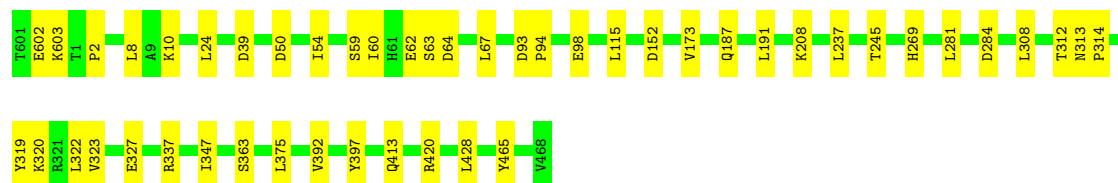
- Molecule 1: glutamine synthetase

Chain 5-C:  90% 10%



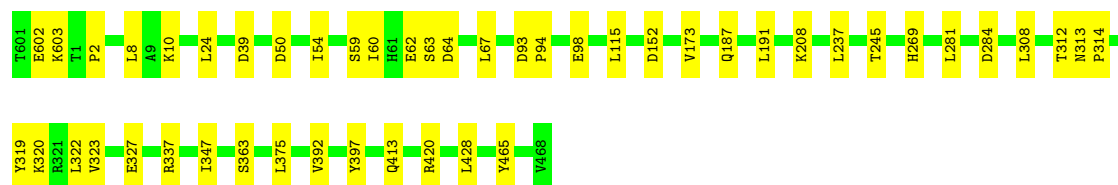
- Molecule 1: glutamine synthetase

Chain 5-D:  90% 10%



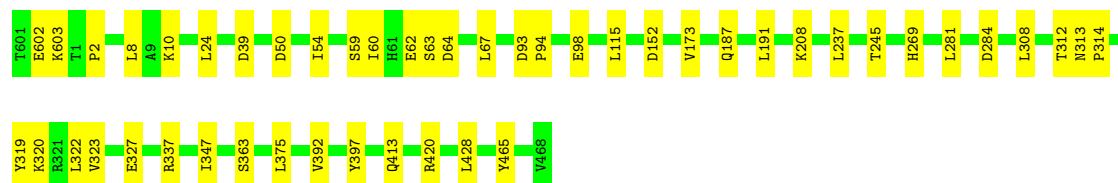
- Molecule 1: glutamine synthetase

Chain 5-E:  90% 10%



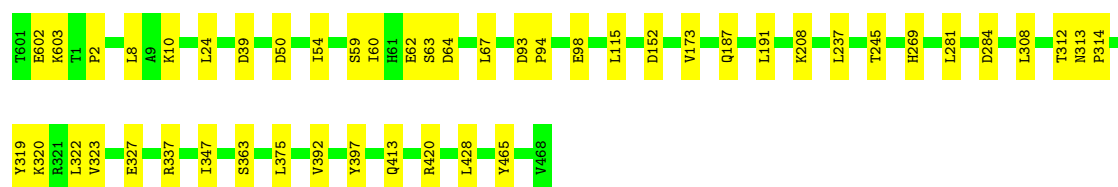
- Molecule 1: glutamine synthetase

Chain 5-F:  90% 10%



- Molecule 1: glutamine synthetase

Chain 5-G:  90% 10%



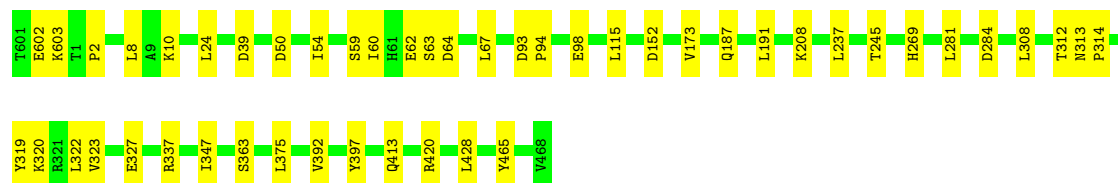
- Molecule 1: glutamine synthetase

Chain 5-H: 90% 10%



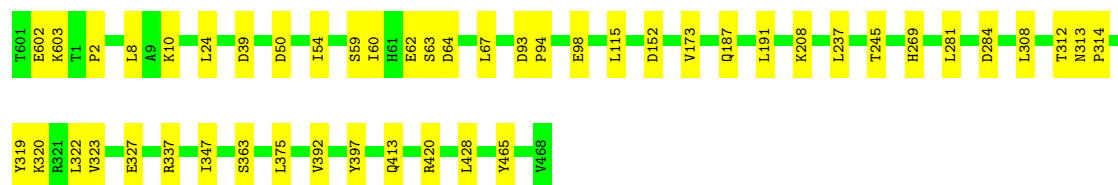
- Molecule 1: glutamine synthetase

Chain 5-I: 90% 10%



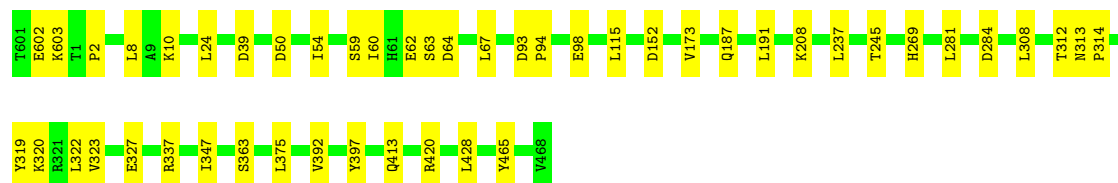
- Molecule 1: glutamine synthetase

Chain 5-J: 90% 10%



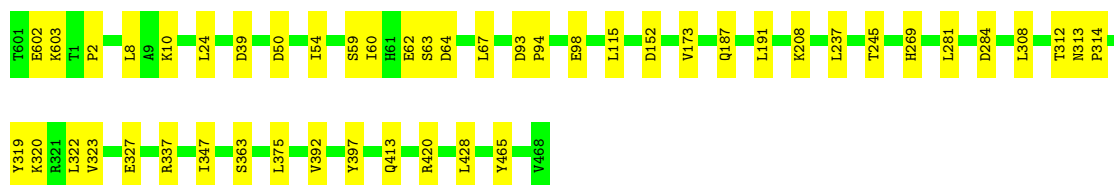
- Molecule 1: glutamine synthetase

Chain 5-K: 90% 10%



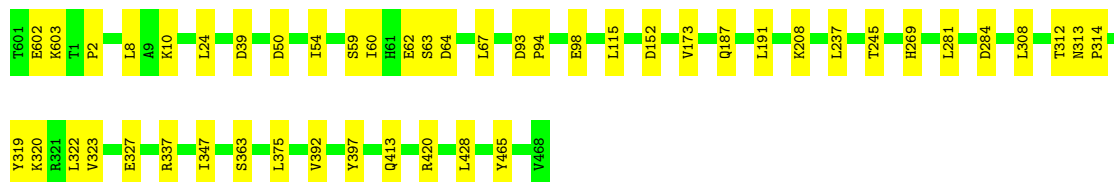
- Molecule 1: glutamine synthetase

Chain 5-L: 90% 10%



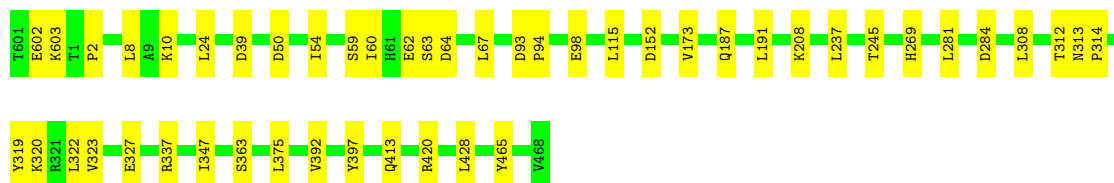
- Molecule 1: glutamine synthetase

Chain 5-M:  90% 10%



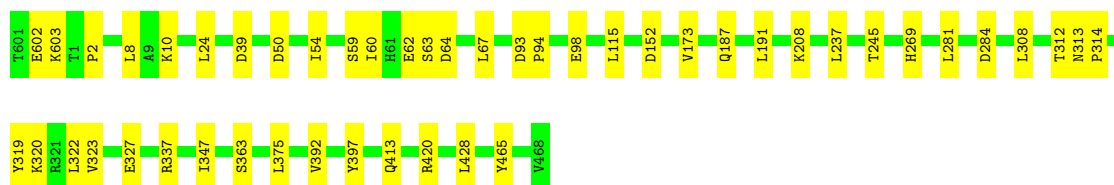
- Molecule 1: glutamine synthetase

Chain 5-N:  90% 10%



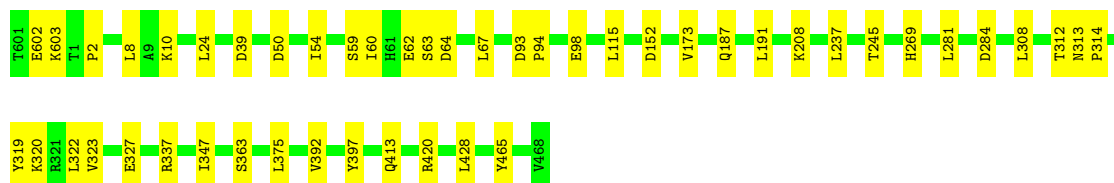
- Molecule 1: glutamine synthetase

Chain 5-O:  90% 10%



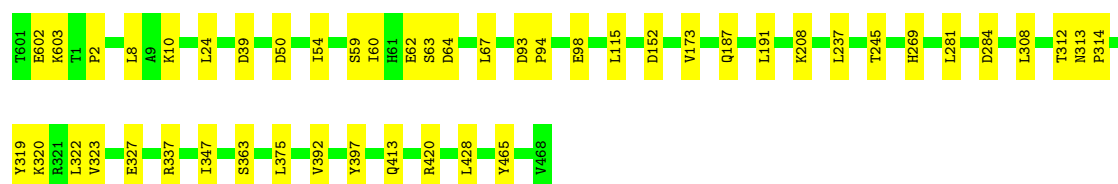
- Molecule 1: glutamine synthetase

Chain 5-P:  90% 10%



- Molecule 1: glutamine synthetase

Chain 5-Q:  90% 10%



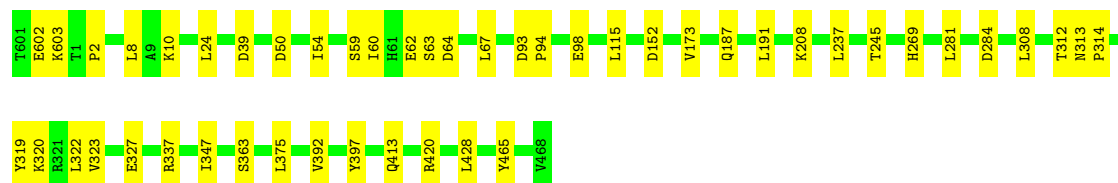
- Molecule 1: glutamine synthetase

Chain 5-R: 90% 10%



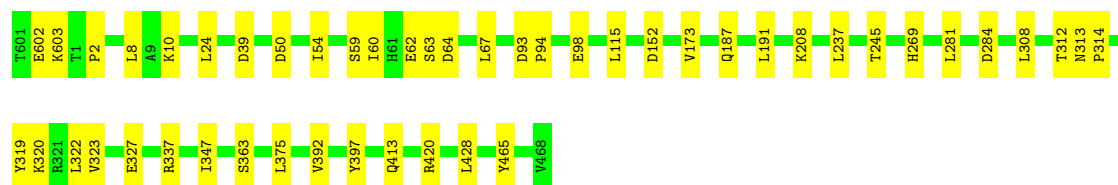
- Molecule 1: glutamine synthetase

Chain 5-S: 90% 10%



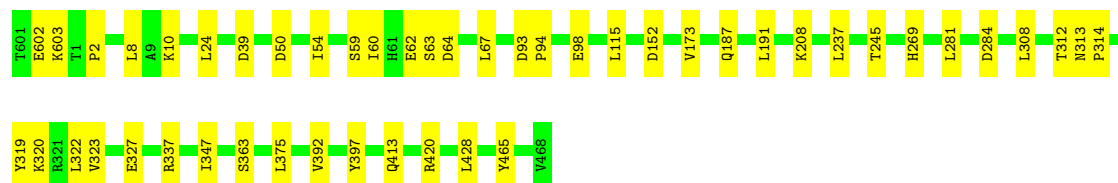
- Molecule 1: glutamine synthetase

Chain 5-T: 90% 10%



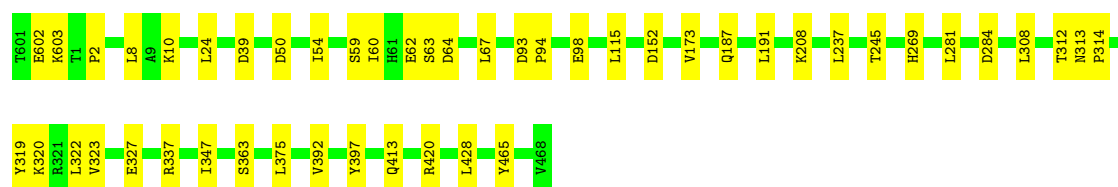
- Molecule 1: glutamine synthetase

Chain 5-U: 90% 10%



- Molecule 1: glutamine synthetase

Chain 5-V: 90% 10%



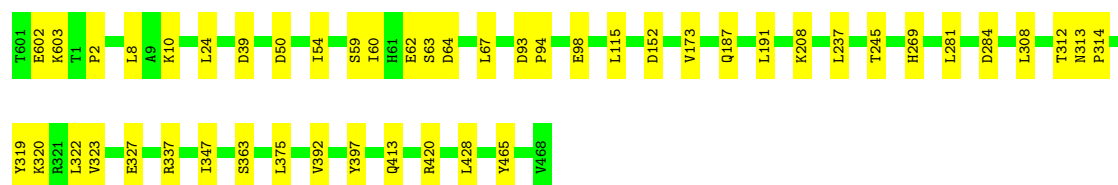
- Molecule 1: glutamine synthetase

Chain 5-W: 90% 10%



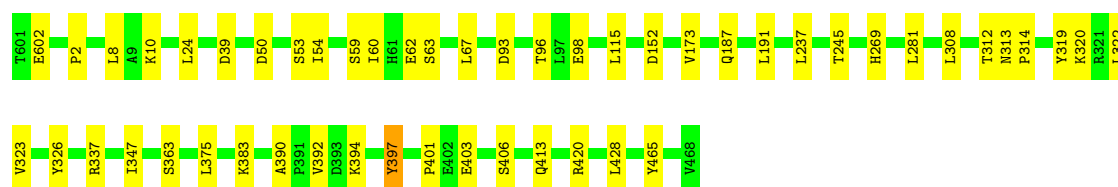
- Molecule 1: glutamine synthetase

Chain 5-X: 90% 10%



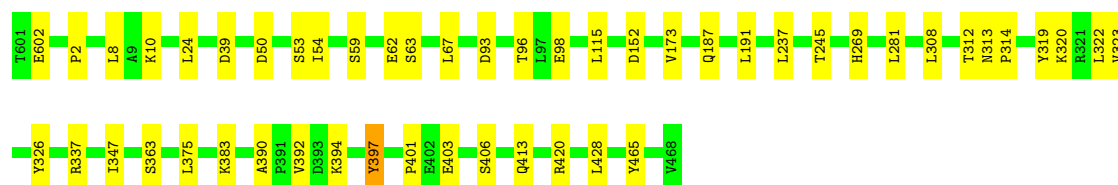
- Molecule 1: glutamine synthetase

Chain 6-A: 89% 10%



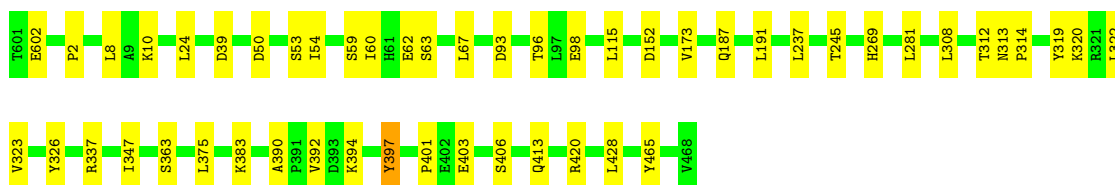
- Molecule 1: glutamine synthetase

Chain 6-B: 90% 10%



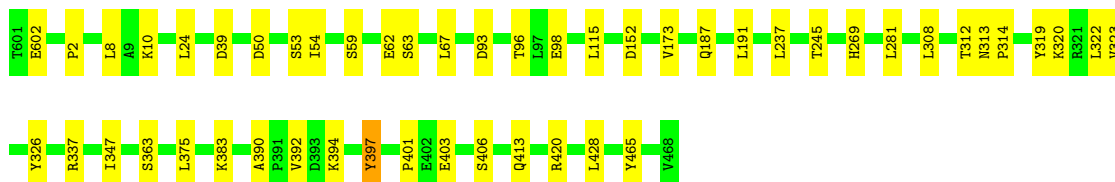
- Molecule 1: glutamine synthetase

Chain 6-C: 89% 10%



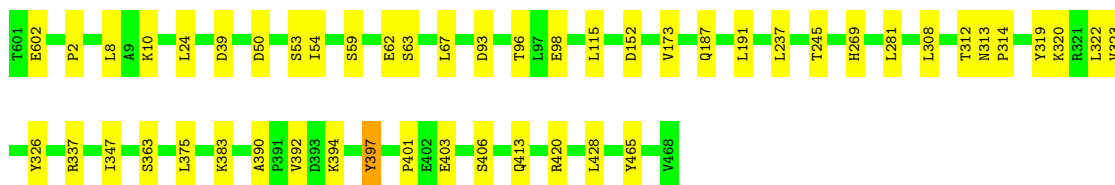
- Molecule 1: glutamine synthetase

Chain 6-D: 90% 10%



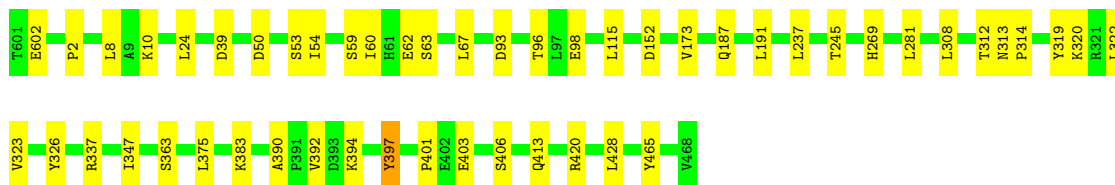
- Molecule 1: glutamine synthetase

Chain 6-E: 90% 10%



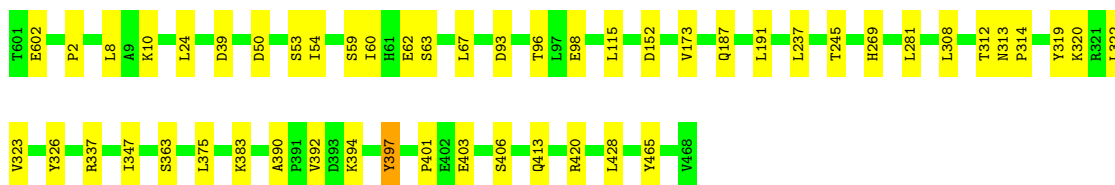
- Molecule 1: glutamine synthetase

Chain 6-F: 89% 10%



- Molecule 1: glutamine synthetase

Chain 6-G: 89% 10%



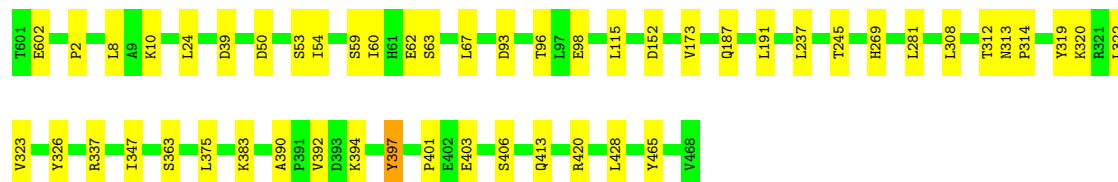
- Molecule 1: glutamine synthetase

Chain 6-H: 90% 10%



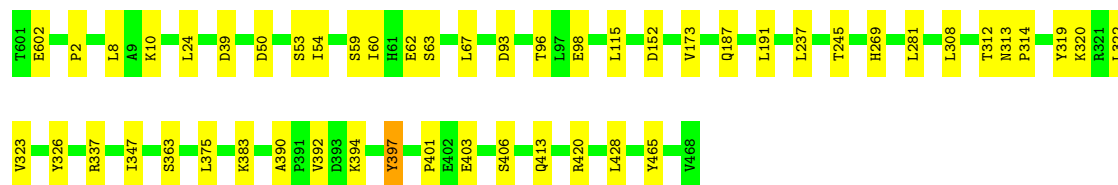
- Molecule 1: glutamine synthetase

Chain 6-I: 89% 10%



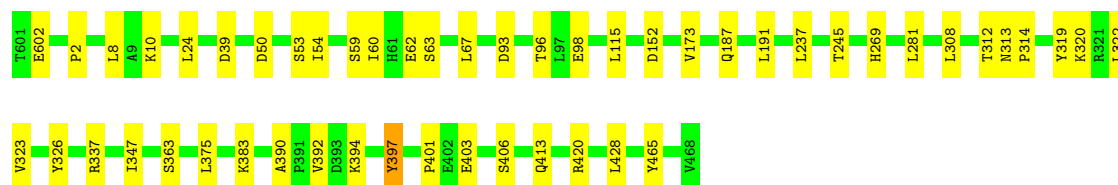
- Molecule 1: glutamine synthetase

Chain 6-J: 89% 10%



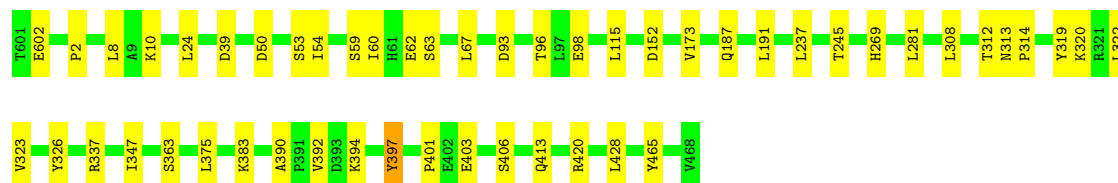
- Molecule 1: glutamine synthetase

Chain 6-K: 89% 10%



- Molecule 1: glutamine synthetase

Chain 6-L: 89% 10%



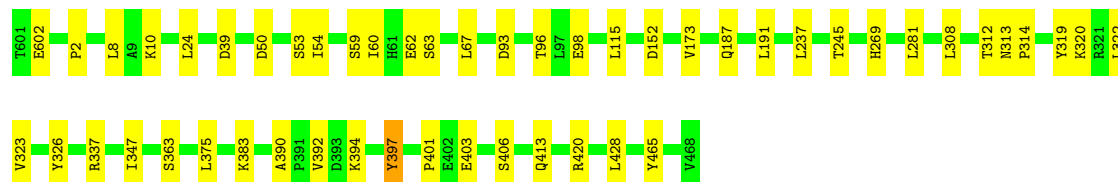
- Molecule 1: glutamine synthetase

Chain 6-M: 90% 10%



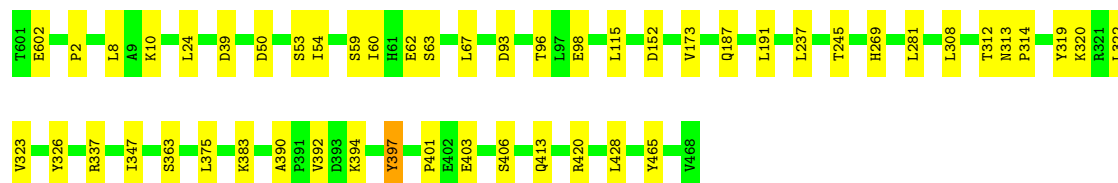
- Molecule 1: glutamine synthetase

Chain 6-N: 89% 10%



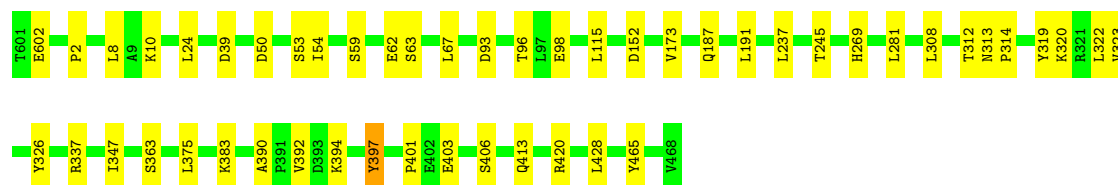
- Molecule 1: glutamine synthetase

Chain 6-O: 89% 10%



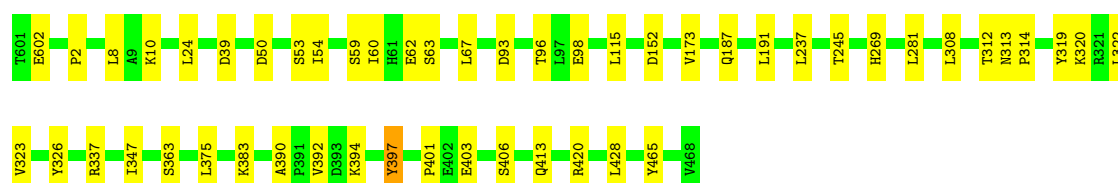
- Molecule 1: glutamine synthetase

Chain 6-P: 90% 10%



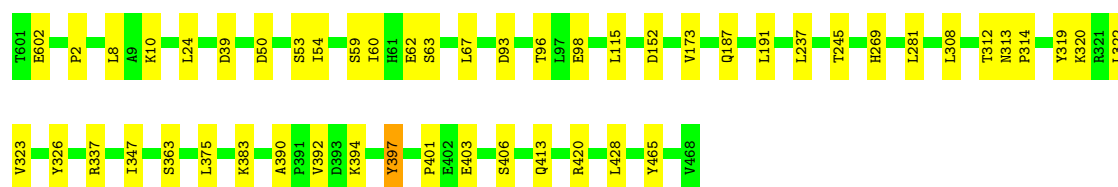
- Molecule 1: glutamine synthetase

Chain 6-Q: 89% 10%



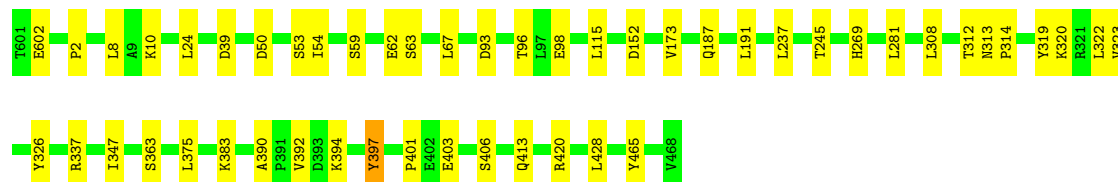
- Molecule 1: glutamine synthetase

Chain 6-R: 89% 10%



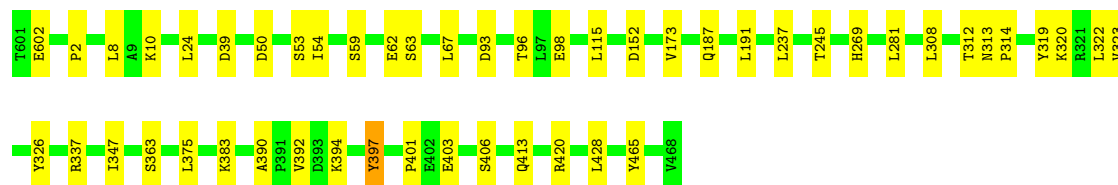
- Molecule 1: glutamine synthetase

Chain 6-S: 90% 10%



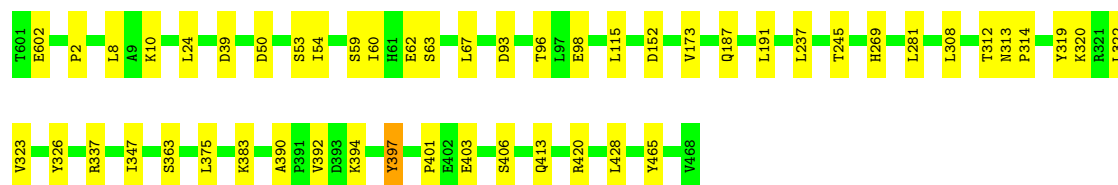
- Molecule 1: glutamine synthetase

Chain 6-T: 90% 10%



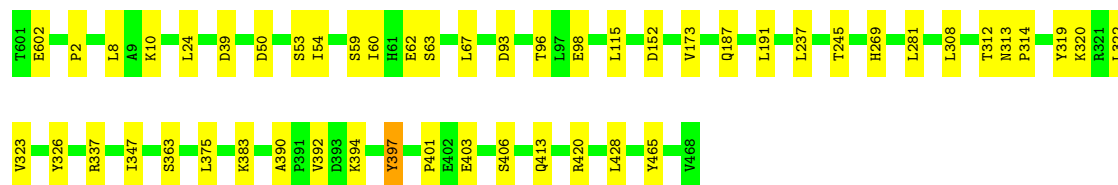
- Molecule 1: glutamine synthetase

Chain 6-U: 89% 10%



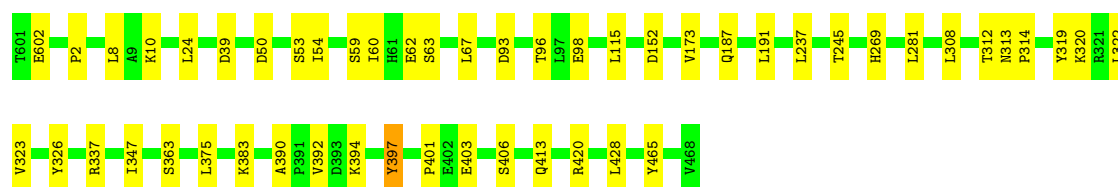
- Molecule 1: glutamine synthetase

Chain 6-V: 89% 10%



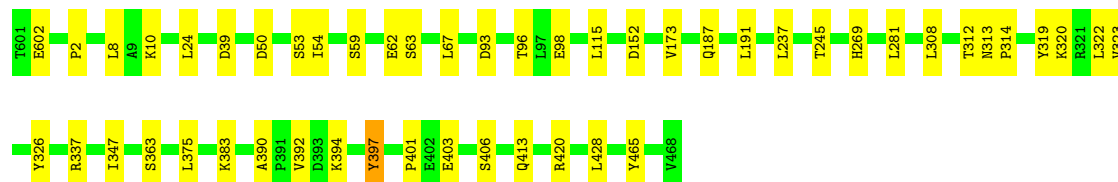
- Molecule 1: glutamine synthetase

Chain 6-W: 89% 10%



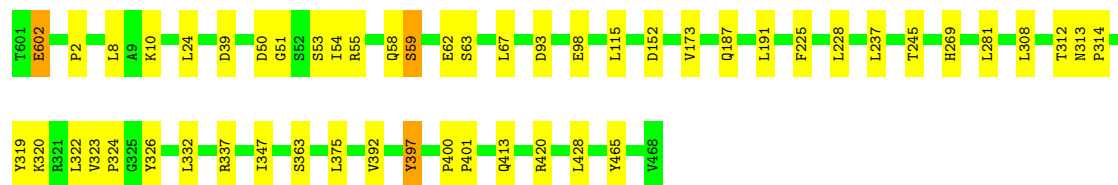
- Molecule 1: glutamine synthetase

Chain 6-X: 90% 10%



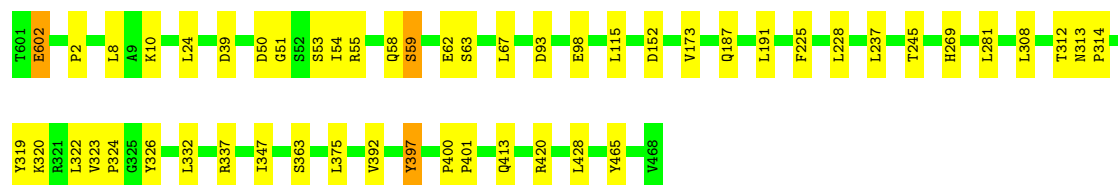
- Molecule 1: glutamine synthetase

Chain 7-A: 89% 10%



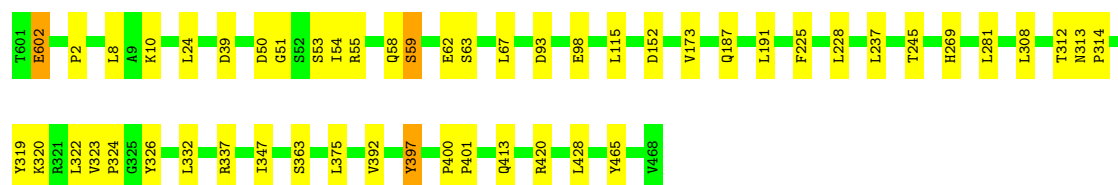
- Molecule 1: glutamine synthetase

Chain 7-B: 89% 10%



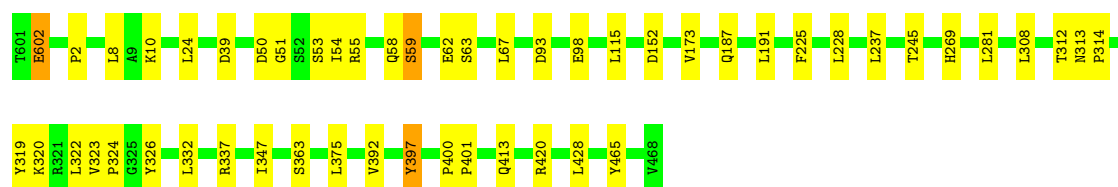
- Molecule 1: glutamine synthetase

Chain 7-C: 89% 10%



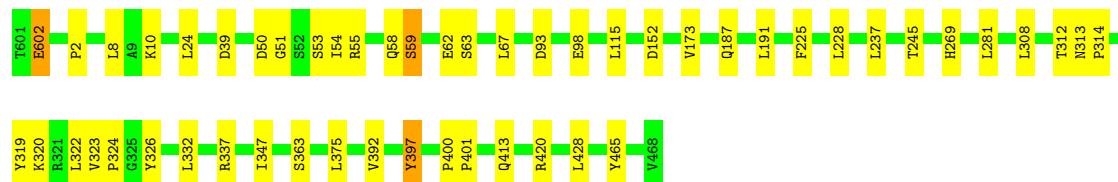
- Molecule 1: glutamine synthetase

Chain 7-D: 89% 10%



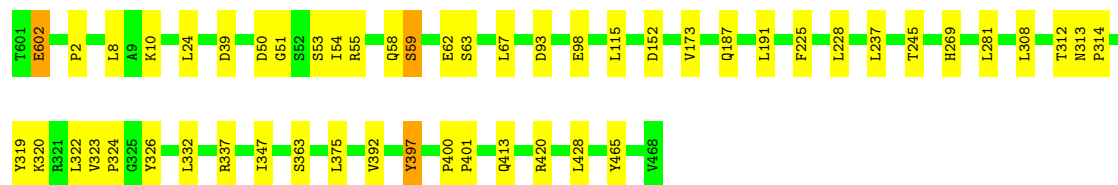
- Molecule 1: glutamine synthetase

Chain 7-E: 89% 10%



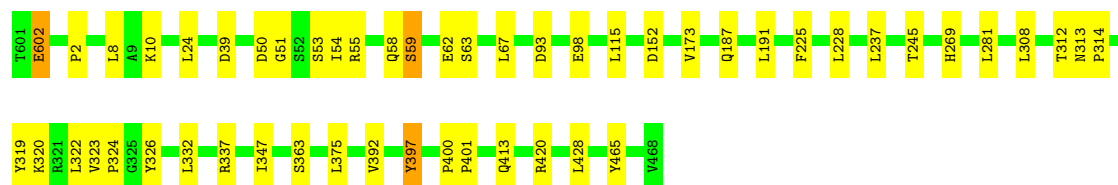
- Molecule 1: glutamine synthetase

Chain 7-F: 89% 10%



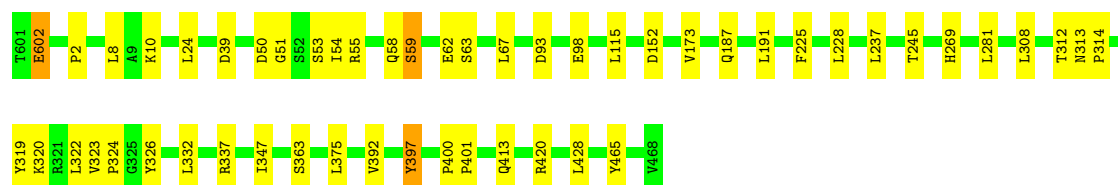
- Molecule 1: glutamine synthetase

Chain 7-G: 89% 10%



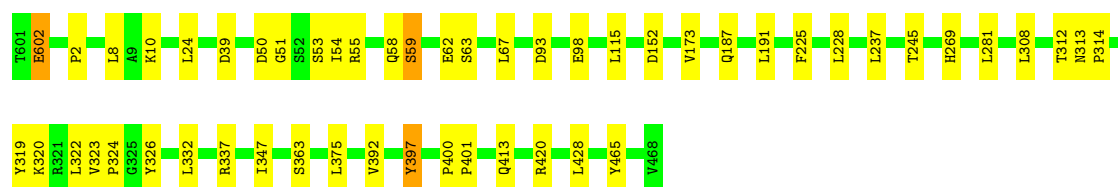
- Molecule 1: glutamine synthetase

Chain 7-H: 89% 10%



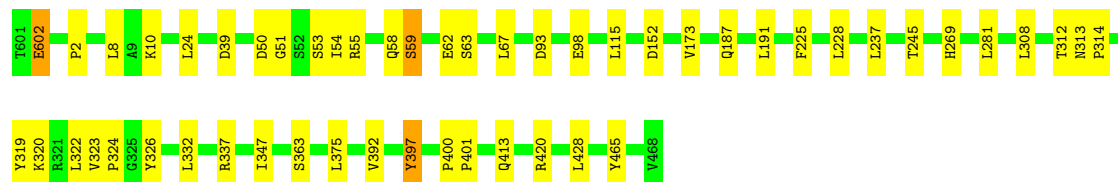
- Molecule 1: glutamine synthetase

Chain 7-I: 89% 10%



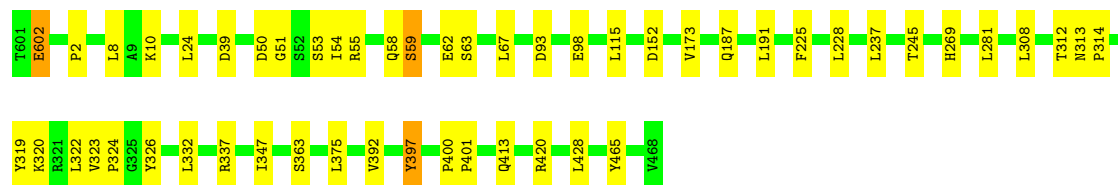
- Molecule 1: glutamine synthetase

Chain 7-J: 89% 10%



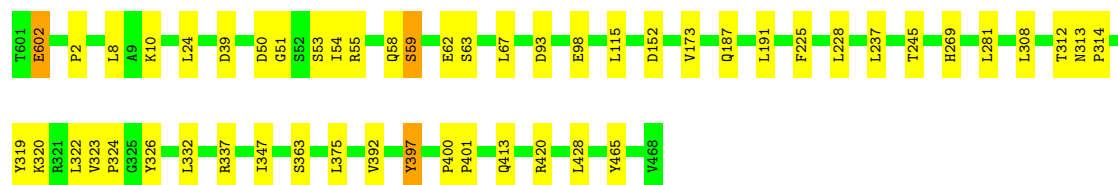
- Molecule 1: glutamine synthetase

Chain 7-K: 89% 10%



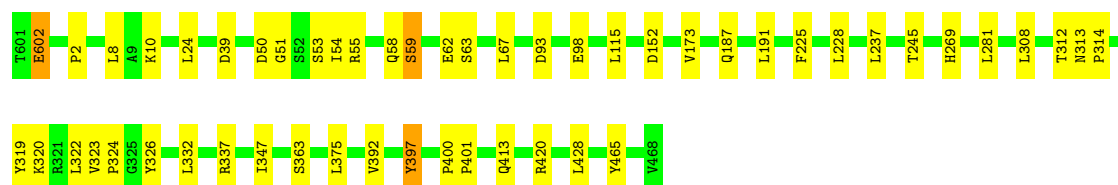
- Molecule 1: glutamine synthetase

Chain 7-L: 89% 10%



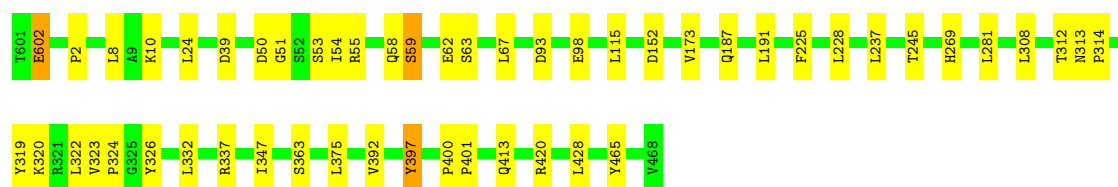
- Molecule 1: glutamine synthetase

Chain 7-M: 89% 10%



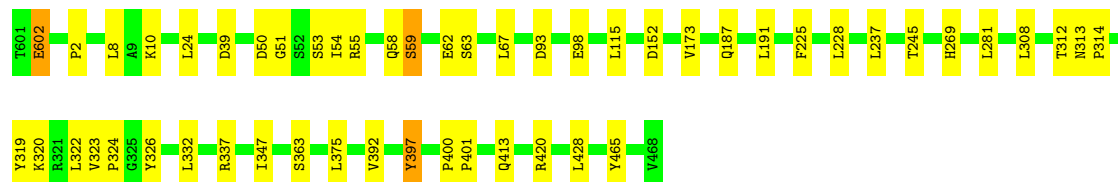
- Molecule 1: glutamine synthetase

Chain 7-N: 89% 10%



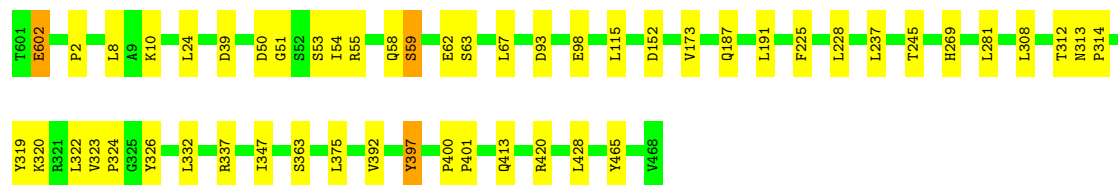
- Molecule 1: glutamine synthetase

Chain 7-O: 89% 10% .



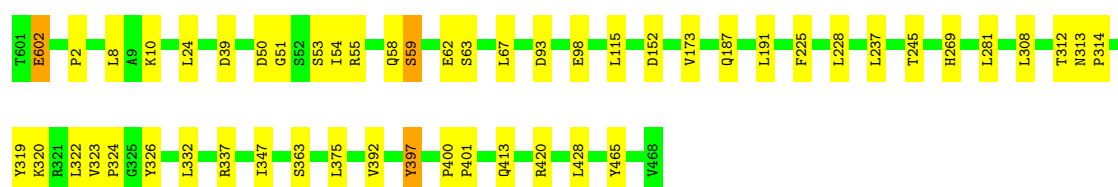
- Molecule 1: glutamine synthetase

Chain 7-P: 89% 10% .



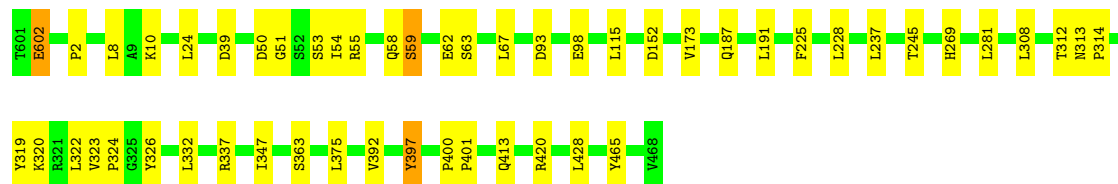
- Molecule 1: glutamine synthetase

Chain 7-Q: 89% 10% .



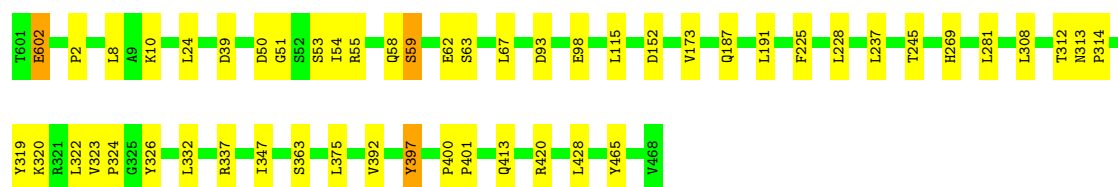
- Molecule 1: glutamine synthetase

Chain 7-R: 89% 10% .



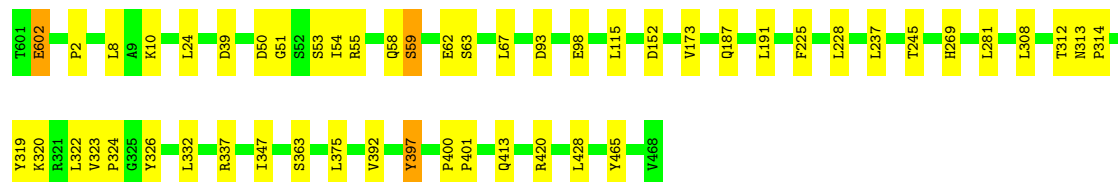
- Molecule 1: glutamine synthetase

Chain 7-S: 89% 10% .



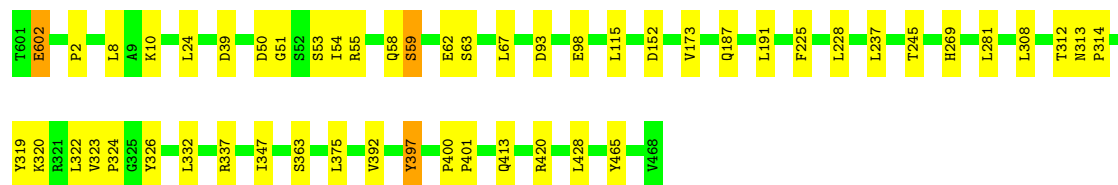
- Molecule 1: glutamine synthetase

Chain 7-T:  89% 10% .



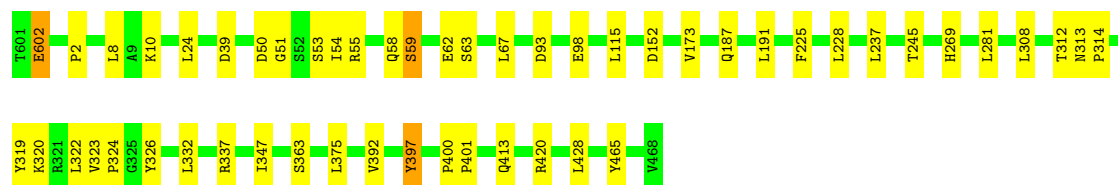
- Molecule 1: glutamine synthetase

Chain 7-U:  89% 10% .



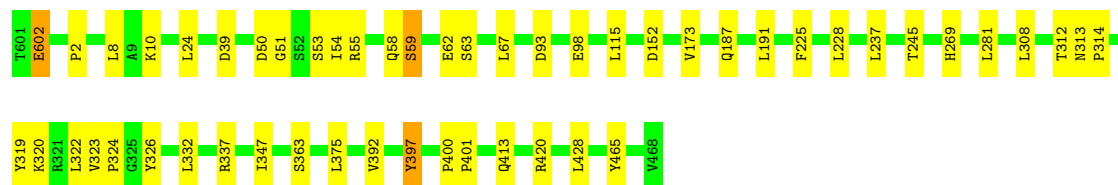
- Molecule 1: glutamine synthetase

Chain 7-V:  89% 10% .



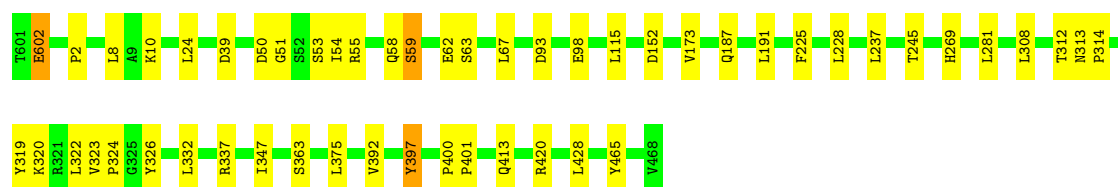
- Molecule 1: glutamine synthetase

Chain 7-W:  89% 10% .



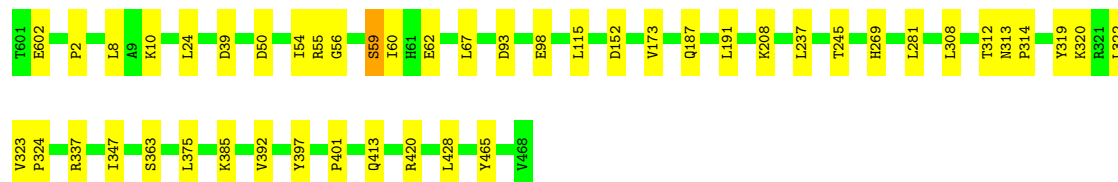
- Molecule 1: glutamine synthetase

Chain 7-X:  89% 10% .



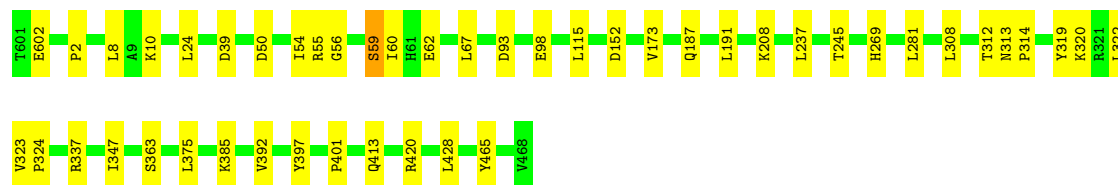
- Molecule 1: glutamine synthetase

Chain 8-A: 90% 10%



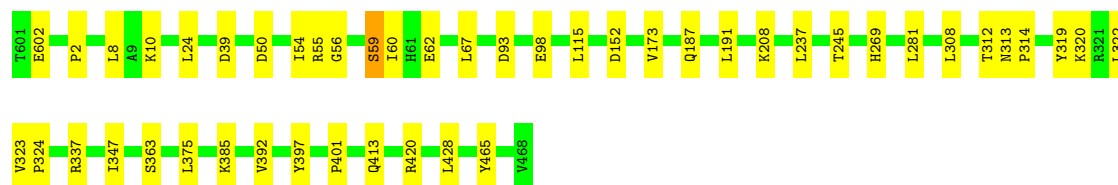
- Molecule 1: glutamine synthetase

Chain 8-B: 90% 10%



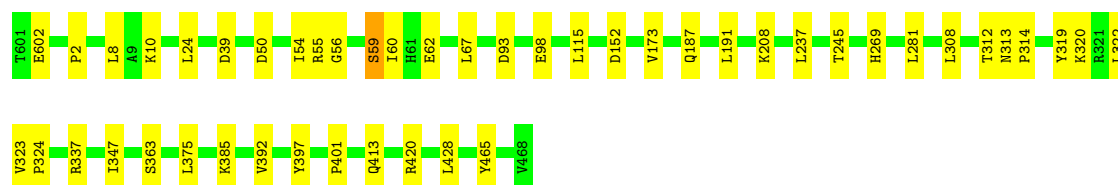
- Molecule 1: glutamine synthetase

Chain 8-C: 90% 10%



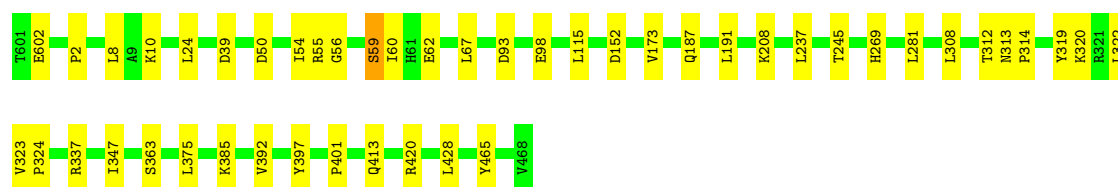
- Molecule 1: glutamine synthetase

Chain 8-D: 90% 10%



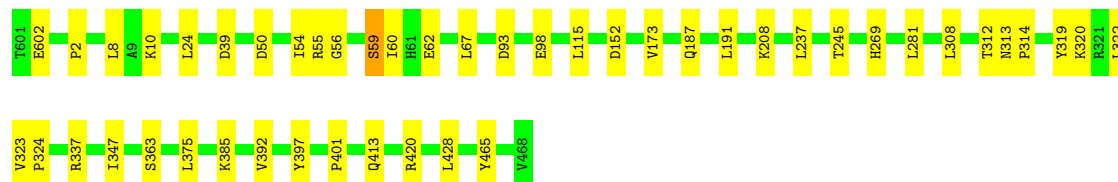
- Molecule 1: glutamine synthetase

Chain 8-E: 90% 10%



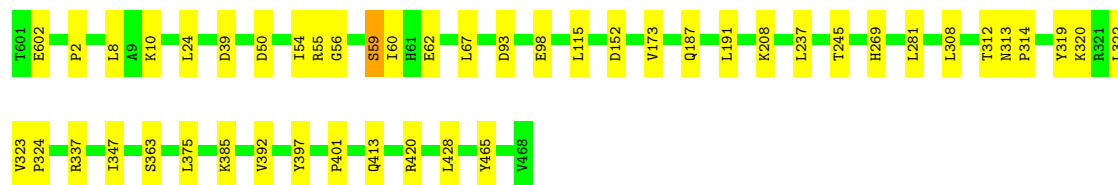
- Molecule 1: glutamine synthetase

Chain 8-F: 90% 10%



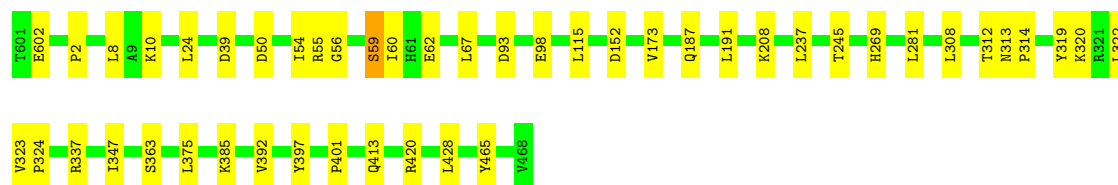
- Molecule 1: glutamine synthetase

Chain 8-G: 90% 10%



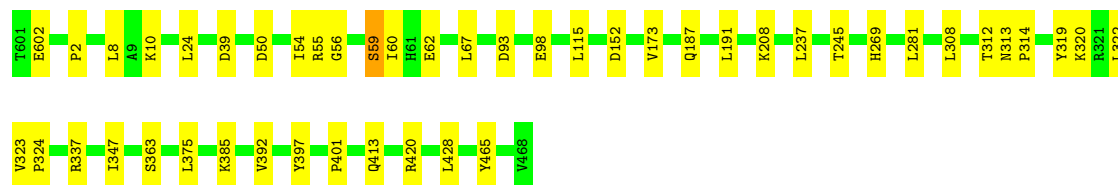
- Molecule 1: glutamine synthetase

Chain 8-H: 90% 10%



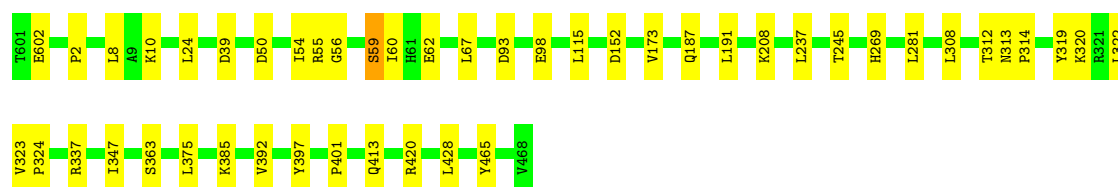
- Molecule 1: glutamine synthetase

Chain 8-I: 90% 10%



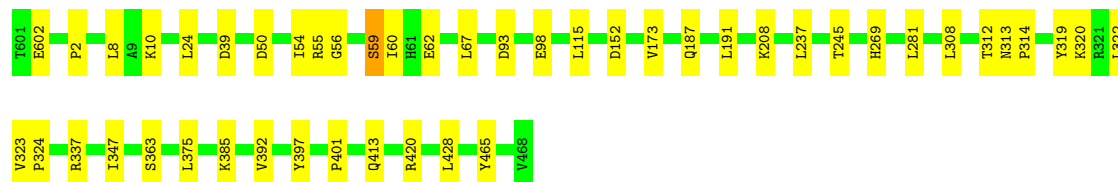
- Molecule 1: glutamine synthetase

Chain 8-J: 90% 10%



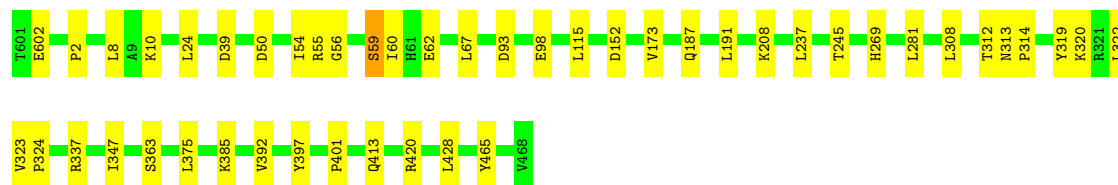
- Molecule 1: glutamine synthetase

Chain 8-K: 90% 10%



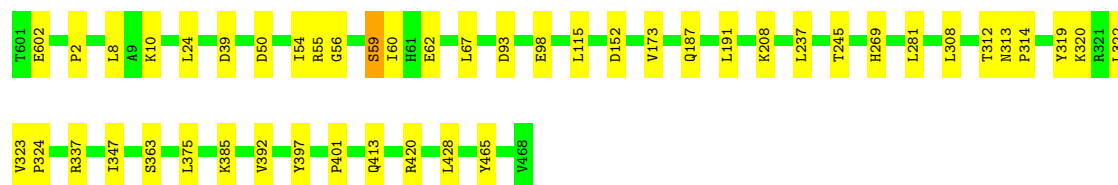
- Molecule 1: glutamine synthetase

Chain 8-L: 90% 10%



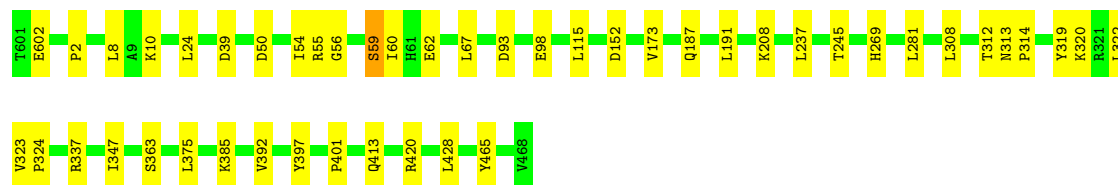
- Molecule 1: glutamine synthetase

Chain 8-M: 90% 10%



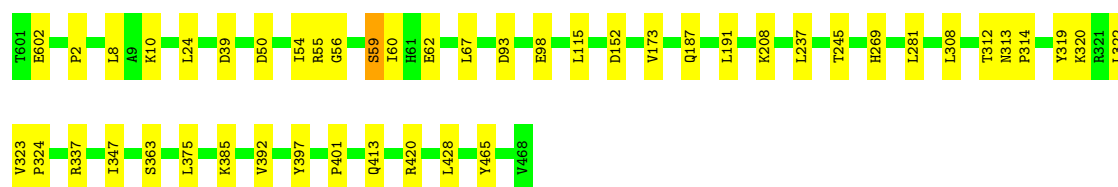
- Molecule 1: glutamine synthetase

Chain 8-N: 90% 10%



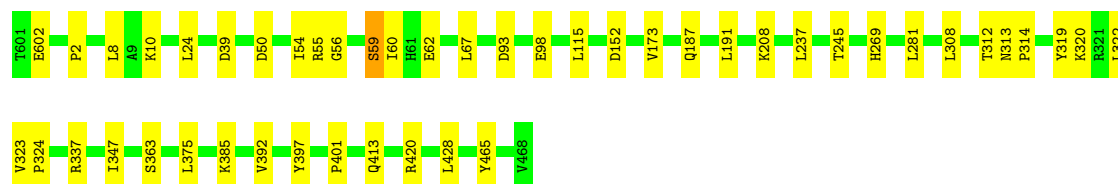
- Molecule 1: glutamine synthetase

Chain 8-O: 90% 10%



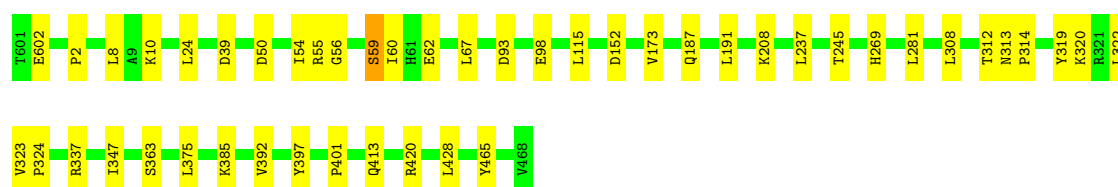
- Molecule 1: glutamine synthetase

Chain 8-P: 90% 10%



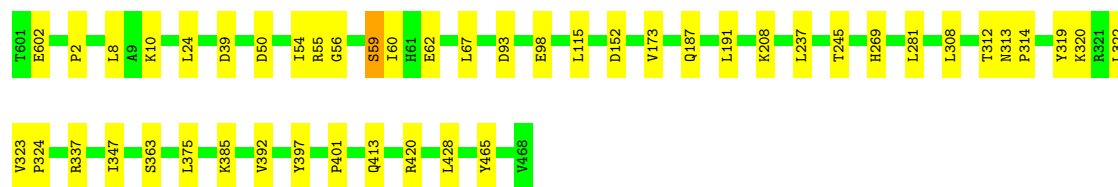
- Molecule 1: glutamine synthetase

Chain 8-Q: 90% 10%



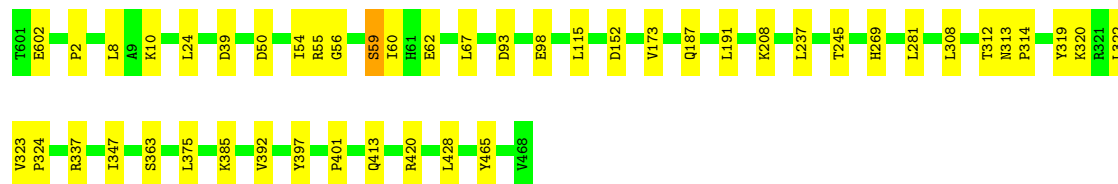
- Molecule 1: glutamine synthetase

Chain 8-R: 90% 10%



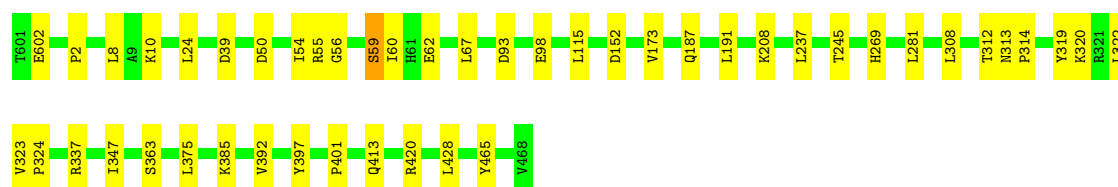
- Molecule 1: glutamine synthetase

Chain 8-S: 90% 10%



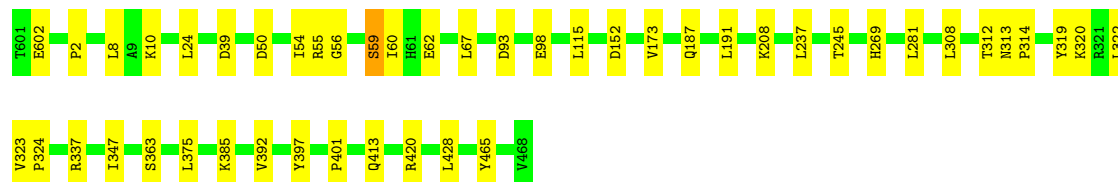
- Molecule 1: glutamine synthetase

Chain 8-T: 90% 10%



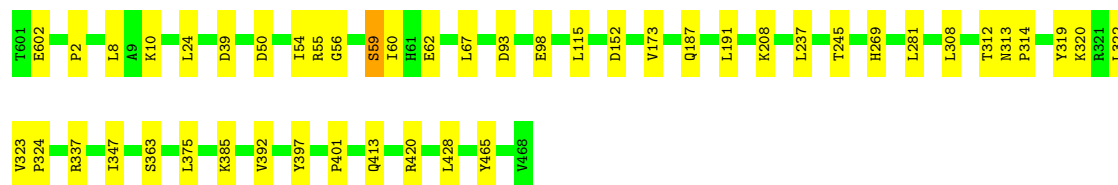
- Molecule 1: glutamine synthetase

Chain 8-U: 90% 10%



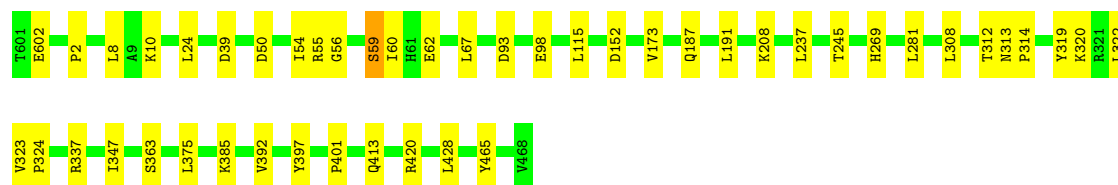
- Molecule 1: glutamine synthetase

Chain 8-V: 90% 10%



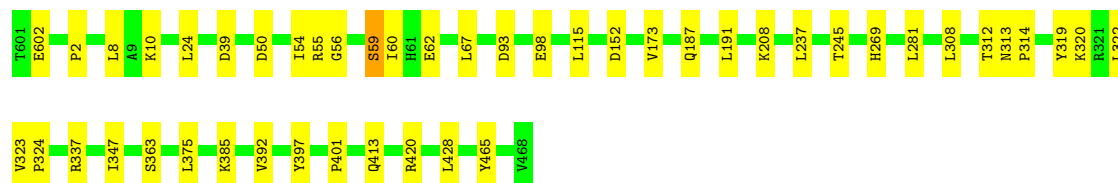
- Molecule 1: glutamine synthetase

Chain 8-W: 90% 10%



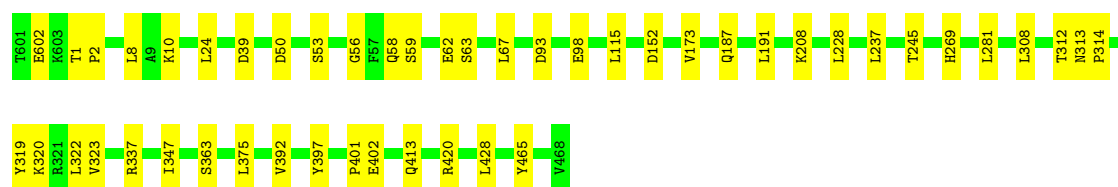
- Molecule 1: glutamine synthetase

Chain 8-X: 90% 10%



- Molecule 1: glutamine synthetase

Chain 9-A: 90% 10%



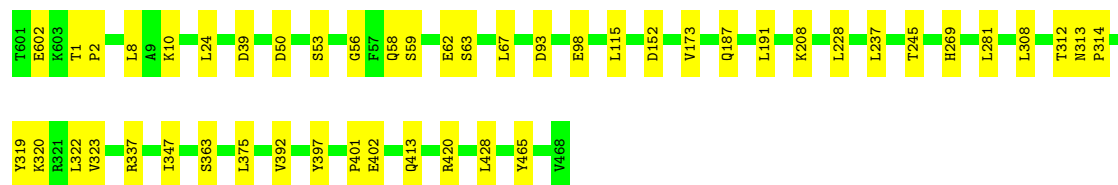
- Molecule 1: glutamine synthetase

Chain 9-B:  90% 10%



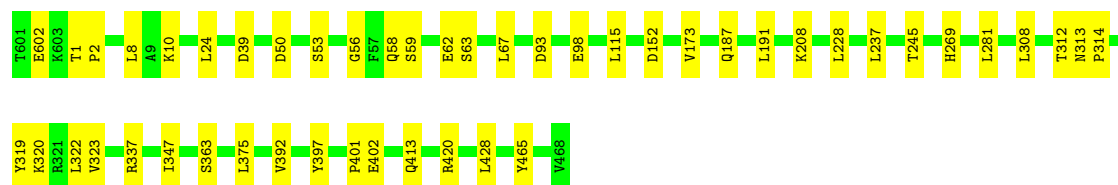
- Molecule 1: glutamine synthetase

Chain 9-C:  90% 10%



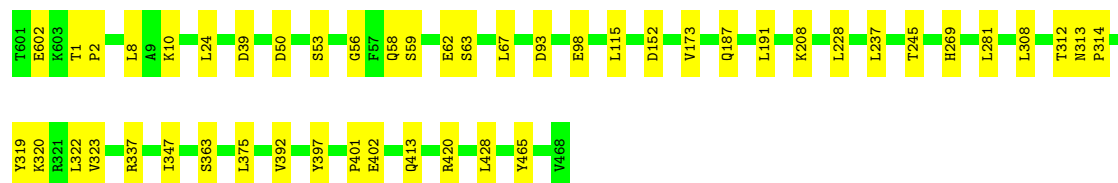
- Molecule 1: glutamine synthetase

Chain 9-D:  90% 10%



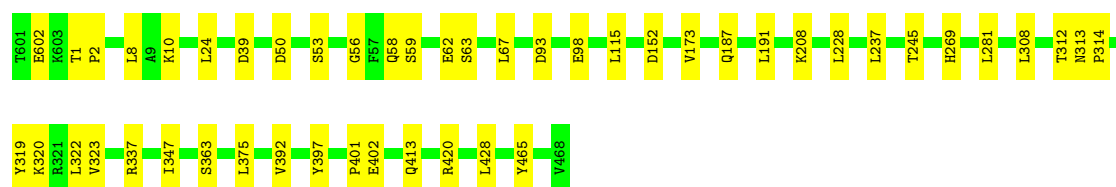
- Molecule 1: glutamine synthetase

Chain 9-E:  90% 10%



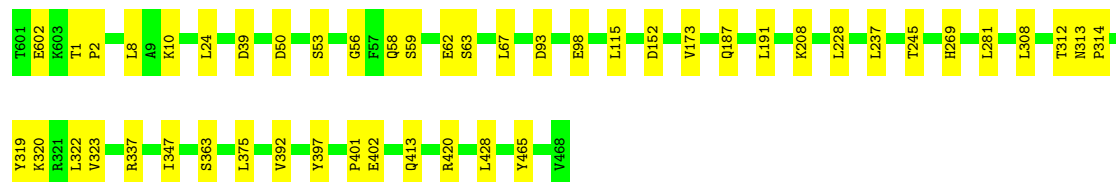
- Molecule 1: glutamine synthetase

Chain 9-F:  90% 10%



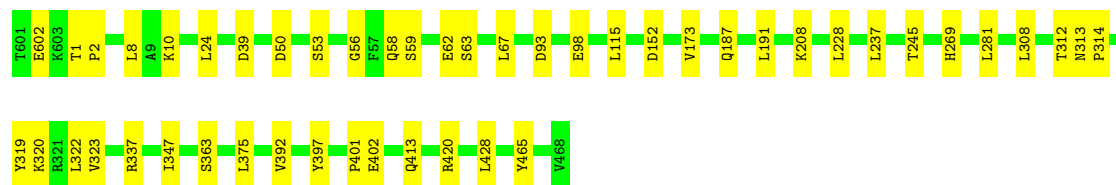
- Molecule 1: glutamine synthetase

Chain 9-G:  90% 10%



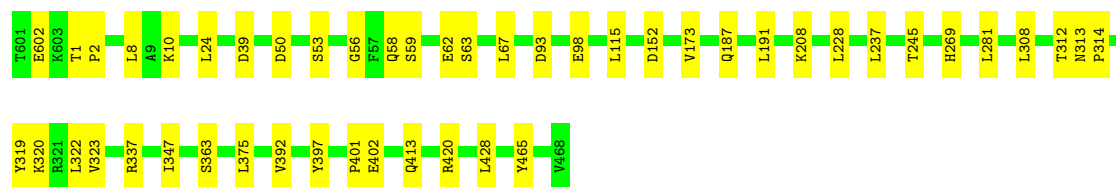
- Molecule 1: glutamine synthetase

Chain 9-H:  90% 10%



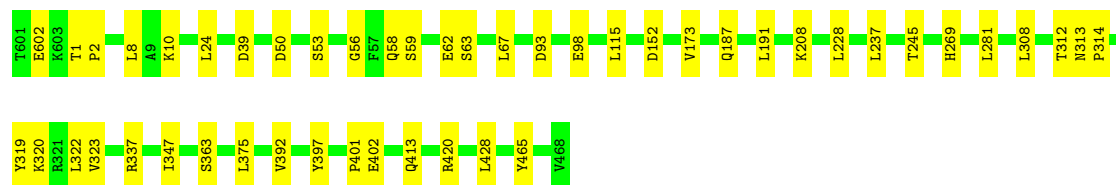
- Molecule 1: glutamine synthetase

Chain 9-I:  90% 10%



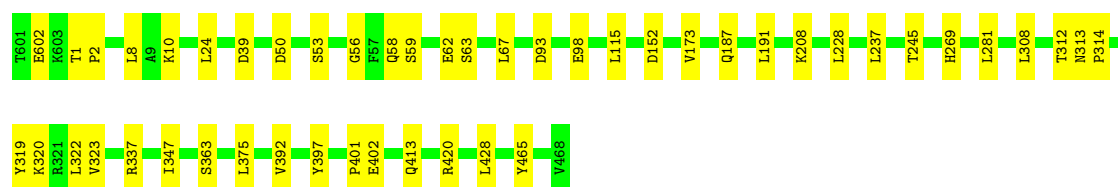
- Molecule 1: glutamine synthetase

Chain 9-J:  90% 10%



- Molecule 1: glutamine synthetase

Chain 9-K:  90% 10%



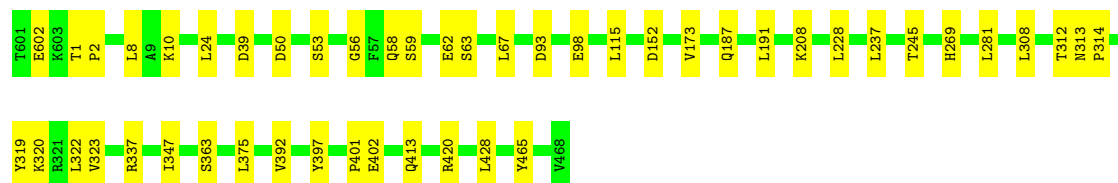
• Molecule 1: glutamine synthetase

Chain 9-L: 90% 10%



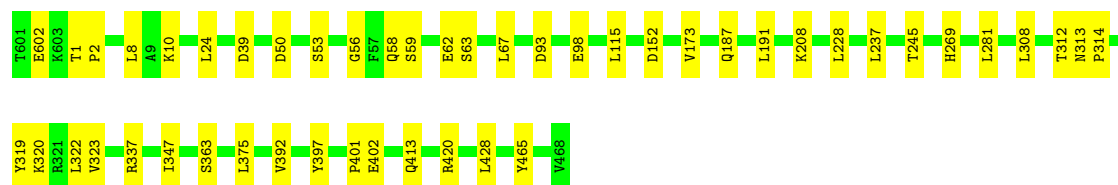
• Molecule 1: glutamine synthetase

Chain 9-M: 90% 10%



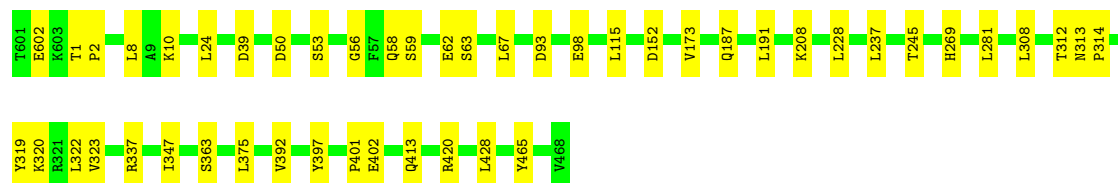
• Molecule 1: glutamine synthetase

Chain 9-N: 90% 10%



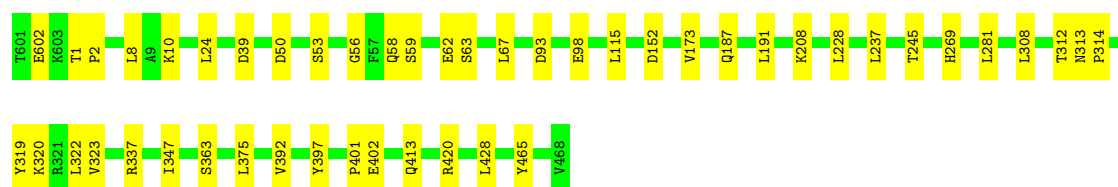
• Molecule 1: glutamine synthetase

Chain 9-O: 90% 10%



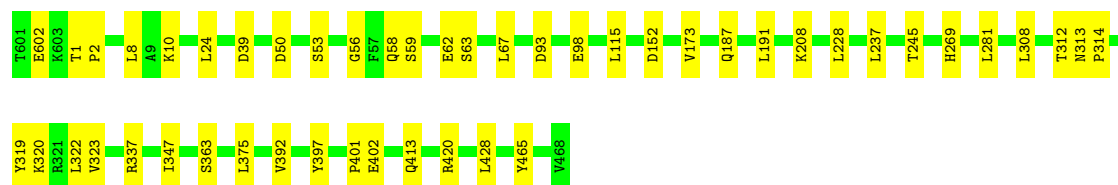
• Molecule 1: glutamine synthetase

Chain 9-P: 90% 10%



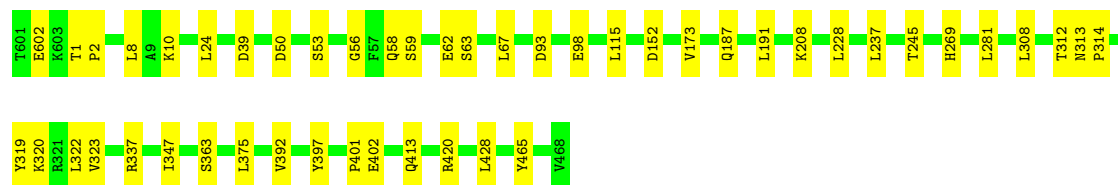
- Molecule 1: glutamine synthetase

Chain 9-Q:
90% 10%



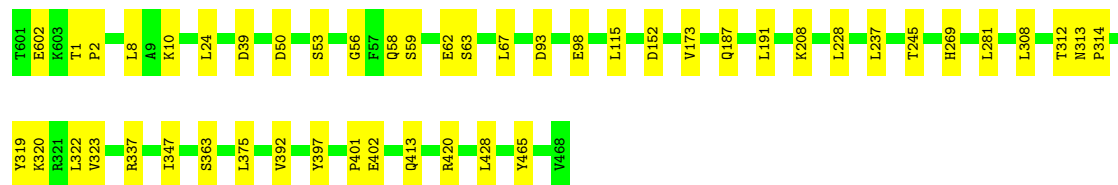
- Molecule 1: glutamine synthetase

Chain 9-R:
90% 10%



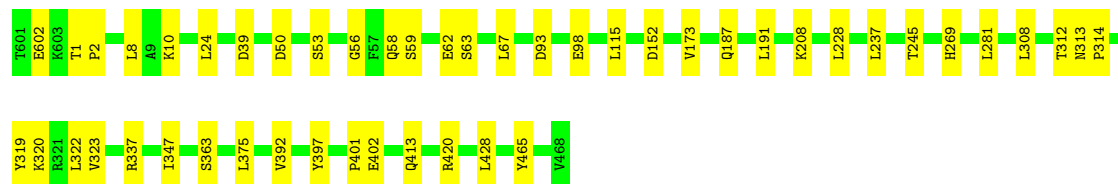
- Molecule 1: glutamine synthetase

Chain 9-S:
90% 10%



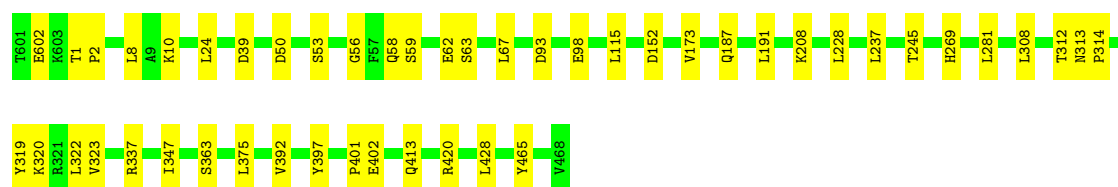
- Molecule 1: glutamine synthetase

Chain 9-T:
90% 10%



- Molecule 1: glutamine synthetase

Chain 9-U:
90% 10%



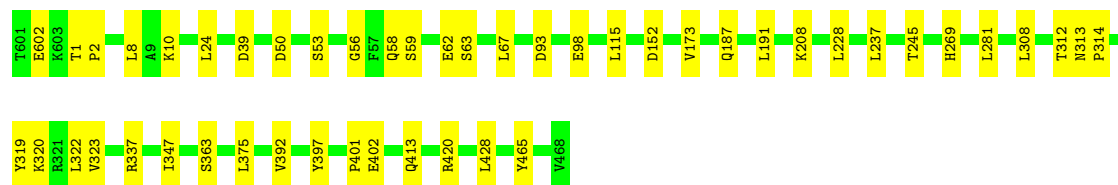
- Molecule 1: glutamine synthetase

Chain 9-V: 90% 10%



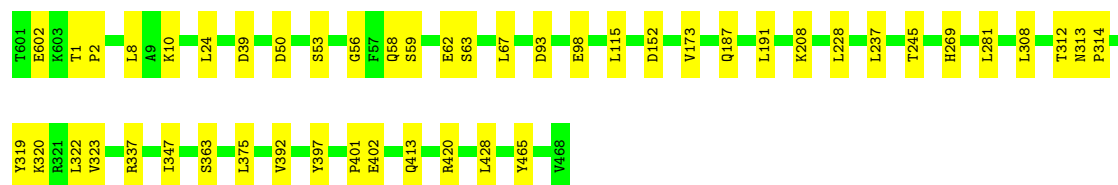
- Molecule 1: glutamine synthetase

Chain 9-W: 90% 10%



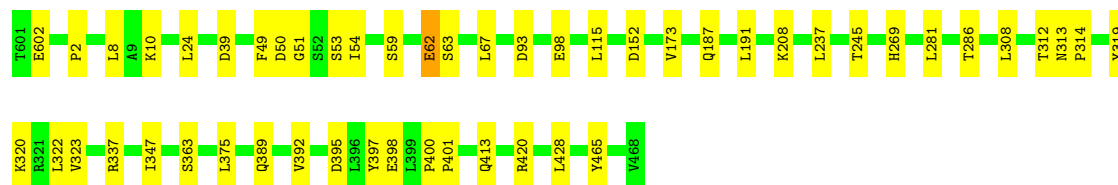
- Molecule 1: glutamine synthetase

Chain 9-X: 90% 10%



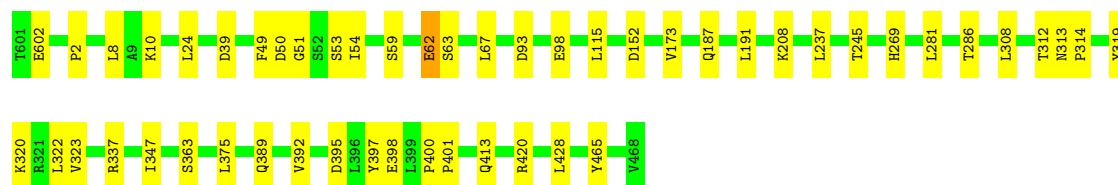
- Molecule 1: glutamine synthetase

Chain 10-A: 89% 10%



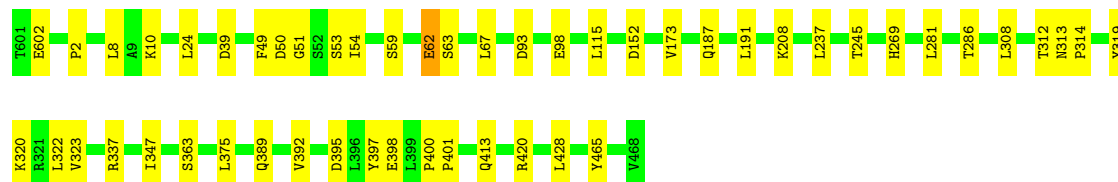
- Molecule 1: glutamine synthetase

Chain 10-B: 89% 10%



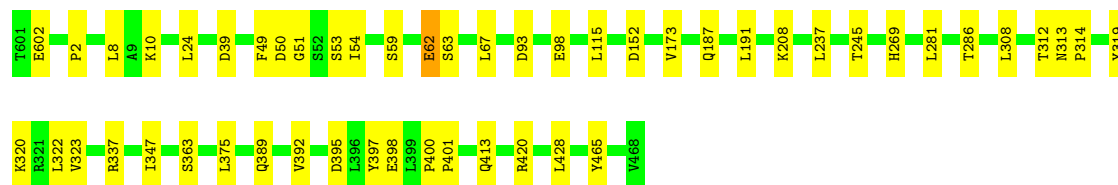
- Molecule 1: glutamine synthetase

Chain 10-C: 89% 10%



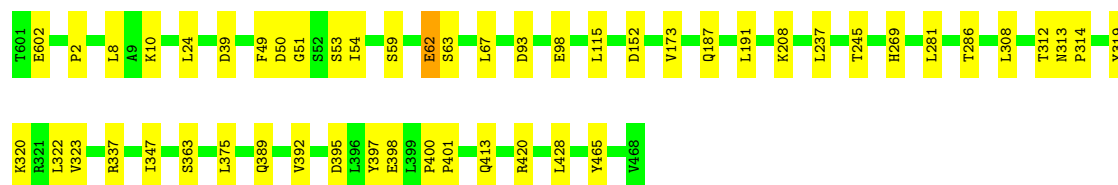
- Molecule 1: glutamine synthetase

Chain 10-D: 89% 10%



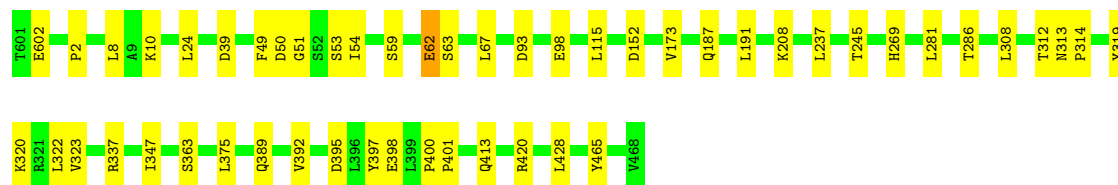
- Molecule 1: glutamine synthetase

Chain 10-E: 89% 10%



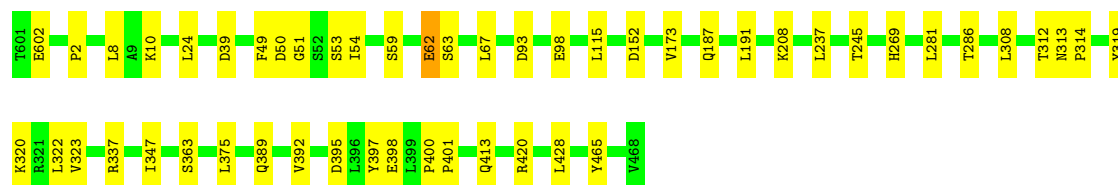
- Molecule 1: glutamine synthetase

Chain 10-F: 89% 10%



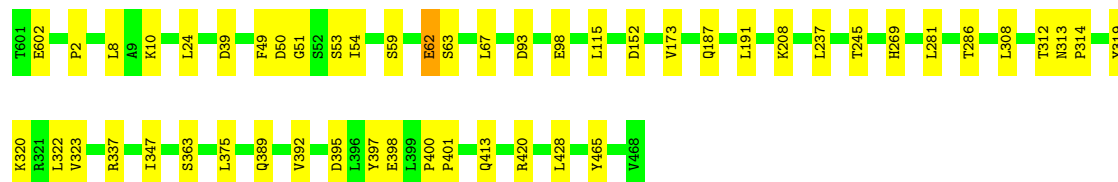
- Molecule 1: glutamine synthetase

Chain 10-G: 89% 10%



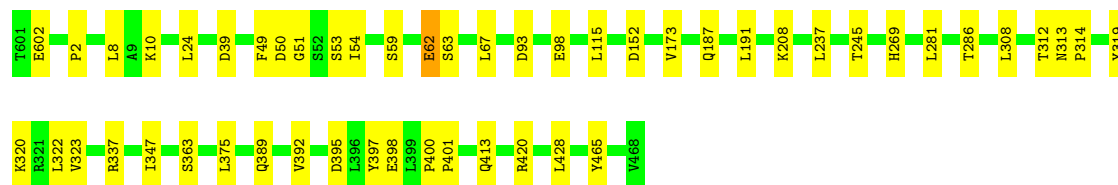
- Molecule 1: glutamine synthetase

Chain 10-H: 89% 10%



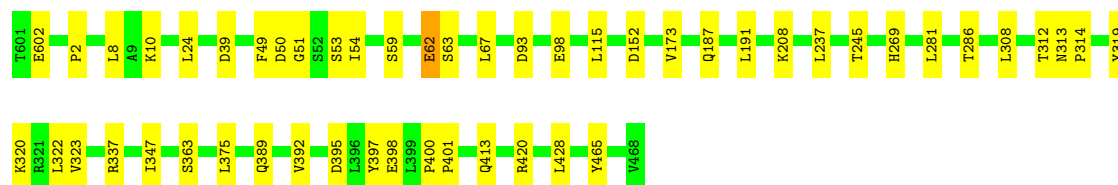
- Molecule 1: glutamine synthetase

Chain 10-I: 89% 10%



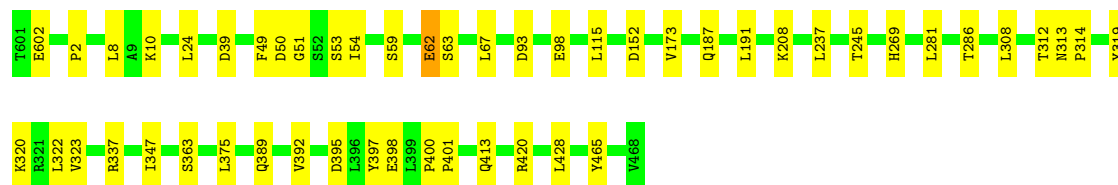
- Molecule 1: glutamine synthetase

Chain 10-J: 89% 10%



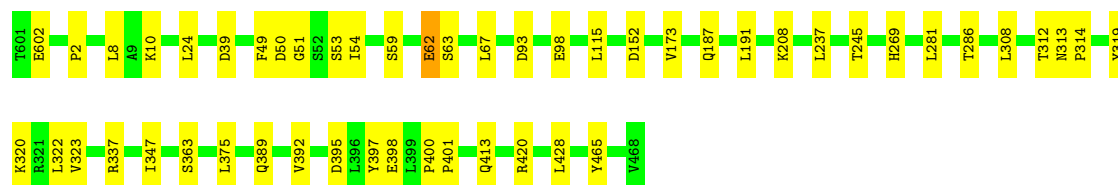
- Molecule 1: glutamine synthetase

Chain 10-K: 89% 10%



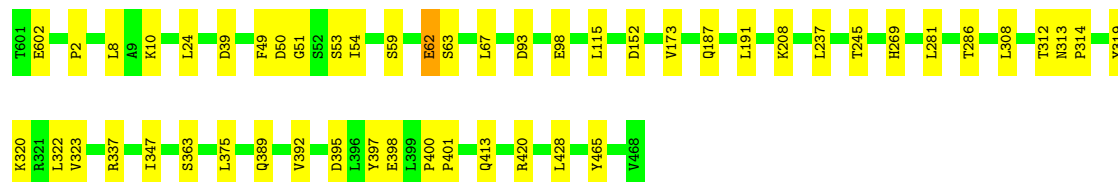
- Molecule 1: glutamine synthetase

Chain 10-L: 89% 10%



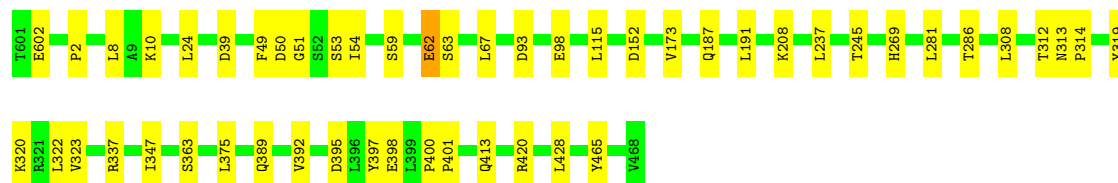
- Molecule 1: glutamine synthetase

Chain 10-M: 89% 10%



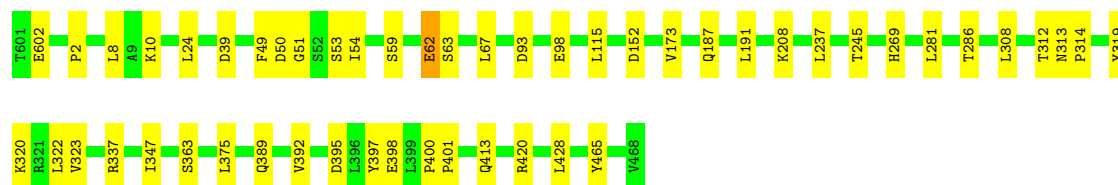
- Molecule 1: glutamine synthetase

Chain 10-N: 89% 10%



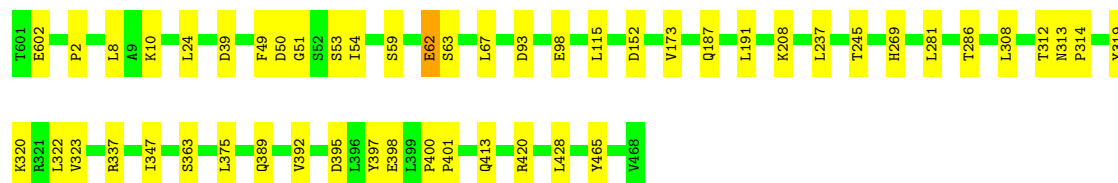
- Molecule 1: glutamine synthetase

Chain 10-O: 89% 10%



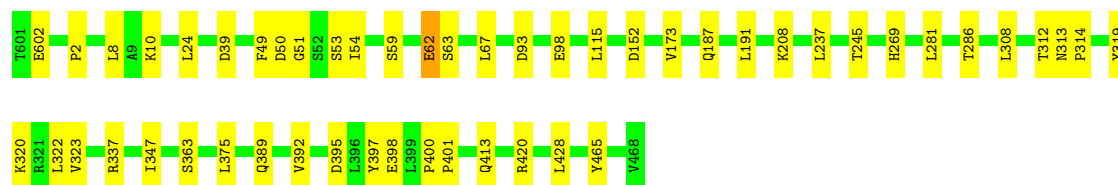
- Molecule 1: glutamine synthetase

Chain 10-P: 89% 10%



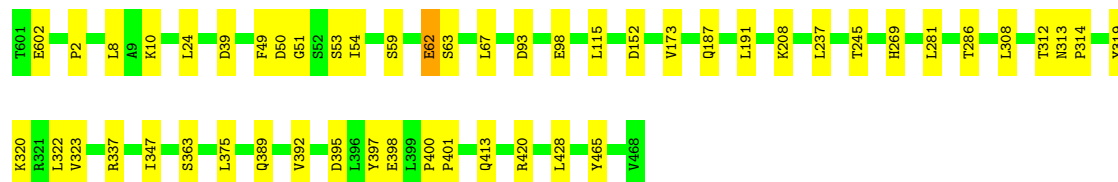
- Molecule 1: glutamine synthetase

Chain 10-Q: 89% 10%



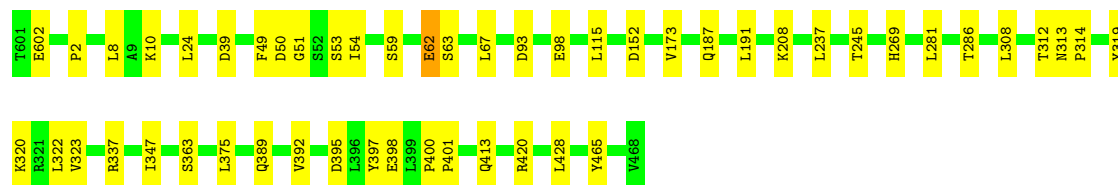
- Molecule 1: glutamine synthetase

Chain 10-R: 89% 10%



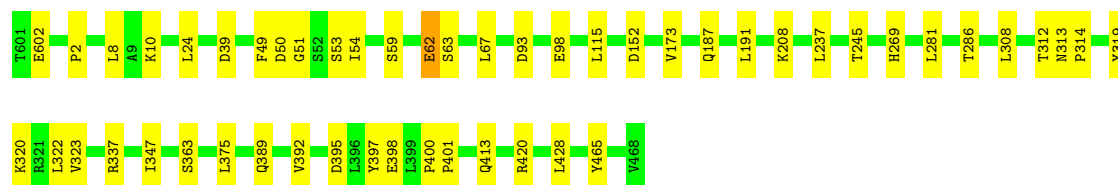
- Molecule 1: glutamine synthetase

Chain 10-S: 89% 10%



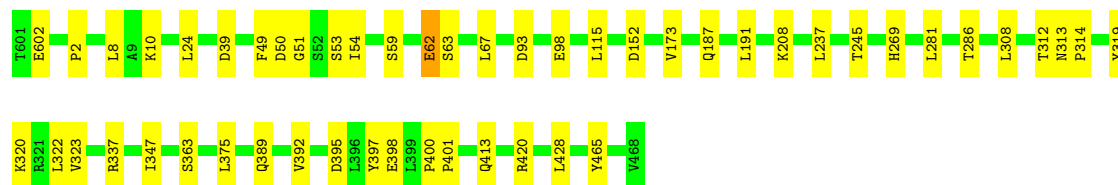
- Molecule 1: glutamine synthetase

Chain 10-T: 89% 10%



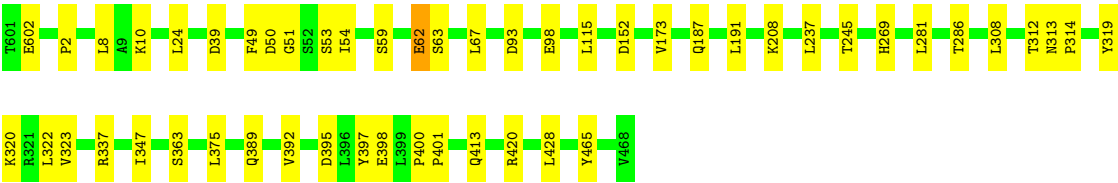
- Molecule 1: glutamine synthetase

Chain 10-U: 89% 10%

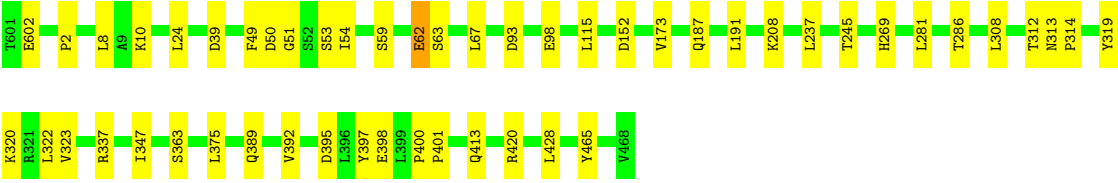


- Molecule 1: glutamine synthetase

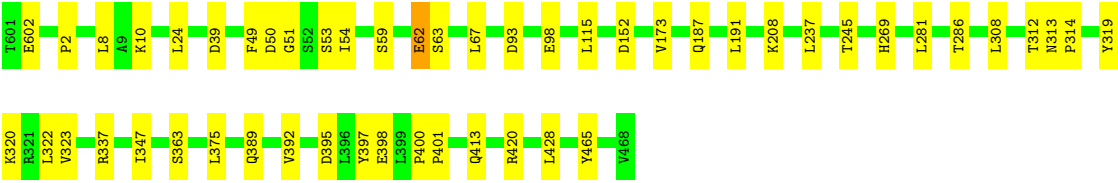
Chain 10-V: 89% 10%



• Molecule 1: glutamine synthetase



• Molecule 1: glutamine synthetase



• Molecule 1: glutamine synthetase

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	207.72Å 257.69Å 274.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.40) 99.5 (20.00-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.38 (at 2.41Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.204 , 0.223 0.219 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.03 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	978720	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.31 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.0949e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MN, AMP, CIT

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	1-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	1-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-H	0.28	0/3884	0.58	6/5279 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	2-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	3-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-C	0.28	0/3884	0.58	6/5279 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	4-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	4-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-V	0.28	0/3884	0.58	6/5279 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	5-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	5-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	6-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-Q	0.28	0/3884	0.58	6/5279 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	7-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	7-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	8-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-L	0.28	0/3884	0.58	6/5279 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	9-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	9-X	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-A	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-B	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-C	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-D	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-E	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-F	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-G	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-H	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-I	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-J	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-K	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-L	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-M	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-N	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-O	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-P	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-Q	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-R	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-S	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-T	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-U	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-V	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-W	0.28	0/3884	0.58	6/5279 (0.1%)
1	10-X	0.28	0/3884	0.58	6/5279 (0.1%)
All	All	0.28	0/932160	0.58	1440/1266960 (0.1%)

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	1-A	0	1
1	1-B	0	1
1	1-C	0	1
1	1-D	0	1
1	1-E	0	1
1	1-F	0	1
1	1-G	0	1
1	1-H	0	1
1	1-I	0	1
1	1-J	0	1
1	1-K	0	1
1	1-L	0	1
1	1-M	0	1
1	1-N	0	1
1	1-O	0	1
1	1-P	0	1
1	1-Q	0	1
1	1-R	0	1
1	1-S	0	1
1	1-T	0	1
1	1-U	0	1
1	1-V	0	1
1	1-W	0	1
1	1-X	0	1
1	2-A	0	1
1	2-B	0	1
1	2-C	0	1
1	2-D	0	1
1	2-E	0	1
1	2-F	0	1
1	2-G	0	1
1	2-H	0	1
1	2-I	0	1
1	2-J	0	1
1	2-K	0	1
1	2-L	0	1
1	2-M	0	1
1	2-N	0	1
1	2-O	0	1
1	2-P	0	1
1	2-Q	0	1
1	2-R	0	1
1	2-S	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	2-T	0	1
1	2-U	0	1
1	2-V	0	1
1	2-W	0	1
1	2-X	0	1
1	3-A	0	1
1	3-B	0	1
1	3-C	0	1
1	3-D	0	1
1	3-E	0	1
1	3-F	0	1
1	3-G	0	1
1	3-H	0	1
1	3-I	0	1
1	3-J	0	1
1	3-K	0	1
1	3-L	0	1
1	3-M	0	1
1	3-N	0	1
1	3-O	0	1
1	3-P	0	1
1	3-Q	0	1
1	3-R	0	1
1	3-S	0	1
1	3-T	0	1
1	3-U	0	1
1	3-V	0	1
1	3-W	0	1
1	3-X	0	1
1	4-A	0	1
1	4-B	0	1
1	4-C	0	1
1	4-D	0	1
1	4-E	0	1
1	4-F	0	1
1	4-G	0	1
1	4-H	0	1
1	4-I	0	1
1	4-J	0	1
1	4-K	0	1
1	4-L	0	1
1	4-M	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	4-N	0	1
1	4-O	0	1
1	4-P	0	1
1	4-Q	0	1
1	4-R	0	1
1	4-S	0	1
1	4-T	0	1
1	4-U	0	1
1	4-V	0	1
1	4-W	0	1
1	4-X	0	1
1	5-A	0	1
1	5-B	0	1
1	5-C	0	1
1	5-D	0	1
1	5-E	0	1
1	5-F	0	1
1	5-G	0	1
1	5-H	0	1
1	5-I	0	1
1	5-J	0	1
1	5-K	0	1
1	5-L	0	1
1	5-M	0	1
1	5-N	0	1
1	5-O	0	1
1	5-P	0	1
1	5-Q	0	1
1	5-R	0	1
1	5-S	0	1
1	5-T	0	1
1	5-U	0	1
1	5-V	0	1
1	5-W	0	1
1	5-X	0	1
1	6-A	0	1
1	6-B	0	1
1	6-C	0	1
1	6-D	0	1
1	6-E	0	1
1	6-F	0	1
1	6-G	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	6-H	0	1
1	6-I	0	1
1	6-J	0	1
1	6-K	0	1
1	6-L	0	1
1	6-M	0	1
1	6-N	0	1
1	6-O	0	1
1	6-P	0	1
1	6-Q	0	1
1	6-R	0	1
1	6-S	0	1
1	6-T	0	1
1	6-U	0	1
1	6-V	0	1
1	6-W	0	1
1	6-X	0	1
1	7-A	0	1
1	7-B	0	1
1	7-C	0	1
1	7-D	0	1
1	7-E	0	1
1	7-F	0	1
1	7-G	0	1
1	7-H	0	1
1	7-I	0	1
1	7-J	0	1
1	7-K	0	1
1	7-L	0	1
1	7-M	0	1
1	7-N	0	1
1	7-O	0	1
1	7-P	0	1
1	7-Q	0	1
1	7-R	0	1
1	7-S	0	1
1	7-T	0	1
1	7-U	0	1
1	7-V	0	1
1	7-W	0	1
1	7-X	0	1
1	8-A	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	8-B	0	1
1	8-C	0	1
1	8-D	0	1
1	8-E	0	1
1	8-F	0	1
1	8-G	0	1
1	8-H	0	1
1	8-I	0	1
1	8-J	0	1
1	8-K	0	1
1	8-L	0	1
1	8-M	0	1
1	8-N	0	1
1	8-O	0	1
1	8-P	0	1
1	8-Q	0	1
1	8-R	0	1
1	8-S	0	1
1	8-T	0	1
1	8-U	0	1
1	8-V	0	1
1	8-W	0	1
1	8-X	0	1
1	9-A	0	1
1	9-B	0	1
1	9-C	0	1
1	9-D	0	1
1	9-E	0	1
1	9-F	0	1
1	9-G	0	1
1	9-H	0	1
1	9-I	0	1
1	9-J	0	1
1	9-K	0	1
1	9-L	0	1
1	9-M	0	1
1	9-N	0	1
1	9-O	0	1
1	9-P	0	1
1	9-Q	0	1
1	9-R	0	1
1	9-S	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	9-T	0	1
1	9-U	0	1
1	9-V	0	1
1	9-W	0	1
1	9-X	0	1
1	10-A	0	1
1	10-B	0	1
1	10-C	0	1
1	10-D	0	1
1	10-E	0	1
1	10-F	0	1
1	10-G	0	1
1	10-H	0	1
1	10-I	0	1
1	10-J	0	1
1	10-K	0	1
1	10-L	0	1
1	10-M	0	1
1	10-N	0	1
1	10-O	0	1
1	10-P	0	1
1	10-Q	0	1
1	10-R	0	1
1	10-S	0	1
1	10-T	0	1
1	10-U	0	1
1	10-V	0	1
1	10-W	0	1
1	10-X	0	1
All	All	0	240

There are no bond length outliers.

The worst 5 of 1440 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-U	320	LYS	N-CA-C	-7.00	104.56	113.23
1	2-U	320	LYS	N-CA-C	-7.00	104.56	113.23
1	3-U	320	LYS	N-CA-C	-7.00	104.56	113.23
1	4-U	320	LYS	N-CA-C	-7.00	104.56	113.23
1	5-U	320	LYS	N-CA-C	-7.00	104.56	113.23

There are no chirality outliers.

5 of 240 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	319	TYR	Sidechain
1	1-B	319	TYR	Sidechain
1	1-C	319	TYR	Sidechain
1	1-D	319	TYR	Sidechain
1	1-E	319	TYR	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	3778	0	3604	0	0
1	1-B	3778	0	3604	0	0
1	1-C	3778	0	3604	0	0
1	1-D	3778	0	3604	0	0
1	1-E	3778	0	3604	0	0
1	1-F	3778	0	3604	0	0
1	1-G	3778	0	3604	0	0
1	1-H	3778	0	3604	0	0
1	1-I	3778	0	3604	0	0
1	1-J	3778	0	3604	0	0
1	1-K	3778	0	3604	0	0
1	1-L	3778	0	3604	0	0
1	1-M	3778	0	3604	0	0
1	1-N	3778	0	3604	0	0
1	1-O	3778	0	3604	0	0
1	1-P	3778	0	3604	0	0
1	1-Q	3778	0	3604	0	0
1	1-R	3778	0	3604	0	0
1	1-S	3778	0	3604	0	0
1	1-T	3778	0	3604	0	0
1	1-U	3778	0	3604	0	0
1	1-V	3778	0	3604	0	0
1	1-W	3778	0	3604	0	0
1	1-X	3778	0	3604	0	0
1	2-A	3778	0	3604	0	0
1	2-B	3778	0	3604	0	0
1	2-C	3778	0	3604	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2-D	3778	0	3604	0	0
1	2-E	3778	0	3604	0	0
1	2-F	3778	0	3604	0	0
1	2-G	3778	0	3604	0	0
1	2-H	3778	0	3604	0	0
1	2-I	3778	0	3604	0	0
1	2-J	3778	0	3604	0	0
1	2-K	3778	0	3604	0	0
1	2-L	3778	0	3604	0	0
1	2-M	3778	0	3604	0	0
1	2-N	3778	0	3604	0	0
1	2-O	3778	0	3604	0	0
1	2-P	3778	0	3604	0	0
1	2-Q	3778	0	3604	0	0
1	2-R	3778	0	3604	0	0
1	2-S	3778	0	3604	0	0
1	2-T	3778	0	3604	0	0
1	2-U	3778	0	3604	0	0
1	2-V	3778	0	3604	0	0
1	2-W	3778	0	3604	0	0
1	2-X	3778	0	3604	0	0
1	3-A	3778	0	3604	0	0
1	3-B	3778	0	3604	0	0
1	3-C	3778	0	3604	0	0
1	3-D	3778	0	3604	0	0
1	3-E	3778	0	3604	0	0
1	3-F	3778	0	3604	0	0
1	3-G	3778	0	3604	0	0
1	3-H	3778	0	3604	0	0
1	3-I	3778	0	3604	0	0
1	3-J	3778	0	3604	0	0
1	3-K	3778	0	3604	0	0
1	3-L	3778	0	3604	0	0
1	3-M	3778	0	3604	0	0
1	3-N	3778	0	3604	0	0
1	3-O	3778	0	3604	0	0
1	3-P	3778	0	3604	0	0
1	3-Q	3778	0	3604	0	0
1	3-R	3778	0	3604	0	0
1	3-S	3778	0	3604	0	0
1	3-T	3778	0	3604	0	0
1	3-U	3778	0	3602	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3-V	3778	0	3604	0	0
1	3-W	3778	0	3604	0	0
1	3-X	3778	0	3604	0	0
1	4-A	3778	0	3604	0	0
1	4-B	3778	0	3604	0	0
1	4-C	3778	0	3604	0	0
1	4-D	3778	0	3604	0	0
1	4-E	3778	0	3604	0	0
1	4-F	3778	0	3604	0	0
1	4-G	3778	0	3604	0	0
1	4-H	3778	0	3604	0	0
1	4-I	3778	0	3604	0	0
1	4-J	3778	0	3604	0	0
1	4-K	3778	0	3604	0	0
1	4-L	3778	0	3604	0	0
1	4-M	3778	0	3604	0	0
1	4-N	3778	0	3604	0	0
1	4-O	3778	0	3604	0	0
1	4-P	3778	0	3604	0	0
1	4-Q	3778	0	3604	0	0
1	4-R	3778	0	3604	0	0
1	4-S	3778	0	3602	0	0
1	4-T	3778	0	3604	0	0
1	4-U	3778	0	3604	0	0
1	4-V	3778	0	3604	0	0
1	4-W	3778	0	3604	0	0
1	4-X	3778	0	3604	0	0
1	5-A	3778	0	3604	0	0
1	5-B	3778	0	3604	0	0
1	5-C	3778	0	3604	0	0
1	5-D	3778	0	3604	0	0
1	5-E	3778	0	3604	0	0
1	5-F	3778	0	3604	0	0
1	5-G	3778	0	3604	0	0
1	5-H	3778	0	3604	0	0
1	5-I	3778	0	3604	0	0
1	5-J	3778	0	3604	0	0
1	5-K	3778	0	3604	0	0
1	5-L	3778	0	3604	0	0
1	5-M	3778	0	3604	0	0
1	5-N	3778	0	3604	0	0
1	5-O	3778	0	3604	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5-P	3778	0	3604	0	0
1	5-Q	3778	0	3604	0	0
1	5-R	3778	0	3604	0	0
1	5-S	3778	0	3604	0	0
1	5-T	3778	0	3604	0	0
1	5-U	3778	0	3604	0	0
1	5-V	3778	0	3604	0	0
1	5-W	3778	0	3604	0	0
1	5-X	3778	0	3604	0	0
1	6-A	3778	0	3604	0	0
1	6-B	3778	0	3604	0	0
1	6-C	3778	0	3604	0	0
1	6-D	3778	0	3604	0	0
1	6-E	3778	0	3604	0	0
1	6-F	3778	0	3604	0	0
1	6-G	3778	0	3604	0	0
1	6-H	3778	0	3604	0	0
1	6-I	3778	0	3604	0	0
1	6-J	3778	0	3604	0	0
1	6-K	3778	0	3604	0	0
1	6-L	3778	0	3604	0	0
1	6-M	3778	0	3604	0	0
1	6-N	3778	0	3604	0	0
1	6-O	3778	0	3604	0	0
1	6-P	3778	0	3604	0	0
1	6-Q	3778	0	3604	0	0
1	6-R	3778	0	3604	0	0
1	6-S	3778	0	3604	0	0
1	6-T	3778	0	3604	0	0
1	6-U	3778	0	3604	0	0
1	6-V	3778	0	3604	0	0
1	6-W	3778	0	3604	0	0
1	6-X	3778	0	3604	0	0
1	7-A	3778	0	3604	0	0
1	7-B	3778	0	3604	0	0
1	7-C	3778	0	3604	0	0
1	7-D	3778	0	3604	0	0
1	7-E	3778	0	3604	0	0
1	7-F	3778	0	3604	0	0
1	7-G	3778	0	3604	0	0
1	7-H	3778	0	3604	0	0
1	7-I	3778	0	3604	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	7-J	3778	0	3604	0	0
1	7-K	3778	0	3604	0	0
1	7-L	3778	0	3604	0	0
1	7-M	3778	0	3604	0	0
1	7-N	3778	0	3604	0	0
1	7-O	3778	0	3604	0	0
1	7-P	3778	0	3604	0	0
1	7-Q	3778	0	3604	0	0
1	7-R	3778	0	3604	0	0
1	7-S	3778	0	3601	0	0
1	7-T	3778	0	3604	0	0
1	7-U	3778	0	3604	0	0
1	7-V	3778	0	3604	0	0
1	7-W	3778	0	3604	0	0
1	7-X	3778	0	3604	0	0
1	8-A	3778	0	3604	0	0
1	8-B	3778	0	3604	0	0
1	8-C	3778	0	3604	0	0
1	8-D	3778	0	3604	0	0
1	8-E	3778	0	3604	0	0
1	8-F	3778	0	3604	0	0
1	8-G	3778	0	3604	0	0
1	8-H	3778	0	3604	0	0
1	8-I	3778	0	3604	0	0
1	8-J	3778	0	3604	0	0
1	8-K	3778	0	3604	0	0
1	8-L	3778	0	3604	0	0
1	8-M	3778	0	3604	0	0
1	8-N	3778	0	3604	0	0
1	8-O	3778	0	3604	0	0
1	8-P	3778	0	3604	0	0
1	8-Q	3778	0	3604	0	0
1	8-R	3778	0	3604	0	0
1	8-S	3778	0	3604	0	0
1	8-T	3778	0	3604	0	0
1	8-U	3778	0	3604	0	0
1	8-V	3778	0	3604	0	0
1	8-W	3778	0	3604	0	0
1	8-X	3778	0	3604	0	0
1	9-A	3778	0	3604	0	0
1	9-B	3778	0	3604	0	0
1	9-C	3778	0	3604	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	9-D	3778	0	3604	0	0
1	9-E	3778	0	3604	0	0
1	9-F	3778	0	3604	0	0
1	9-G	3778	0	3604	0	0
1	9-H	3778	0	3604	0	0
1	9-I	3778	0	3604	0	0
1	9-J	3778	0	3604	0	0
1	9-K	3778	0	3604	0	0
1	9-L	3778	0	3604	0	0
1	9-M	3778	0	3604	0	0
1	9-N	3778	0	3604	0	0
1	9-O	3778	0	3604	0	0
1	9-P	3778	0	3604	0	0
1	9-Q	3778	0	3604	0	0
1	9-R	3778	0	3604	0	0
1	9-S	3778	0	3602	0	0
1	9-T	3778	0	3604	0	0
1	9-U	3778	0	3604	0	0
1	9-V	3778	0	3604	0	0
1	9-W	3778	0	3604	0	0
1	9-X	3778	0	3604	0	0
1	10-A	3778	0	3604	0	0
1	10-B	3778	0	3604	0	0
1	10-C	3778	0	3604	0	0
1	10-D	3778	0	3604	0	0
1	10-E	3778	0	3604	0	0
1	10-F	3778	0	3604	0	0
1	10-G	3778	0	3604	0	0
1	10-H	3778	0	3604	0	0
1	10-I	3778	0	3604	0	0
1	10-J	3778	0	3604	0	0
1	10-K	3778	0	3604	0	0
1	10-L	3778	0	3604	0	0
1	10-M	3778	0	3604	0	0
1	10-N	3778	0	3604	0	0
1	10-O	3778	0	3604	0	0
1	10-P	3778	0	3604	0	0
1	10-Q	3778	0	3604	0	0
1	10-R	3778	0	3604	0	0
1	10-S	3778	0	3604	0	0
1	10-T	3778	0	3604	0	0
1	10-U	3778	0	3604	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	10-V	3778	0	3604	0	0
1	10-W	3778	0	3604	0	0
1	10-X	3778	0	3604	0	0
2	1-A	1	0	0	0	0
2	1-B	1	0	0	0	0
2	1-C	1	0	0	0	0
2	1-D	1	0	0	0	0
2	1-E	1	0	0	0	0
2	1-F	1	0	0	0	0
2	1-G	1	0	0	0	0
2	1-H	1	0	0	0	0
2	1-I	1	0	0	0	0
2	1-J	1	0	0	0	0
2	1-K	1	0	0	0	0
2	1-L	1	0	0	0	0
2	1-M	1	0	0	0	0
2	1-N	1	0	0	0	0
2	1-O	1	0	0	0	0
2	1-P	1	0	0	0	0
2	1-Q	1	0	0	0	0
2	1-R	1	0	0	0	0
2	1-S	1	0	0	0	0
2	1-T	1	0	0	0	0
2	1-U	1	0	0	0	0
2	1-V	1	0	0	0	0
2	1-W	1	0	0	0	0
2	1-X	1	0	0	0	0
2	2-A	1	0	0	0	0
2	2-B	1	0	0	0	0
2	2-C	1	0	0	0	0
2	2-D	1	0	0	0	0
2	2-E	1	0	0	0	0
2	2-F	1	0	0	0	0
2	2-G	1	0	0	0	0
2	2-H	1	0	0	0	0
2	2-I	1	0	0	0	0
2	2-J	1	0	0	0	0
2	2-K	1	0	0	0	0
2	2-L	1	0	0	0	0
2	2-M	1	0	0	0	0
2	2-N	1	0	0	0	0
2	2-O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	2-P	1	0	0	0	0
2	2-Q	1	0	0	0	0
2	2-R	1	0	0	0	0
2	2-S	1	0	0	0	0
2	2-T	1	0	0	0	0
2	2-U	1	0	0	0	0
2	2-V	1	0	0	0	0
2	2-W	1	0	0	0	0
2	2-X	1	0	0	0	0
2	3-A	1	0	0	0	0
2	3-B	1	0	0	0	0
2	3-C	1	0	0	0	0
2	3-D	1	0	0	0	0
2	3-E	1	0	0	0	0
2	3-F	1	0	0	0	0
2	3-G	1	0	0	0	0
2	3-H	1	0	0	0	0
2	3-I	1	0	0	0	0
2	3-J	1	0	0	0	0
2	3-K	1	0	0	0	0
2	3-L	1	0	0	0	0
2	3-M	1	0	0	0	0
2	3-N	1	0	0	0	0
2	3-O	1	0	0	0	0
2	3-P	1	0	0	0	0
2	3-Q	1	0	0	0	0
2	3-R	1	0	0	0	0
2	3-S	1	0	0	0	0
2	3-T	1	0	0	0	0
2	3-U	1	0	0	0	0
2	3-V	1	0	0	0	0
2	3-W	1	0	0	0	0
2	3-X	1	0	0	0	0
2	4-A	1	0	0	0	0
2	4-B	1	0	0	0	0
2	4-C	1	0	0	0	0
2	4-D	1	0	0	0	0
2	4-E	1	0	0	0	0
2	4-F	1	0	0	0	0
2	4-G	1	0	0	0	0
2	4-H	1	0	0	0	0
2	4-I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	4-J	1	0	0	0	0
2	4-K	1	0	0	0	0
2	4-L	1	0	0	0	0
2	4-M	1	0	0	0	0
2	4-N	1	0	0	0	0
2	4-O	1	0	0	0	0
2	4-P	1	0	0	0	0
2	4-Q	1	0	0	0	0
2	4-R	1	0	0	0	0
2	4-S	1	0	0	0	0
2	4-T	1	0	0	0	0
2	4-U	1	0	0	0	0
2	4-V	1	0	0	0	0
2	4-W	1	0	0	0	0
2	4-X	1	0	0	0	0
2	5-A	1	0	0	0	0
2	5-B	1	0	0	0	0
2	5-C	1	0	0	0	0
2	5-D	1	0	0	0	0
2	5-E	1	0	0	0	0
2	5-F	1	0	0	0	0
2	5-G	1	0	0	0	0
2	5-H	1	0	0	0	0
2	5-I	1	0	0	0	0
2	5-J	1	0	0	0	0
2	5-K	1	0	0	0	0
2	5-L	1	0	0	0	0
2	5-M	1	0	0	0	0
2	5-N	1	0	0	0	0
2	5-O	1	0	0	0	0
2	5-P	1	0	0	0	0
2	5-Q	1	0	0	0	0
2	5-R	1	0	0	0	0
2	5-S	1	0	0	0	0
2	5-T	1	0	0	0	0
2	5-U	1	0	0	0	0
2	5-V	1	0	0	0	0
2	5-W	1	0	0	0	0
2	5-X	1	0	0	0	0
2	6-A	1	0	0	0	0
2	6-B	1	0	0	0	0
2	6-C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	6-D	1	0	0	0	0
2	6-E	1	0	0	0	0
2	6-F	1	0	0	0	0
2	6-G	1	0	0	0	0
2	6-H	1	0	0	0	0
2	6-I	1	0	0	0	0
2	6-J	1	0	0	0	0
2	6-K	1	0	0	0	0
2	6-L	1	0	0	0	0
2	6-M	1	0	0	0	0
2	6-N	1	0	0	0	0
2	6-O	1	0	0	0	0
2	6-P	1	0	0	0	0
2	6-Q	1	0	0	0	0
2	6-R	1	0	0	0	0
2	6-S	1	0	0	0	0
2	6-T	1	0	0	0	0
2	6-U	1	0	0	0	0
2	6-V	1	0	0	0	0
2	6-W	1	0	0	0	0
2	6-X	1	0	0	0	0
2	7-A	1	0	0	0	0
2	7-B	1	0	0	0	0
2	7-C	1	0	0	0	0
2	7-D	1	0	0	0	0
2	7-E	1	0	0	0	0
2	7-F	1	0	0	0	0
2	7-G	1	0	0	0	0
2	7-H	1	0	0	0	0
2	7-I	1	0	0	0	0
2	7-J	1	0	0	0	0
2	7-K	1	0	0	0	0
2	7-L	1	0	0	0	0
2	7-M	1	0	0	0	0
2	7-N	1	0	0	0	0
2	7-O	1	0	0	0	0
2	7-P	1	0	0	0	0
2	7-Q	1	0	0	0	0
2	7-R	1	0	0	0	0
2	7-S	1	0	0	0	0
2	7-T	1	0	0	0	0
2	7-U	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	7-V	1	0	0	0	0
2	7-W	1	0	0	0	0
2	7-X	1	0	0	0	0
2	8-A	1	0	0	0	0
2	8-B	1	0	0	0	0
2	8-C	1	0	0	0	0
2	8-D	1	0	0	0	0
2	8-E	1	0	0	0	0
2	8-F	1	0	0	0	0
2	8-G	1	0	0	0	0
2	8-H	1	0	0	0	0
2	8-I	1	0	0	0	0
2	8-J	1	0	0	0	0
2	8-K	1	0	0	0	0
2	8-L	1	0	0	0	0
2	8-M	1	0	0	0	0
2	8-N	1	0	0	0	0
2	8-O	1	0	0	0	0
2	8-P	1	0	0	0	0
2	8-Q	1	0	0	0	0
2	8-R	1	0	0	0	0
2	8-S	1	0	0	0	0
2	8-T	1	0	0	0	0
2	8-U	1	0	0	0	0
2	8-V	1	0	0	0	0
2	8-W	1	0	0	0	0
2	8-X	1	0	0	0	0
2	9-A	1	0	0	0	0
2	9-B	1	0	0	0	0
2	9-C	1	0	0	0	0
2	9-D	1	0	0	0	0
2	9-E	1	0	0	0	0
2	9-F	1	0	0	0	0
2	9-G	1	0	0	0	0
2	9-H	1	0	0	0	0
2	9-I	1	0	0	0	0
2	9-J	1	0	0	0	0
2	9-K	1	0	0	0	0
2	9-L	1	0	0	0	0
2	9-M	1	0	0	0	0
2	9-N	1	0	0	0	0
2	9-O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	9-P	1	0	0	0	0
2	9-Q	1	0	0	0	0
2	9-R	1	0	0	0	0
2	9-S	1	0	0	0	0
2	9-T	1	0	0	0	0
2	9-U	1	0	0	0	0
2	9-V	1	0	0	0	0
2	9-W	1	0	0	0	0
2	9-X	1	0	0	0	0
2	10-A	1	0	0	0	0
2	10-B	1	0	0	0	0
2	10-C	1	0	0	0	0
2	10-D	1	0	0	0	0
2	10-E	1	0	0	0	0
2	10-F	1	0	0	0	0
2	10-G	1	0	0	0	0
2	10-H	1	0	0	0	0
2	10-I	1	0	0	0	0
2	10-J	1	0	0	0	0
2	10-K	1	0	0	0	0
2	10-L	1	0	0	0	0
2	10-M	1	0	0	0	0
2	10-N	1	0	0	0	0
2	10-O	1	0	0	0	0
2	10-P	1	0	0	0	0
2	10-Q	1	0	0	0	0
2	10-R	1	0	0	0	0
2	10-S	1	0	0	0	0
2	10-T	1	0	0	0	0
2	10-U	1	0	0	0	0
2	10-V	1	0	0	0	0
2	10-W	1	0	0	0	0
2	10-X	1	0	0	0	0
3	1-A	23	0	10	0	0
3	1-B	23	0	10	0	0
3	1-C	23	0	10	0	0
3	1-D	23	0	10	0	0
3	1-E	23	0	10	0	0
3	1-F	23	0	10	0	0
3	1-G	23	0	10	0	0
3	1-H	23	0	10	0	0
3	1-I	23	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	1-J	23	0	10	0	0
3	1-K	23	0	10	0	0
3	1-L	23	0	10	0	0
3	1-M	23	0	10	0	0
3	1-N	23	0	10	0	0
3	1-O	23	0	10	0	0
3	1-P	23	0	10	0	0
3	1-Q	23	0	10	0	0
3	1-R	23	0	10	0	0
3	1-S	23	0	10	0	0
3	1-T	23	0	10	0	0
3	1-U	23	0	10	0	0
3	1-V	23	0	10	0	0
3	1-W	23	0	10	0	0
3	1-X	23	0	10	0	0
3	2-A	23	0	10	0	0
3	2-B	23	0	10	0	0
3	2-C	23	0	10	0	0
3	2-D	23	0	10	0	0
3	2-E	23	0	10	0	0
3	2-F	23	0	10	0	0
3	2-G	23	0	10	0	0
3	2-H	23	0	10	0	0
3	2-I	23	0	10	0	0
3	2-J	23	0	10	0	0
3	2-K	23	0	10	0	0
3	2-L	23	0	10	0	0
3	2-M	23	0	10	0	0
3	2-N	23	0	10	0	0
3	2-O	23	0	10	0	0
3	2-P	23	0	10	0	0
3	2-Q	23	0	10	0	0
3	2-R	23	0	10	0	0
3	2-S	23	0	10	0	0
3	2-T	23	0	10	0	0
3	2-U	23	0	10	0	0
3	2-V	23	0	10	0	0
3	2-W	23	0	10	0	0
3	2-X	23	0	10	0	0
3	3-A	23	0	10	0	0
3	3-B	23	0	10	0	0
3	3-C	23	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3-D	23	0	10	0	0
3	3-E	23	0	10	0	0
3	3-F	23	0	10	0	0
3	3-G	23	0	10	0	0
3	3-H	23	0	10	0	0
3	3-I	23	0	10	0	0
3	3-J	23	0	10	0	0
3	3-K	23	0	10	0	0
3	3-L	23	0	10	0	0
3	3-M	23	0	10	0	0
3	3-N	23	0	10	0	0
3	3-O	23	0	10	0	0
3	3-P	23	0	10	0	0
3	3-Q	23	0	10	0	0
3	3-R	23	0	10	0	0
3	3-S	23	0	10	0	0
3	3-T	23	0	10	0	0
3	3-U	23	0	10	0	0
3	3-V	23	0	10	0	0
3	3-W	23	0	10	0	0
3	3-X	23	0	10	0	0
3	4-A	23	0	10	0	0
3	4-B	23	0	10	0	0
3	4-C	23	0	10	0	0
3	4-D	23	0	10	0	0
3	4-E	23	0	10	0	0
3	4-F	23	0	10	0	0
3	4-G	23	0	10	0	0
3	4-H	23	0	10	0	0
3	4-I	23	0	10	0	0
3	4-J	23	0	10	0	0
3	4-K	23	0	10	0	0
3	4-L	23	0	10	0	0
3	4-M	23	0	10	0	0
3	4-N	23	0	10	0	0
3	4-O	23	0	10	0	0
3	4-P	23	0	10	0	0
3	4-Q	23	0	10	0	0
3	4-R	23	0	10	0	0
3	4-S	23	0	10	0	0
3	4-T	23	0	10	0	0
3	4-U	23	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	4-V	23	0	10	0	0
3	4-W	23	0	10	0	0
3	4-X	23	0	10	0	0
3	5-A	23	0	10	0	0
3	5-B	23	0	10	0	0
3	5-C	23	0	10	0	0
3	5-D	23	0	10	0	0
3	5-E	23	0	10	0	0
3	5-F	23	0	10	0	0
3	5-G	23	0	10	0	0
3	5-H	23	0	10	0	0
3	5-I	23	0	10	0	0
3	5-J	23	0	10	0	0
3	5-K	23	0	10	0	0
3	5-L	23	0	10	0	0
3	5-M	23	0	10	0	0
3	5-N	23	0	10	0	0
3	5-O	23	0	10	0	0
3	5-P	23	0	10	0	0
3	5-Q	23	0	10	0	0
3	5-R	23	0	10	0	0
3	5-S	23	0	10	0	0
3	5-T	23	0	10	0	0
3	5-U	23	0	10	0	0
3	5-V	23	0	10	0	0
3	5-W	23	0	10	0	0
3	5-X	23	0	10	0	0
3	6-A	23	0	10	0	0
3	6-B	23	0	10	0	0
3	6-C	23	0	10	0	0
3	6-D	23	0	10	0	0
3	6-E	23	0	10	0	0
3	6-F	23	0	10	0	0
3	6-G	23	0	10	0	0
3	6-H	23	0	10	0	0
3	6-I	23	0	10	0	0
3	6-J	23	0	10	0	0
3	6-K	23	0	10	0	0
3	6-L	23	0	10	0	0
3	6-M	23	0	10	0	0
3	6-N	23	0	10	0	0
3	6-O	23	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	6-P	23	0	10	0	0
3	6-Q	23	0	10	0	0
3	6-R	23	0	10	0	0
3	6-S	23	0	10	0	0
3	6-T	23	0	10	0	0
3	6-U	23	0	10	0	0
3	6-V	23	0	10	0	0
3	6-W	23	0	10	0	0
3	6-X	23	0	10	0	0
3	7-A	23	0	10	0	0
3	7-B	23	0	10	0	0
3	7-C	23	0	10	0	0
3	7-D	23	0	10	0	0
3	7-E	23	0	10	0	0
3	7-F	23	0	10	0	0
3	7-G	23	0	10	0	0
3	7-H	23	0	10	0	0
3	7-I	23	0	10	0	0
3	7-J	23	0	10	0	0
3	7-K	23	0	10	0	0
3	7-L	23	0	10	0	0
3	7-M	23	0	10	0	0
3	7-N	23	0	10	0	0
3	7-O	23	0	10	0	0
3	7-P	23	0	10	0	0
3	7-Q	23	0	10	0	0
3	7-R	23	0	10	0	0
3	7-S	23	0	10	0	0
3	7-T	23	0	10	0	0
3	7-U	23	0	10	0	0
3	7-V	23	0	10	0	0
3	7-W	23	0	10	0	0
3	7-X	23	0	10	0	0
3	8-A	23	0	10	0	0
3	8-B	23	0	10	0	0
3	8-C	23	0	10	0	0
3	8-D	23	0	10	0	0
3	8-E	23	0	10	0	0
3	8-F	23	0	10	0	0
3	8-G	23	0	10	0	0
3	8-H	23	0	10	0	0
3	8-I	23	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	8-J	23	0	10	0	0
3	8-K	23	0	10	0	0
3	8-L	23	0	10	0	0
3	8-M	23	0	10	0	0
3	8-N	23	0	10	0	0
3	8-O	23	0	10	0	0
3	8-P	23	0	10	0	0
3	8-Q	23	0	10	0	0
3	8-R	23	0	10	0	0
3	8-S	23	0	10	0	0
3	8-T	23	0	10	0	0
3	8-U	23	0	10	0	0
3	8-V	23	0	10	0	0
3	8-W	23	0	10	0	0
3	8-X	23	0	10	0	0
3	9-A	23	0	10	0	0
3	9-B	23	0	10	0	0
3	9-C	23	0	10	0	0
3	9-D	23	0	10	0	0
3	9-E	23	0	10	0	0
3	9-F	23	0	10	0	0
3	9-G	23	0	10	0	0
3	9-H	23	0	10	0	0
3	9-I	23	0	10	0	0
3	9-J	23	0	10	0	0
3	9-K	23	0	10	0	0
3	9-L	23	0	10	0	0
3	9-M	23	0	10	0	0
3	9-N	23	0	10	0	0
3	9-O	23	0	10	0	0
3	9-P	23	0	10	0	0
3	9-Q	23	0	10	0	0
3	9-R	23	0	10	0	0
3	9-S	23	0	10	0	0
3	9-T	23	0	10	0	0
3	9-U	23	0	10	0	0
3	9-V	23	0	10	0	0
3	9-W	23	0	10	0	0
3	9-X	23	0	10	0	0
3	10-A	23	0	10	0	0
3	10-B	23	0	10	0	0
3	10-C	23	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	10-D	23	0	10	0	0
3	10-E	23	0	10	0	0
3	10-F	23	0	10	0	0
3	10-G	23	0	10	0	0
3	10-H	23	0	10	0	0
3	10-I	23	0	10	0	0
3	10-J	23	0	10	0	0
3	10-K	23	0	10	0	0
3	10-L	23	0	10	0	0
3	10-M	23	0	10	0	0
3	10-N	23	0	10	0	0
3	10-O	23	0	10	0	0
3	10-P	23	0	10	0	0
3	10-Q	23	0	10	0	0
3	10-R	23	0	10	0	0
3	10-S	23	0	10	0	0
3	10-T	23	0	10	0	0
3	10-U	23	0	10	0	0
3	10-V	23	0	10	0	0
3	10-W	23	0	10	0	0
3	10-X	23	0	10	0	0
4	1-A	13	0	5	0	0
4	1-B	13	0	5	0	0
4	1-C	13	0	5	0	0
4	1-D	13	0	5	0	0
4	1-E	13	0	5	0	0
4	1-F	13	0	5	0	0
4	1-G	13	0	5	0	0
4	1-H	13	0	5	0	0
4	1-I	13	0	5	0	0
4	1-J	13	0	5	0	0
4	1-K	13	0	5	0	0
4	1-L	13	0	5	0	0
4	1-M	13	0	5	0	0
4	1-N	13	0	5	0	0
4	1-O	13	0	5	0	0
4	1-P	13	0	5	0	0
4	1-Q	13	0	5	0	0
4	1-R	13	0	5	0	0
4	1-S	13	0	5	0	0
4	1-T	13	0	5	0	0
4	1-U	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	1-V	13	0	5	0	0
4	1-W	13	0	5	0	0
4	1-X	13	0	5	0	0
4	2-A	13	0	5	0	0
4	2-B	13	0	5	0	0
4	2-C	13	0	5	0	0
4	2-D	13	0	5	0	0
4	2-E	13	0	5	0	0
4	2-F	13	0	5	0	0
4	2-G	13	0	5	0	0
4	2-H	13	0	5	0	0
4	2-I	13	0	5	0	0
4	2-J	13	0	5	0	0
4	2-K	13	0	5	0	0
4	2-L	13	0	5	0	0
4	2-M	13	0	5	0	0
4	2-N	13	0	5	0	0
4	2-O	13	0	5	0	0
4	2-P	13	0	5	0	0
4	2-Q	13	0	5	0	0
4	2-R	13	0	5	0	0
4	2-S	13	0	5	0	0
4	2-T	13	0	5	0	0
4	2-U	13	0	5	0	0
4	2-V	13	0	5	0	0
4	2-W	13	0	5	0	0
4	2-X	13	0	5	0	0
4	3-A	13	0	5	0	0
4	3-B	13	0	5	0	0
4	3-C	13	0	5	0	0
4	3-D	13	0	5	0	0
4	3-E	13	0	5	0	0
4	3-F	13	0	5	0	0
4	3-G	13	0	5	0	0
4	3-H	13	0	5	0	0
4	3-I	13	0	5	0	0
4	3-J	13	0	5	0	0
4	3-K	13	0	5	0	0
4	3-L	13	0	5	0	0
4	3-M	13	0	5	0	0
4	3-N	13	0	5	0	0
4	3-O	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	3-P	13	0	5	0	0
4	3-Q	13	0	5	0	0
4	3-R	13	0	5	0	0
4	3-S	13	0	5	0	0
4	3-T	13	0	5	0	0
4	3-U	13	0	5	0	0
4	3-V	13	0	5	0	0
4	3-W	13	0	5	0	0
4	3-X	13	0	5	0	0
4	4-A	13	0	5	0	0
4	4-B	13	0	5	0	0
4	4-C	13	0	5	0	0
4	4-D	13	0	5	0	0
4	4-E	13	0	5	0	0
4	4-F	13	0	5	0	0
4	4-G	13	0	5	0	0
4	4-H	13	0	5	0	0
4	4-I	13	0	5	0	0
4	4-J	13	0	5	0	0
4	4-K	13	0	5	0	0
4	4-L	13	0	5	0	0
4	4-M	13	0	5	0	0
4	4-N	13	0	5	0	0
4	4-O	13	0	5	0	0
4	4-P	13	0	5	0	0
4	4-Q	13	0	5	0	0
4	4-R	13	0	5	0	0
4	4-S	13	0	5	0	0
4	4-T	13	0	5	0	0
4	4-U	13	0	5	0	0
4	4-V	13	0	5	0	0
4	4-W	13	0	5	0	0
4	4-X	13	0	5	0	0
4	5-A	13	0	5	0	0
4	5-B	13	0	5	0	0
4	5-C	13	0	5	0	0
4	5-D	13	0	5	0	0
4	5-E	13	0	5	0	0
4	5-F	13	0	5	0	0
4	5-G	13	0	5	0	0
4	5-H	13	0	5	0	0
4	5-I	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	5-J	13	0	5	0	0
4	5-K	13	0	5	0	0
4	5-L	13	0	5	0	0
4	5-M	13	0	5	0	0
4	5-N	13	0	5	0	0
4	5-O	13	0	5	0	0
4	5-P	13	0	5	0	0
4	5-Q	13	0	5	0	0
4	5-R	13	0	5	0	0
4	5-S	13	0	5	0	0
4	5-T	13	0	5	0	0
4	5-U	13	0	5	0	0
4	5-V	13	0	5	0	0
4	5-W	13	0	5	0	0
4	5-X	13	0	5	0	0
4	6-A	13	0	5	0	0
4	6-B	13	0	5	0	0
4	6-C	13	0	5	0	0
4	6-D	13	0	5	0	0
4	6-E	13	0	5	0	0
4	6-F	13	0	5	0	0
4	6-G	13	0	5	0	0
4	6-H	13	0	5	0	0
4	6-I	13	0	5	0	0
4	6-J	13	0	5	0	0
4	6-K	13	0	5	0	0
4	6-L	13	0	5	0	0
4	6-M	13	0	5	0	0
4	6-N	13	0	5	0	0
4	6-O	13	0	5	0	0
4	6-P	13	0	5	0	0
4	6-Q	13	0	5	0	0
4	6-R	13	0	5	0	0
4	6-S	13	0	5	0	0
4	6-T	13	0	5	0	0
4	6-U	13	0	5	0	0
4	6-V	13	0	5	0	0
4	6-W	13	0	5	0	0
4	6-X	13	0	5	0	0
4	7-A	13	0	5	0	0
4	7-B	13	0	5	0	0
4	7-C	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	7-D	13	0	5	0	0
4	7-E	13	0	5	0	0
4	7-F	13	0	5	0	0
4	7-G	13	0	5	0	0
4	7-H	13	0	5	0	0
4	7-I	13	0	5	0	0
4	7-J	13	0	5	0	0
4	7-K	13	0	5	0	0
4	7-L	13	0	5	0	0
4	7-M	13	0	5	0	0
4	7-N	13	0	5	0	0
4	7-O	13	0	5	0	0
4	7-P	13	0	5	0	0
4	7-Q	13	0	5	0	0
4	7-R	13	0	5	0	0
4	7-S	13	0	5	0	0
4	7-T	13	0	5	0	0
4	7-U	13	0	5	0	0
4	7-V	13	0	5	0	0
4	7-W	13	0	5	0	0
4	7-X	13	0	5	0	0
4	8-A	13	0	5	0	0
4	8-B	13	0	5	0	0
4	8-C	13	0	5	0	0
4	8-D	13	0	5	0	0
4	8-E	13	0	5	0	0
4	8-F	13	0	5	0	0
4	8-G	13	0	5	0	0
4	8-H	13	0	5	0	0
4	8-I	13	0	5	0	0
4	8-J	13	0	5	0	0
4	8-K	13	0	5	0	0
4	8-L	13	0	5	0	0
4	8-M	13	0	5	0	0
4	8-N	13	0	5	0	0
4	8-O	13	0	5	0	0
4	8-P	13	0	5	0	0
4	8-Q	13	0	5	0	0
4	8-R	13	0	5	0	0
4	8-S	13	0	5	0	0
4	8-T	13	0	5	0	0
4	8-U	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	8-V	13	0	5	0	0
4	8-W	13	0	5	0	0
4	8-X	13	0	5	0	0
4	9-A	13	0	5	0	0
4	9-B	13	0	5	0	0
4	9-C	13	0	5	0	0
4	9-D	13	0	5	0	0
4	9-E	13	0	5	0	0
4	9-F	13	0	5	0	0
4	9-G	13	0	5	0	0
4	9-H	13	0	5	0	0
4	9-I	13	0	5	0	0
4	9-J	13	0	5	0	0
4	9-K	13	0	5	0	0
4	9-L	13	0	5	0	0
4	9-M	13	0	5	0	0
4	9-N	13	0	5	0	0
4	9-O	13	0	5	0	0
4	9-P	13	0	5	0	0
4	9-Q	13	0	5	0	0
4	9-R	13	0	5	0	0
4	9-S	13	0	5	0	0
4	9-T	13	0	5	0	0
4	9-U	13	0	5	0	0
4	9-V	13	0	5	0	0
4	9-W	13	0	5	0	0
4	9-X	13	0	5	0	0
4	10-A	13	0	5	0	0
4	10-B	13	0	5	0	0
4	10-C	13	0	5	0	0
4	10-D	13	0	5	0	0
4	10-E	13	0	5	0	0
4	10-F	13	0	5	0	0
4	10-G	13	0	5	0	0
4	10-H	13	0	5	0	0
4	10-I	13	0	5	0	0
4	10-J	13	0	5	0	0
4	10-K	13	0	5	0	0
4	10-L	13	0	5	0	0
4	10-M	13	0	5	0	0
4	10-N	13	0	5	0	0
4	10-O	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	10-P	13	0	5	0	0
4	10-Q	13	0	5	0	0
4	10-R	13	0	5	0	0
4	10-S	13	0	5	0	0
4	10-T	13	0	5	0	0
4	10-U	13	0	5	0	0
4	10-V	13	0	5	0	0
4	10-W	13	0	5	0	0
4	10-X	13	0	5	0	0
5	1-A	261	0	0	0	0
5	1-B	264	0	0	0	0
5	1-C	261	0	0	0	0
5	1-D	260	0	0	0	0
5	1-E	261	0	0	0	0
5	1-F	262	0	0	0	0
5	1-G	265	0	0	0	0
5	1-H	262	0	0	0	0
5	1-I	265	0	0	0	0
5	1-J	262	0	0	0	0
5	1-K	272	0	0	0	0
5	1-L	261	0	0	0	0
5	1-M	261	0	0	0	0
5	1-N	263	0	0	0	0
5	1-O	263	0	0	0	0
5	1-P	261	0	0	0	0
5	1-Q	260	0	0	0	0
5	1-R	261	0	0	0	0
5	1-S	265	0	0	0	0
5	1-T	261	0	0	0	0
5	1-U	263	0	0	0	0
5	1-V	265	0	0	0	0
5	1-W	269	0	0	0	0
5	1-X	264	0	0	0	0
5	2-A	262	0	0	0	0
5	2-B	261	0	0	0	0
5	2-C	264	0	0	0	0
5	2-D	269	0	0	0	0
5	2-E	254	0	0	0	0
5	2-F	263	0	0	0	0
5	2-G	262	0	0	0	0
5	2-H	263	0	0	0	0
5	2-I	265	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	2-J	258	0	0	0	0
5	2-K	271	0	0	0	0
5	2-L	264	0	0	0	0
5	2-M	264	0	0	0	0
5	2-N	261	0	0	0	0
5	2-O	267	0	0	0	0
5	2-P	264	0	0	0	0
5	2-Q	257	0	0	0	0
5	2-R	265	0	0	0	0
5	2-S	259	0	0	0	0
5	2-T	259	0	0	0	0
5	2-U	267	0	0	0	0
5	2-V	260	0	0	0	0
5	2-W	266	0	0	0	0
5	2-X	267	0	0	0	0
5	3-A	261	0	0	0	0
5	3-B	263	0	0	0	0
5	3-C	265	0	0	0	0
5	3-D	260	0	0	0	0
5	3-E	257	0	0	0	0
5	3-F	272	0	0	0	0
5	3-G	257	0	0	0	0
5	3-H	261	0	0	0	0
5	3-I	266	0	0	0	0
5	3-J	260	0	0	0	0
5	3-K	268	0	0	0	0
5	3-L	266	0	0	0	0
5	3-M	259	0	0	0	0
5	3-N	263	0	0	0	0
5	3-O	265	0	0	0	0
5	3-P	260	0	0	0	0
5	3-Q	259	0	0	0	0
5	3-R	268	0	0	0	0
5	3-S	264	0	0	0	0
5	3-T	262	0	0	0	0
5	3-U	267	0	0	0	0
5	3-V	258	0	0	0	0
5	3-W	266	0	0	0	0
5	3-X	265	0	0	0	0
5	4-A	263	0	0	0	0
5	4-B	262	0	0	0	0
5	4-C	261	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	4-D	263	0	0	0	0
5	4-E	263	0	0	0	0
5	4-F	264	0	0	0	0
5	4-G	261	0	0	0	0
5	4-H	266	0	0	0	0
5	4-I	263	0	0	0	0
5	4-J	260	0	0	0	0
5	4-K	267	0	0	0	0
5	4-L	263	0	0	0	0
5	4-M	264	0	0	0	0
5	4-N	263	0	0	0	0
5	4-O	263	0	0	0	0
5	4-P	259	0	0	0	0
5	4-Q	264	0	0	0	0
5	4-R	263	0	0	0	0
5	4-S	260	0	0	0	0
5	4-T	262	0	0	0	0
5	4-U	264	0	0	0	0
5	4-V	266	0	0	0	0
5	4-W	263	0	0	0	0
5	4-X	265	0	0	0	0
5	5-A	261	0	0	0	0
5	5-B	261	0	0	0	0
5	5-C	263	0	0	0	0
5	5-D	262	0	0	0	0
5	5-E	259	0	0	0	0
5	5-F	266	0	0	0	0
5	5-G	263	0	0	0	0
5	5-H	270	0	0	0	0
5	5-I	260	0	0	0	0
5	5-J	263	0	0	0	0
5	5-K	268	0	0	0	0
5	5-L	260	0	0	0	0
5	5-M	264	0	0	0	0
5	5-N	265	0	0	0	0
5	5-O	267	0	0	0	0
5	5-P	262	0	0	0	0
5	5-Q	261	0	0	0	0
5	5-R	265	0	0	0	0
5	5-S	263	0	0	0	0
5	5-T	258	0	0	0	0
5	5-U	263	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	5-V	261	0	0	0	0
5	5-W	262	0	0	0	0
5	5-X	265	0	0	0	0
5	6-A	257	0	0	0	0
5	6-B	265	0	0	0	0
5	6-C	262	0	0	0	0
5	6-D	265	0	0	0	0
5	6-E	262	0	0	0	0
5	6-F	263	0	0	0	0
5	6-G	267	0	0	0	0
5	6-H	263	0	0	0	0
5	6-I	263	0	0	0	0
5	6-J	259	0	0	0	0
5	6-K	270	0	0	0	0
5	6-L	260	0	0	0	0
5	6-M	262	0	0	0	0
5	6-N	260	0	0	0	0
5	6-O	265	0	0	0	0
5	6-P	262	0	0	0	0
5	6-Q	260	0	0	0	0
5	6-R	266	0	0	0	0
5	6-S	266	0	0	0	0
5	6-T	257	0	0	0	0
5	6-U	265	0	0	0	0
5	6-V	265	0	0	0	0
5	6-W	264	0	0	0	0
5	6-X	264	0	0	0	0
5	7-A	265	0	0	0	0
5	7-B	264	0	0	0	0
5	7-C	262	0	0	0	0
5	7-D	261	0	0	0	0
5	7-E	265	0	0	0	0
5	7-F	262	0	0	0	0
5	7-G	259	0	0	0	0
5	7-H	262	0	0	0	0
5	7-I	261	0	0	0	0
5	7-J	266	0	0	0	0
5	7-K	263	0	0	0	0
5	7-L	266	0	0	0	0
5	7-M	260	0	0	0	0
5	7-N	266	0	0	0	0
5	7-O	262	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	7-P	261	0	0	0	0
5	7-Q	264	0	0	0	0
5	7-R	264	0	0	0	0
5	7-S	263	0	0	0	0
5	7-T	263	0	0	0	0
5	7-U	262	0	0	0	0
5	7-V	265	0	0	0	0
5	7-W	265	0	0	0	0
5	7-X	261	0	0	0	0
5	8-A	259	0	0	0	0
5	8-B	264	0	0	0	0
5	8-C	263	0	0	0	0
5	8-D	265	0	0	0	0
5	8-E	257	0	0	0	0
5	8-F	268	0	0	0	0
5	8-G	265	0	0	0	0
5	8-H	261	0	0	0	0
5	8-I	265	0	0	0	0
5	8-J	263	0	0	0	0
5	8-K	264	0	0	0	0
5	8-L	262	0	0	0	0
5	8-M	260	0	0	0	0
5	8-N	263	0	0	0	0
5	8-O	265	0	0	0	0
5	8-P	263	0	0	0	0
5	8-Q	257	0	0	0	0
5	8-R	265	0	0	0	0
5	8-S	269	0	0	0	0
5	8-T	259	0	0	0	0
5	8-U	263	0	0	0	0
5	8-V	264	0	0	0	0
5	8-W	263	0	0	0	0
5	8-X	265	0	0	0	0
5	9-A	265	0	0	0	0
5	9-B	258	0	0	0	0
5	9-C	261	0	0	0	0
5	9-D	266	0	0	0	0
5	9-E	262	0	0	0	0
5	9-F	262	0	0	0	0
5	9-G	263	0	0	0	0
5	9-H	268	0	0	0	0
5	9-I	262	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	9-J	260	0	0	0	0
5	9-K	269	0	0	0	0
5	9-L	260	0	0	0	0
5	9-M	265	0	0	0	0
5	9-N	261	0	0	0	0
5	9-O	263	0	0	0	0
5	9-P	265	0	0	0	0
5	9-Q	263	0	0	0	0
5	9-R	264	0	0	0	0
5	9-S	259	0	0	0	0
5	9-T	265	0	0	0	0
5	9-U	265	0	0	0	0
5	9-V	259	0	0	0	0
5	9-W	261	0	0	0	0
5	9-X	266	0	0	0	0
5	10-A	262	0	0	0	0
5	10-B	263	0	0	0	0
5	10-C	262	0	0	0	0
5	10-D	262	0	0	0	0
5	10-E	257	0	0	0	0
5	10-F	261	0	0	0	0
5	10-G	264	0	0	0	0
5	10-H	264	0	0	0	0
5	10-I	263	0	0	0	0
5	10-J	264	0	0	0	0
5	10-K	271	0	0	0	0
5	10-L	263	0	0	0	0
5	10-M	263	0	0	0	0
5	10-N	259	0	0	0	0
5	10-O	263	0	0	0	0
5	10-P	264	0	0	0	0
5	10-Q	257	0	0	0	0
5	10-R	262	0	0	0	0
5	10-S	266	0	0	0	0
5	10-T	262	0	0	0	0
5	10-U	264	0	0	0	0
5	10-V	265	0	0	0	0
5	10-W	265	0	0	0	0
5	10-X	266	0	0	0	0
All	All	978720	0	868551	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	1-A	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-B	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-C	475/477 (100%)	430 (90%)	28 (6%)	17 (4%)	2	2
1	1-D	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-E	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-F	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-G	475/477 (100%)	430 (90%)	28 (6%)	17 (4%)	2	2
1	1-H	475/477 (100%)	430 (90%)	28 (6%)	17 (4%)	2	2
1	1-I	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-J	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-K	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-L	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-M	475/477 (100%)	430 (90%)	28 (6%)	17 (4%)	2	2
1	1-N	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-O	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-P	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-Q	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-R	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-S	475/477 (100%)	430 (90%)	28 (6%)	17 (4%)	2	2
1	1-T	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-U	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-V	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-W	475/477 (100%)	429 (90%)	29 (6%)	17 (4%)	2	2
1	1-X	475/477 (100%)	430 (90%)	28 (6%)	17 (4%)	2	2
1	2-A	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-B	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-C	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-D	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-E	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-F	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-G	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-H	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-I	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-J	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-K	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-L	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-M	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-N	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-O	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-P	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-Q	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-R	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-S	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-T	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-U	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-V	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-W	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	2-X	475/477 (100%)	429 (90%)	28 (6%)	18 (4%)	2	2
1	3-A	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-B	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-C	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-D	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3-E	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-F	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-G	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-H	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-I	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-J	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-K	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-L	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-M	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-N	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-O	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-P	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-Q	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-R	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-S	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-T	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-U	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-V	475/477 (100%)	433 (91%)	30 (6%)	12 (2%)	4	5
1	3-W	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	3-X	475/477 (100%)	432 (91%)	31 (6%)	12 (2%)	4	5
1	4-A	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-B	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-C	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-D	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-E	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-F	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-G	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-H	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-I	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-J	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-K	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	4-L	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-M	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-N	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-O	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-P	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-Q	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-R	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-S	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-T	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-U	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-V	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-W	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	4-X	475/477 (100%)	428 (90%)	33 (7%)	14 (3%)	3	3
1	5-A	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-B	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-C	475/477 (100%)	423 (89%)	43 (9%)	9 (2%)	6	8
1	5-D	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-E	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-F	475/477 (100%)	423 (89%)	43 (9%)	9 (2%)	6	8
1	5-G	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-H	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-I	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-J	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-K	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-L	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-M	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-N	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-O	475/477 (100%)	423 (89%)	43 (9%)	9 (2%)	6	8
1	5-P	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-Q	475/477 (100%)	423 (89%)	43 (9%)	9 (2%)	6	8
1	5-R	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	5-S	475/477 (100%)	423 (89%)	43 (9%)	9 (2%)	6	8
1	5-T	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-U	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-V	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-W	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	5-X	475/477 (100%)	424 (89%)	42 (9%)	9 (2%)	6	8
1	6-A	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-B	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-C	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-D	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-E	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-F	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-G	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-H	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-I	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-J	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-K	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-L	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-M	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-N	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-O	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-P	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-Q	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-R	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-S	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-T	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	6-U	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-V	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-W	475/477 (100%)	423 (89%)	39 (8%)	13 (3%)	4	4
1	6-X	475/477 (100%)	423 (89%)	40 (8%)	12 (2%)	4	5
1	7-A	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	7-B	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-C	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-D	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-E	475/477 (100%)	424 (89%)	35 (7%)	16 (3%)	3	2
1	7-F	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-G	475/477 (100%)	424 (89%)	35 (7%)	16 (3%)	3	2
1	7-H	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-I	475/477 (100%)	424 (89%)	35 (7%)	16 (3%)	3	2
1	7-J	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-K	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-L	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-M	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-N	475/477 (100%)	424 (89%)	35 (7%)	16 (3%)	3	2
1	7-O	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-P	475/477 (100%)	424 (89%)	35 (7%)	16 (3%)	3	2
1	7-Q	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-R	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-S	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-T	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-U	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-V	475/477 (100%)	424 (89%)	35 (7%)	16 (3%)	3	2
1	7-W	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	7-X	475/477 (100%)	423 (89%)	36 (8%)	16 (3%)	3	2
1	8-A	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-B	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-C	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-D	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-E	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-F	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-G	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-H	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	8-I	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-J	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-K	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-L	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-M	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-N	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-O	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-P	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-Q	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-R	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-S	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-T	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-U	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-V	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-W	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	8-X	475/477 (100%)	434 (91%)	32 (7%)	9 (2%)	6	8
1	9-A	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-B	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-C	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-D	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-E	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-F	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-G	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-H	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-I	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-J	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-K	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-L	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-M	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-N	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-O	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	9-P	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-Q	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-R	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-S	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-T	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-U	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-V	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	9-W	475/477 (100%)	425 (90%)	41 (9%)	9 (2%)	6	8
1	9-X	475/477 (100%)	426 (90%)	40 (8%)	9 (2%)	6	8
1	10-A	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-B	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-C	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-D	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-E	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-F	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-G	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-H	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-I	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-J	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-K	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-L	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-M	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-N	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-O	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-P	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-Q	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-R	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-S	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-T	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-U	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-V	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	10-W	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
1	10-X	475/477 (100%)	421 (89%)	41 (9%)	13 (3%)	4	4
All	All	114000/114480 (100%)	102469 (90%)	8420 (7%)	3111 (3%)	4	4

5 of 3111 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	57	PHE
1	1-A	59	SER
1	1-A	63	SER
1	1-A	327	GLU
1	1-B	57	PHE

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	1-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-N	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	1-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-U	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	2-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	3-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-D	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	4-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-K	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	5-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	5-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-R	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	6-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	6-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	7-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-A	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	8-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	8-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-H	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	9-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-O	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	9-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-A	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-B	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-C	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-D	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-E	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-F	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-G	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-H	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-I	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-J	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-K	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-L	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-M	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-N	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-O	404/404 (100%)	371 (92%)	33 (8%)	10	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	10-P	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-Q	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-R	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-S	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-T	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-U	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-V	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-W	404/404 (100%)	371 (92%)	33 (8%)	10	18
1	10-X	404/404 (100%)	371 (92%)	33 (8%)	10	18
All	All	96960/96960 (100%)	89040 (92%)	7920 (8%)	10	18

5 of 7920 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5-Q	67	LEU
1	9-W	413	GLN
1	6-S	420	ARG
1	9-U	323	VAL
1	10-N	173	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 4099 such sidechains are listed below:

Mol	Chain	Res	Type
1	9-X	210	HIS
1	10-F	458	HIS
1	9-X	86	ASN
1	4-V	272	GLN
1	4-S	272	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 720 ligands modelled in this entry, 240 are monoatomic - leaving 480 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	AMP	9-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	2-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	10-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	9-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	9-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	9-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	1-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	7-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	2-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	1-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	7-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	6-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	8-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	3-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	3-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	7-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	6-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	2-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	3-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	1-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	5-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	10-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	4-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	5-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	10-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	10-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	9-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	2-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CIT	3-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	5-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	1-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	7-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	4-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	9-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	7-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	2-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	2-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	5-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	9-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	9-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	6-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	5-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	1-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	8-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	5-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	6-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	10-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	10-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	1-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	4-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	10-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	1-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	10-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	2-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	9-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	9-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	10-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	5-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	9-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	8-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	7-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	9-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	9-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	2-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	3-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	6-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	2-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	10-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	8-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	10-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	4-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	8-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	1-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	10-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	3-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	2-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	3-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	1-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	2-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	6-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	8-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	9-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CIT	1-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	7-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	3-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	5-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	9-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	4-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	3-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	3-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	2-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	6-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	6-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	10-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	5-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	3-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	2-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	6-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CIT	5-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	4-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	5-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	5-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	5-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	4-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	8-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	2-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	1-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	10-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	10-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	9-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	8-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	1-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	8-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	7-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	8-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	5-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	5-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	9-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	1-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	10-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	10-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	1-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	8-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	3-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	5-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	5-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	2-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	3-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	2-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	5-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	4-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	10-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	4-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	9-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	3-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	1-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	5-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	8-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	10-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	2-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	1-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	2-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	10-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	4-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	2-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	2-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	10-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	6-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	8-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	8-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	8-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	7-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	10-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	2-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	3-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	8-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	3-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	6-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	2-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	1-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	9-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	1-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-N	7501	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	7-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	7-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	7-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	2-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	5-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	9-D	7482	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	10-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	6-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	7-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	9-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	1-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	5-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	5-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	6-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	1-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	5-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-H	7490	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	7-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	3-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	4-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	9-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	9-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	4-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	1-C	7480	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	4-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	7-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	5-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	6-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	4-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CIT	10-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	1-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	6-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	4-W	7520	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	10-H	7489	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	9-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	2-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	10-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	5-U	7516	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	1-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	9-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	1-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	10-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	6-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	3-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	3-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	9-C	7479	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	9-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	9-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	9-A	7476	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	7-A	7475	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	5-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	7-B	7477	-	25,25,25	4.11	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	8-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	10-I	7491	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	9-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	1-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	1-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	5-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	10-V	7517	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	10-L	7498	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
3	AMP	7-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-N	7502	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	6 (35%)
4	CIT	3-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-O	7503	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
3	AMP	6-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-E	7484	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	6-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	5-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	7-K	7495	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-K	7496	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	4-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	9-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	7-J	7494	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	4-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	6-T	7513	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	3-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	10-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	8-O	7504	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	2-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	1-G	7487	-	25,25,25	4.09	16 (64%)	37,38,38	3.17	14 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CIT	8-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	7-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-I	7492	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-P	7506	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	5-L	7497	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	9-M	7499	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	10-V	7518	-	12,12,12	3.43	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	8-B	7478	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	7-F	7486	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
4	CIT	10-Q	7508	-	12,12,12	3.41	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	9-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	3-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	2-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	8-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	3-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-Q	7507	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	9-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	2-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	7-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	1-R	7510	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	6-P	7505	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	6-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	2-S	7512	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-J	7493	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	10-W	7519	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	7-G	7488	-	12,12,12	3.41	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-S	7511	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	2-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	2-D	7481	-	25,25,25	4.10	16 (64%)	37,38,38	3.18	14 (37%)
4	CIT	4-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)
4	CIT	6-T	7514	-	12,12,12	3.40	9 (75%)	17,17,17	1.83	7 (41%)
3	AMP	6-F	7485	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	5-X	7522	-	12,12,12	3.39	9 (75%)	17,17,17	1.84	7 (41%)
3	AMP	7-X	7521	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	6-E	7483	-	25,25,25	4.09	16 (64%)	37,38,38	3.18	14 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	AMP	10-R	7509	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
3	AMP	6-U	7515	-	25,25,25	4.10	16 (64%)	37,38,38	3.17	14 (37%)
4	CIT	8-M	7500	-	12,12,12	3.40	9 (75%)	17,17,17	1.84	7 (41%)

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	AMP	9-I	7491	-	-	6/10/26/26	0/3/3/3
3	AMP	2-G	7487	-	-	6/10/26/26	0/3/3/3
3	AMP	10-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	2-P	7506	-	-	3/16/16/16	-
4	CIT	9-R	7510	-	-	3/16/16/16	-
3	AMP	2-A	7475	-	-	6/10/26/26	0/3/3/3
4	CIT	9-N	7502	-	-	3/16/16/16	-
3	AMP	9-A	7475	-	-	6/10/26/26	0/3/3/3
4	CIT	8-K	7496	-	-	3/16/16/16	-
4	CIT	5-L	7498	-	-	3/16/16/16	-
3	AMP	9-S	7511	-	-	6/10/26/26	0/3/3/3
3	AMP	1-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	7-V	7518	-	-	3/16/16/16	-
3	AMP	7-H	7489	-	-	6/10/26/26	0/3/3/3
4	CIT	2-K	7496	-	-	3/16/16/16	-
4	CIT	7-E	7484	-	-	3/16/16/16	-
4	CIT	9-Q	7508	-	-	3/16/16/16	-
3	AMP	1-J	7493	-	-	6/10/26/26	0/3/3/3
3	AMP	5-A	7475	-	-	6/10/26/26	0/3/3/3
3	AMP	2-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	6-C	7480	-	-	3/16/16/16	-
4	CIT	1-M	7500	-	-	3/16/16/16	-
3	AMP	7-F	7485	-	-	6/10/26/26	0/3/3/3
3	AMP	4-J	7493	-	-	6/10/26/26	0/3/3/3
4	CIT	3-N	7502	-	-	3/16/16/16	-
3	AMP	6-O	7503	-	-	6/10/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	8-U	7515	-	-	6/10/26/26	0/3/3/3
3	AMP	5-B	7477	-	-	6/10/26/26	0/3/3/3
3	AMP	4-D	7481	-	-	6/10/26/26	0/3/3/3
3	AMP	3-S	7511	-	-	6/10/26/26	0/3/3/3
3	AMP	8-R	7509	-	-	6/10/26/26	0/3/3/3
3	AMP	4-R	7509	-	-	6/10/26/26	0/3/3/3
4	CIT	5-C	7480	-	-	3/16/16/16	-
4	CIT	3-H	7490	-	-	3/16/16/16	-
3	AMP	7-R	7509	-	-	6/10/26/26	0/3/3/3
4	CIT	8-R	7510	-	-	3/16/16/16	-
4	CIT	7-Q	7508	-	-	3/16/16/16	-
4	CIT	6-R	7510	-	-	3/16/16/16	-
4	CIT	2-A	7476	-	-	3/16/16/16	-
4	CIT	7-W	7520	-	-	3/16/16/16	-
3	AMP	3-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	1-P	7506	-	-	3/16/16/16	-
3	AMP	5-S	7511	-	-	6/10/26/26	0/3/3/3
3	AMP	10-S	7511	-	-	6/10/26/26	0/3/3/3
4	CIT	4-J	7494	-	-	3/16/16/16	-
3	AMP	5-D	7481	-	-	6/10/26/26	0/3/3/3
4	CIT	10-H	7490	-	-	3/16/16/16	-
3	AMP	10-M	7499	-	-	6/10/26/26	0/3/3/3
3	AMP	9-J	7493	-	-	6/10/26/26	0/3/3/3
4	CIT	8-T	7514	-	-	3/16/16/16	-
3	AMP	2-L	7497	-	-	6/10/26/26	0/3/3/3
4	CIT	8-U	7516	-	-	3/16/16/16	-
4	CIT	9-M	7500	-	-	3/16/16/16	-
4	CIT	1-D	7482	-	-	3/16/16/16	-
3	AMP	1-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	5-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	10-P	7506	-	-	3/16/16/16	-
4	CIT	3-K	7496	-	-	3/16/16/16	-
3	AMP	5-N	7501	-	-	6/10/26/26	0/3/3/3
3	AMP	1-P	7505	-	-	6/10/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	7-T	7513	-	-	6/10/26/26	0/3/3/3
3	AMP	4-C	7479	-	-	6/10/26/26	0/3/3/3
3	AMP	9-T	7513	-	-	6/10/26/26	0/3/3/3
3	AMP	7-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	6-A	7476	-	-	3/16/16/16	-
3	AMP	4-M	7499	-	-	6/10/26/26	0/3/3/3
3	AMP	8-J	7493	-	-	6/10/26/26	0/3/3/3
3	AMP	3-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	4-H	7490	-	-	3/16/16/16	-
3	AMP	3-F	7485	-	-	6/10/26/26	0/3/3/3
3	AMP	2-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	2-R	7509	-	-	6/10/26/26	0/3/3/3
3	AMP	3-T	7513	-	-	6/10/26/26	0/3/3/3
3	AMP	5-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	9-K	7496	-	-	3/16/16/16	-
3	AMP	9-R	7509	-	-	6/10/26/26	0/3/3/3
3	AMP	8-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	6-I	7492	-	-	3/16/16/16	-
4	CIT	6-D	7482	-	-	3/16/16/16	-
3	AMP	1-W	7519	-	-	6/10/26/26	0/3/3/3
3	AMP	7-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	3-C	7480	-	-	3/16/16/16	-
3	AMP	5-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	1-U	7516	-	-	3/16/16/16	-
4	CIT	8-H	7490	-	-	3/16/16/16	-
3	AMP	6-C	7479	-	-	6/10/26/26	0/3/3/3
4	CIT	5-G	7488	-	-	3/16/16/16	-
4	CIT	6-E	7484	-	-	3/16/16/16	-
3	AMP	10-K	7495	-	-	6/10/26/26	0/3/3/3
4	CIT	10-B	7478	-	-	3/16/16/16	-
4	CIT	1-F	7486	-	-	3/16/16/16	-
4	CIT	1-N	7502	-	-	3/16/16/16	-
3	AMP	4-L	7497	-	-	6/10/26/26	0/3/3/3
4	CIT	2-I	7492	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	1-D	7481	-	-	6/10/26/26	0/3/3/3
4	CIT	10-U	7516	-	-	3/16/16/16	-
4	CIT	4-X	7522	-	-	3/16/16/16	-
3	AMP	4-A	7475	-	-	6/10/26/26	0/3/3/3
4	CIT	8-Q	7508	-	-	3/16/16/16	-
4	CIT	1-V	7518	-	-	3/16/16/16	-
3	AMP	10-J	7493	-	-	6/10/26/26	0/3/3/3
3	AMP	7-N	7501	-	-	6/10/26/26	0/3/3/3
3	AMP	10-N	7501	-	-	6/10/26/26	0/3/3/3
3	AMP	2-T	7513	-	-	6/10/26/26	0/3/3/3
3	AMP	10-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	9-N	7501	-	-	6/10/26/26	0/3/3/3
4	CIT	4-Q	7508	-	-	3/16/16/16	-
3	AMP	9-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	5-H	7490	-	-	3/16/16/16	-
3	AMP	10-C	7479	-	-	6/10/26/26	0/3/3/3
4	CIT	5-O	7504	-	-	3/16/16/16	-
3	AMP	9-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	7-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	8-L	7498	-	-	3/16/16/16	-
3	AMP	7-C	7479	-	-	6/10/26/26	0/3/3/3
3	AMP	9-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	10-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	9-F	7486	-	-	3/16/16/16	-
3	AMP	2-B	7477	-	-	6/10/26/26	0/3/3/3
4	CIT	3-X	7522	-	-	3/16/16/16	-
4	CIT	1-T	7514	-	-	3/16/16/16	-
4	CIT	3-R	7510	-	-	3/16/16/16	-
3	AMP	2-X	7521	-	-	6/10/26/26	0/3/3/3
4	CIT	2-H	7490	-	-	3/16/16/16	-
3	AMP	8-A	7475	-	-	6/10/26/26	0/3/3/3
3	AMP	6-M	7499	-	-	6/10/26/26	0/3/3/3
4	CIT	2-L	7498	-	-	3/16/16/16	-
3	AMP	2-V	7517	-	-	6/10/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	10-F	7486	-	-	3/16/16/16	-
3	AMP	1-L	7497	-	-	6/10/26/26	0/3/3/3
3	AMP	7-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	8-V	7518	-	-	3/16/16/16	-
4	CIT	10-C	7480	-	-	3/16/16/16	-
3	AMP	4-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	4-L	7498	-	-	3/16/16/16	-
3	AMP	8-C	7479	-	-	6/10/26/26	0/3/3/3
4	CIT	1-W	7520	-	-	3/16/16/16	-
4	CIT	10-I	7492	-	-	3/16/16/16	-
4	CIT	5-W	7520	-	-	3/16/16/16	-
4	CIT	3-U	7516	-	-	3/16/16/16	-
3	AMP	6-R	7509	-	-	6/10/26/26	0/3/3/3
3	AMP	8-D	7481	-	-	6/10/26/26	0/3/3/3
4	CIT	2-C	7480	-	-	3/16/16/16	-
4	CIT	3-B	7478	-	-	3/16/16/16	-
3	AMP	3-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	10-M	7500	-	-	3/16/16/16	-
3	AMP	3-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	8-K	7495	-	-	6/10/26/26	0/3/3/3
4	CIT	1-Q	7508	-	-	3/16/16/16	-
4	CIT	2-V	7518	-	-	3/16/16/16	-
4	CIT	6-H	7490	-	-	3/16/16/16	-
4	CIT	9-X	7522	-	-	3/16/16/16	-
4	CIT	8-J	7494	-	-	3/16/16/16	-
3	AMP	1-A	7475	-	-	6/10/26/26	0/3/3/3
4	CIT	9-G	7488	-	-	3/16/16/16	-
3	AMP	4-B	7477	-	-	6/10/26/26	0/3/3/3
4	CIT	6-Q	7508	-	-	3/16/16/16	-
3	AMP	9-L	7497	-	-	6/10/26/26	0/3/3/3
4	CIT	3-E	7484	-	-	3/16/16/16	-
4	CIT	5-B	7478	-	-	3/16/16/16	-
4	CIT	1-I	7492	-	-	3/16/16/16	-
4	CIT	4-V	7518	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	1-S	7512	-	-	3/16/16/16	-
3	AMP	7-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	2-W	7520	-	-	3/16/16/16	-
3	AMP	3-D	7481	-	-	6/10/26/26	0/3/3/3
3	AMP	5-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	9-W	7520	-	-	3/16/16/16	-
3	AMP	4-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	3-S	7512	-	-	3/16/16/16	-
4	CIT	1-L	7498	-	-	3/16/16/16	-
3	AMP	3-E	7483	-	-	6/10/26/26	0/3/3/3
4	CIT	2-B	7478	-	-	3/16/16/16	-
3	AMP	1-T	7513	-	-	6/10/26/26	0/3/3/3
3	AMP	6-L	7497	-	-	6/10/26/26	0/3/3/3
3	AMP	8-P	7505	-	-	6/10/26/26	0/3/3/3
3	AMP	10-D	7481	-	-	6/10/26/26	0/3/3/3
3	AMP	6-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	10-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	8-S	7511	-	-	6/10/26/26	0/3/3/3
3	AMP	3-M	7499	-	-	6/10/26/26	0/3/3/3
4	CIT	10-E	7484	-	-	3/16/16/16	-
3	AMP	6-H	7489	-	-	6/10/26/26	0/3/3/3
4	CIT	7-S	7512	-	-	3/16/16/16	-
3	AMP	6-J	7493	-	-	6/10/26/26	0/3/3/3
3	AMP	10-T	7513	-	-	6/10/26/26	0/3/3/3
4	CIT	5-V	7518	-	-	3/16/16/16	-
3	AMP	1-B	7477	-	-	6/10/26/26	0/3/3/3
3	AMP	8-T	7513	-	-	6/10/26/26	0/3/3/3
3	AMP	3-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	9-S	7512	-	-	3/16/16/16	-
3	AMP	8-I	7491	-	-	6/10/26/26	0/3/3/3
3	AMP	4-N	7501	-	-	6/10/26/26	0/3/3/3
4	CIT	2-X	7522	-	-	3/16/16/16	-
4	CIT	6-B	7478	-	-	3/16/16/16	-
3	AMP	3-L	7497	-	-	6/10/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	8-A	7476	-	-	3/16/16/16	-
4	CIT	5-D	7482	-	-	3/16/16/16	-
4	CIT	9-L	7498	-	-	3/16/16/16	-
3	AMP	4-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	10-E	7483	-	-	6/10/26/26	0/3/3/3
4	CIT	5-N	7502	-	-	3/16/16/16	-
4	CIT	5-S	7512	-	-	3/16/16/16	-
3	AMP	1-S	7511	-	-	6/10/26/26	0/3/3/3
4	CIT	10-A	7476	-	-	3/16/16/16	-
3	AMP	5-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	4-S	7511	-	-	6/10/26/26	0/3/3/3
4	CIT	9-C	7480	-	-	3/16/16/16	-
4	CIT	8-I	7492	-	-	3/16/16/16	-
4	CIT	4-U	7516	-	-	3/16/16/16	-
3	AMP	6-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	3-W	7520	-	-	3/16/16/16	-
4	CIT	2-U	7516	-	-	3/16/16/16	-
4	CIT	7-C	7480	-	-	3/16/16/16	-
4	CIT	1-K	7496	-	-	3/16/16/16	-
3	AMP	10-L	7497	-	-	6/10/26/26	0/3/3/3
4	CIT	9-B	7478	-	-	3/16/16/16	-
4	CIT	10-S	7512	-	-	3/16/16/16	-
4	CIT	4-C	7480	-	-	3/16/16/16	-
3	AMP	9-B	7477	-	-	6/10/26/26	0/3/3/3
4	CIT	6-K	7496	-	-	3/16/16/16	-
3	AMP	3-C	7479	-	-	6/10/26/26	0/3/3/3
3	AMP	8-M	7499	-	-	6/10/26/26	0/3/3/3
3	AMP	4-F	7485	-	-	6/10/26/26	0/3/3/3
3	AMP	1-N	7501	-	-	6/10/26/26	0/3/3/3
4	CIT	4-R	7510	-	-	3/16/16/16	-
3	AMP	8-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	10-W	7520	-	-	3/16/16/16	-
4	CIT	8-E	7484	-	-	3/16/16/16	-
4	CIT	9-P	7506	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	7-L	7497	-	-	6/10/26/26	0/3/3/3
4	CIT	8-G	7488	-	-	3/16/16/16	-
3	AMP	8-F	7485	-	-	6/10/26/26	0/3/3/3
3	AMP	3-R	7509	-	-	6/10/26/26	0/3/3/3
3	AMP	4-T	7513	-	-	6/10/26/26	0/3/3/3
4	CIT	6-L	7498	-	-	3/16/16/16	-
4	CIT	5-F	7486	-	-	3/16/16/16	-
3	AMP	5-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	7-H	7490	-	-	3/16/16/16	-
3	AMP	9-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	1-X	7522	-	-	3/16/16/16	-
3	AMP	8-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	8-L	7497	-	-	6/10/26/26	0/3/3/3
4	CIT	5-K	7496	-	-	3/16/16/16	-
3	AMP	2-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	8-C	7480	-	-	3/16/16/16	-
4	CIT	10-X	7522	-	-	3/16/16/16	-
3	AMP	10-A	7475	-	-	6/10/26/26	0/3/3/3
4	CIT	1-G	7488	-	-	3/16/16/16	-
4	CIT	4-G	7488	-	-	3/16/16/16	-
3	AMP	6-N	7501	-	-	6/10/26/26	0/3/3/3
4	CIT	8-X	7522	-	-	3/16/16/16	-
3	AMP	1-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	3-V	7517	-	-	6/10/26/26	0/3/3/3
3	AMP	5-F	7485	-	-	6/10/26/26	0/3/3/3
4	CIT	3-O	7504	-	-	3/16/16/16	-
3	AMP	5-T	7513	-	-	6/10/26/26	0/3/3/3
4	CIT	2-F	7486	-	-	3/16/16/16	-
4	CIT	3-A	7476	-	-	3/16/16/16	-
3	AMP	2-N	7501	-	-	6/10/26/26	0/3/3/3
3	AMP	2-H	7489	-	-	6/10/26/26	0/3/3/3
4	CIT	5-A	7476	-	-	3/16/16/16	-
3	AMP	5-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	4-A	7476	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	8-E	7483	-	-	6/10/26/26	0/3/3/3
4	CIT	6-M	7500	-	-	3/16/16/16	-
3	AMP	6-D	7481	-	-	6/10/26/26	0/3/3/3
3	AMP	10-F	7485	-	-	6/10/26/26	0/3/3/3
4	CIT	4-S	7512	-	-	3/16/16/16	-
3	AMP	9-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	3-D	7482	-	-	3/16/16/16	-
3	AMP	4-H	7489	-	-	6/10/26/26	0/3/3/3
3	AMP	1-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	3-N	7501	-	-	6/10/26/26	0/3/3/3
3	AMP	5-X	7521	-	-	6/10/26/26	0/3/3/3
4	CIT	2-E	7484	-	-	3/16/16/16	-
3	AMP	4-X	7521	-	-	6/10/26/26	0/3/3/3
4	CIT	3-V	7518	-	-	3/16/16/16	-
3	AMP	8-H	7489	-	-	6/10/26/26	0/3/3/3
4	CIT	7-B	7478	-	-	3/16/16/16	-
4	CIT	7-D	7482	-	-	3/16/16/16	-
4	CIT	1-E	7484	-	-	3/16/16/16	-
4	CIT	7-N	7502	-	-	3/16/16/16	-
3	AMP	10-B	7477	-	-	6/10/26/26	0/3/3/3
4	CIT	8-W	7520	-	-	3/16/16/16	-
3	AMP	2-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	3-Q	7507	-	-	6/10/26/26	0/3/3/3
4	CIT	1-A	7476	-	-	3/16/16/16	-
4	CIT	4-D	7482	-	-	3/16/16/16	-
4	CIT	2-G	7488	-	-	3/16/16/16	-
4	CIT	10-O	7504	-	-	3/16/16/16	-
3	AMP	4-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	2-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	4-F	7486	-	-	3/16/16/16	-
3	AMP	2-C	7479	-	-	6/10/26/26	0/3/3/3
4	CIT	10-N	7502	-	-	3/16/16/16	-
4	CIT	6-U	7516	-	-	3/16/16/16	-
4	CIT	8-D	7482	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	8-F	7486	-	-	3/16/16/16	-
4	CIT	8-N	7502	-	-	3/16/16/16	-
4	CIT	7-R	7510	-	-	3/16/16/16	-
4	CIT	10-D	7482	-	-	3/16/16/16	-
3	AMP	2-E	7483	-	-	6/10/26/26	0/3/3/3
3	AMP	3-K	7495	-	-	6/10/26/26	0/3/3/3
3	AMP	8-B	7477	-	-	6/10/26/26	0/3/3/3
3	AMP	5-E	7483	-	-	6/10/26/26	0/3/3/3
3	AMP	3-O	7503	-	-	6/10/26/26	0/3/3/3
3	AMP	6-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	5-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	2-N	7502	-	-	3/16/16/16	-
3	AMP	1-I	7491	-	-	6/10/26/26	0/3/3/3
3	AMP	9-H	7489	-	-	6/10/26/26	0/3/3/3
3	AMP	1-H	7489	-	-	6/10/26/26	0/3/3/3
3	AMP	5-H	7489	-	-	6/10/26/26	0/3/3/3
3	AMP	4-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	9-H	7490	-	-	3/16/16/16	-
4	CIT	5-R	7510	-	-	3/16/16/16	-
4	CIT	9-U	7516	-	-	3/16/16/16	-
3	AMP	6-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	2-J	7494	-	-	3/16/16/16	-
3	AMP	8-N	7501	-	-	6/10/26/26	0/3/3/3
3	AMP	7-E	7483	-	-	6/10/26/26	0/3/3/3
4	CIT	7-O	7504	-	-	3/16/16/16	-
4	CIT	7-A	7476	-	-	3/16/16/16	-
3	AMP	6-B	7477	-	-	6/10/26/26	0/3/3/3
4	CIT	10-K	7496	-	-	3/16/16/16	-
4	CIT	2-D	7482	-	-	3/16/16/16	-
3	AMP	4-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	3-Q	7508	-	-	3/16/16/16	-
4	CIT	5-P	7506	-	-	3/16/16/16	-
4	CIT	9-D	7482	-	-	3/16/16/16	-
3	AMP	3-J	7493	-	-	6/10/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	10-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	6-P	7506	-	-	3/16/16/16	-
4	CIT	6-X	7522	-	-	3/16/16/16	-
4	CIT	4-N	7502	-	-	3/16/16/16	-
4	CIT	7-L	7498	-	-	3/16/16/16	-
3	AMP	9-F	7485	-	-	6/10/26/26	0/3/3/3
3	AMP	7-M	7499	-	-	6/10/26/26	0/3/3/3
3	AMP	3-A	7475	-	-	6/10/26/26	0/3/3/3
3	AMP	1-C	7479	-	-	6/10/26/26	0/3/3/3
4	CIT	4-I	7492	-	-	3/16/16/16	-
3	AMP	5-C	7479	-	-	6/10/26/26	0/3/3/3
3	AMP	5-J	7493	-	-	6/10/26/26	0/3/3/3
3	AMP	6-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	1-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	5-J	7494	-	-	3/16/16/16	-
4	CIT	5-M	7500	-	-	3/16/16/16	-
4	CIT	7-I	7492	-	-	3/16/16/16	-
4	CIT	1-H	7490	-	-	3/16/16/16	-
3	AMP	7-J	7493	-	-	6/10/26/26	0/3/3/3
4	CIT	7-X	7522	-	-	3/16/16/16	-
3	AMP	3-B	7477	-	-	6/10/26/26	0/3/3/3
3	AMP	4-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	3-J	7494	-	-	3/16/16/16	-
4	CIT	4-B	7478	-	-	3/16/16/16	-
3	AMP	9-D	7481	-	-	6/10/26/26	0/3/3/3
3	AMP	9-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	3-P	7506	-	-	3/16/16/16	-
3	AMP	4-E	7483	-	-	6/10/26/26	0/3/3/3
4	CIT	6-W	7520	-	-	3/16/16/16	-
4	CIT	1-C	7480	-	-	3/16/16/16	-
3	AMP	4-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	7-U	7516	-	-	3/16/16/16	-
4	CIT	7-K	7496	-	-	3/16/16/16	-
3	AMP	2-F	7485	-	-	6/10/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	9-J	7494	-	-	3/16/16/16	-
3	AMP	5-R	7509	-	-	6/10/26/26	0/3/3/3
4	CIT	6-J	7494	-	-	3/16/16/16	-
3	AMP	2-W	7519	-	-	6/10/26/26	0/3/3/3
3	AMP	6-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	4-E	7484	-	-	3/16/16/16	-
4	CIT	10-R	7510	-	-	3/16/16/16	-
3	AMP	2-M	7499	-	-	6/10/26/26	0/3/3/3
3	AMP	3-H	7489	-	-	6/10/26/26	0/3/3/3
4	CIT	3-L	7498	-	-	3/16/16/16	-
3	AMP	1-F	7485	-	-	6/10/26/26	0/3/3/3
4	CIT	2-T	7514	-	-	3/16/16/16	-
3	AMP	6-A	7475	-	-	6/10/26/26	0/3/3/3
4	CIT	6-V	7518	-	-	3/16/16/16	-
4	CIT	4-W	7520	-	-	3/16/16/16	-
3	AMP	10-H	7489	-	-	6/10/26/26	0/3/3/3
3	AMP	9-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	6-F	7486	-	-	3/16/16/16	-
4	CIT	2-O	7504	-	-	3/16/16/16	-
4	CIT	10-G	7488	-	-	3/16/16/16	-
3	AMP	6-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	4-O	7504	-	-	3/16/16/16	-
4	CIT	5-U	7516	-	-	3/16/16/16	-
3	AMP	8-O	7503	-	-	6/10/26/26	0/3/3/3
4	CIT	1-B	7478	-	-	3/16/16/16	-
4	CIT	4-T	7514	-	-	3/16/16/16	-
3	AMP	9-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	1-O	7504	-	-	3/16/16/16	-
3	AMP	1-R	7509	-	-	6/10/26/26	0/3/3/3
4	CIT	5-E	7484	-	-	3/16/16/16	-
4	CIT	7-T	7514	-	-	3/16/16/16	-
3	AMP	10-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	6-O	7504	-	-	3/16/16/16	-
4	CIT	3-F	7486	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	3-M	7500	-	-	3/16/16/16	-
3	AMP	9-C	7479	-	-	6/10/26/26	0/3/3/3
3	AMP	9-E	7483	-	-	6/10/26/26	0/3/3/3
4	CIT	9-O	7504	-	-	3/16/16/16	-
4	CIT	9-A	7476	-	-	3/16/16/16	-
4	CIT	5-Q	7508	-	-	3/16/16/16	-
3	AMP	1-M	7499	-	-	6/10/26/26	0/3/3/3
3	AMP	7-A	7475	-	-	6/10/26/26	0/3/3/3
3	AMP	5-M	7499	-	-	6/10/26/26	0/3/3/3
4	CIT	8-S	7512	-	-	3/16/16/16	-
3	AMP	7-B	7477	-	-	6/10/26/26	0/3/3/3
3	AMP	8-V	7517	-	-	6/10/26/26	0/3/3/3
3	AMP	10-I	7491	-	-	6/10/26/26	0/3/3/3
4	CIT	7-M	7500	-	-	3/16/16/16	-
4	CIT	9-I	7492	-	-	3/16/16/16	-
4	CIT	1-J	7494	-	-	3/16/16/16	-
3	AMP	1-E	7483	-	-	6/10/26/26	0/3/3/3
3	AMP	5-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	7-S	7511	-	-	6/10/26/26	0/3/3/3
4	CIT	10-J	7494	-	-	3/16/16/16	-
3	AMP	10-V	7517	-	-	6/10/26/26	0/3/3/3
4	CIT	10-L	7498	-	-	3/16/16/16	-
3	AMP	7-D	7481	-	-	6/10/26/26	0/3/3/3
4	CIT	6-N	7502	-	-	3/16/16/16	-
4	CIT	3-T	7514	-	-	3/16/16/16	-
3	AMP	1-O	7503	-	-	6/10/26/26	0/3/3/3
3	AMP	6-S	7511	-	-	6/10/26/26	0/3/3/3
4	CIT	9-E	7484	-	-	3/16/16/16	-
4	CIT	6-G	7488	-	-	3/16/16/16	-
4	CIT	5-T	7514	-	-	3/16/16/16	-
3	AMP	7-K	7495	-	-	6/10/26/26	0/3/3/3
4	CIT	4-K	7496	-	-	3/16/16/16	-
4	CIT	4-P	7506	-	-	3/16/16/16	-
4	CIT	9-V	7518	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	7-J	7494	-	-	3/16/16/16	-
3	AMP	4-G	7487	-	-	6/10/26/26	0/3/3/3
3	AMP	6-T	7513	-	-	6/10/26/26	0/3/3/3
4	CIT	3-I	7492	-	-	3/16/16/16	-
4	CIT	10-T	7514	-	-	3/16/16/16	-
4	CIT	8-O	7504	-	-	3/16/16/16	-
4	CIT	2-Q	7508	-	-	3/16/16/16	-
3	AMP	1-G	7487	-	-	6/10/26/26	0/3/3/3
4	CIT	8-P	7506	-	-	3/16/16/16	-
3	AMP	7-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	5-I	7492	-	-	3/16/16/16	-
4	CIT	7-P	7506	-	-	3/16/16/16	-
3	AMP	5-L	7497	-	-	6/10/26/26	0/3/3/3
3	AMP	9-M	7499	-	-	6/10/26/26	0/3/3/3
4	CIT	10-V	7518	-	-	3/16/16/16	-
4	CIT	8-B	7478	-	-	3/16/16/16	-
4	CIT	7-F	7486	-	-	3/16/16/16	-
4	CIT	10-Q	7508	-	-	3/16/16/16	-
3	AMP	9-Q	7507	-	-	6/10/26/26	0/3/3/3
4	CIT	3-G	7488	-	-	3/16/16/16	-
4	CIT	2-R	7510	-	-	3/16/16/16	-
3	AMP	8-Q	7507	-	-	6/10/26/26	0/3/3/3
3	AMP	3-W	7519	-	-	6/10/26/26	0/3/3/3
3	AMP	7-Q	7507	-	-	6/10/26/26	0/3/3/3
4	CIT	9-T	7514	-	-	3/16/16/16	-
3	AMP	2-U	7515	-	-	6/10/26/26	0/3/3/3
3	AMP	7-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	1-R	7510	-	-	3/16/16/16	-
3	AMP	6-P	7505	-	-	6/10/26/26	0/3/3/3
4	CIT	6-S	7512	-	-	3/16/16/16	-
4	CIT	2-S	7512	-	-	3/16/16/16	-
3	AMP	2-J	7493	-	-	6/10/26/26	0/3/3/3
3	AMP	10-W	7519	-	-	6/10/26/26	0/3/3/3
4	CIT	7-G	7488	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	2-S	7511	-	-	6/10/26/26	0/3/3/3
4	CIT	2-M	7500	-	-	3/16/16/16	-
3	AMP	2-D	7481	-	-	6/10/26/26	0/3/3/3
4	CIT	4-M	7500	-	-	3/16/16/16	-
4	CIT	6-T	7514	-	-	3/16/16/16	-
3	AMP	6-F	7485	-	-	6/10/26/26	0/3/3/3
4	CIT	5-X	7522	-	-	3/16/16/16	-
3	AMP	7-X	7521	-	-	6/10/26/26	0/3/3/3
3	AMP	6-E	7483	-	-	6/10/26/26	0/3/3/3
3	AMP	10-R	7509	-	-	6/10/26/26	0/3/3/3
3	AMP	6-U	7515	-	-	6/10/26/26	0/3/3/3
4	CIT	8-M	7500	-	-	3/16/16/16	-

The worst 5 of 6000 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-R	7509	AMP	C1'-N9	10.96	1.76	1.46
3	2-R	7509	AMP	C1'-N9	10.96	1.76	1.46
3	3-R	7509	AMP	C1'-N9	10.96	1.76	1.46
3	4-R	7509	AMP	C1'-N9	10.96	1.76	1.46
3	5-R	7509	AMP	C1'-N9	10.96	1.76	1.46

The worst 5 of 5010 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-P	7505	AMP	O4'-C1'-C2'	-9.17	87.00	106.62
3	2-P	7505	AMP	O4'-C1'-C2'	-9.17	87.00	106.62
3	3-P	7505	AMP	O4'-C1'-C2'	-9.17	87.00	106.62
3	4-P	7505	AMP	O4'-C1'-C2'	-9.17	87.00	106.62
3	5-P	7505	AMP	O4'-C1'-C2'	-9.17	87.00	106.62

There are no chirality outliers.

5 of 2160 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	1-A	7475	AMP	C5'-O5'-P-O2P
3	1-A	7475	AMP	C5'-O5'-P-O3P
3	2-A	7475	AMP	C5'-O5'-P-O2P
3	2-A	7475	AMP	C5'-O5'-P-O3P

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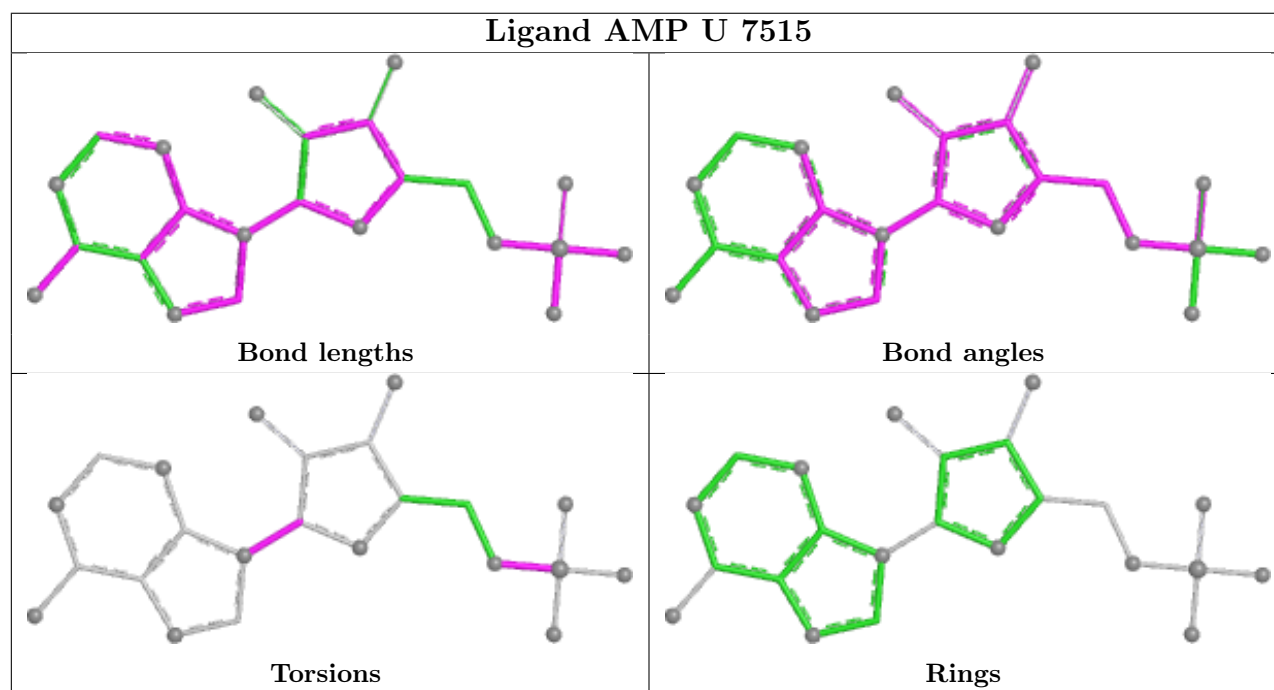
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Mol	Chain	Res	Type	Atoms
3	3-A	7475	AMP	C5'-O5'-P-O2P

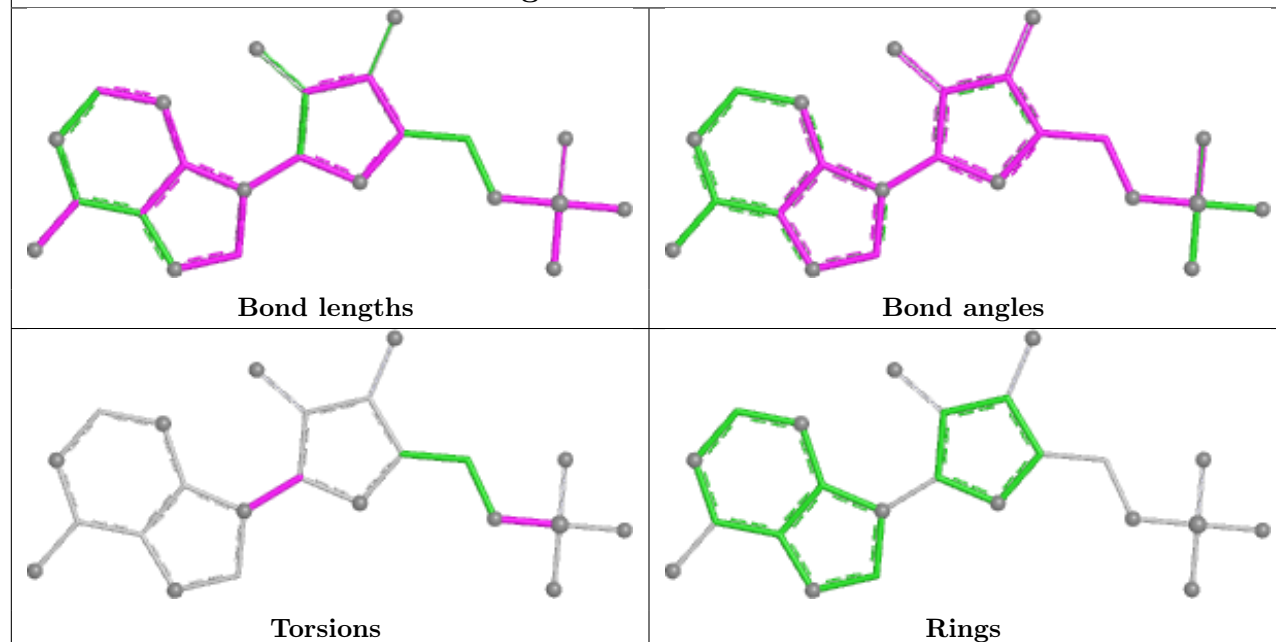
There are no ring outliers.

No monomer is involved in short contacts.

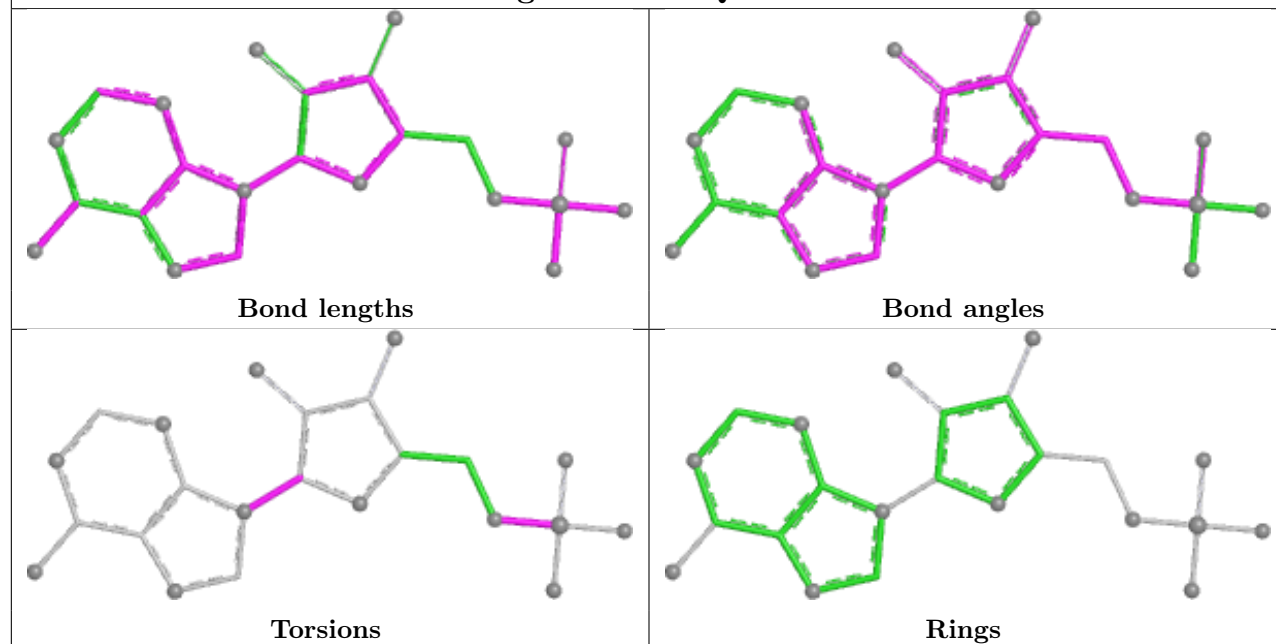
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



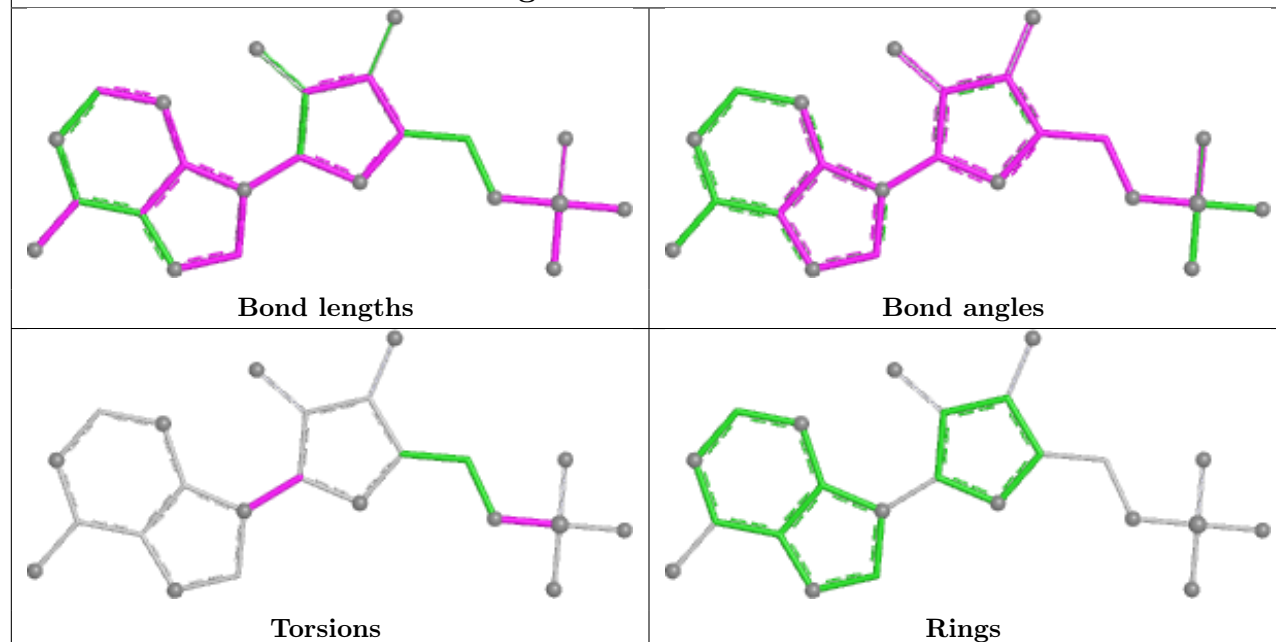
Ligand AMP J 7493



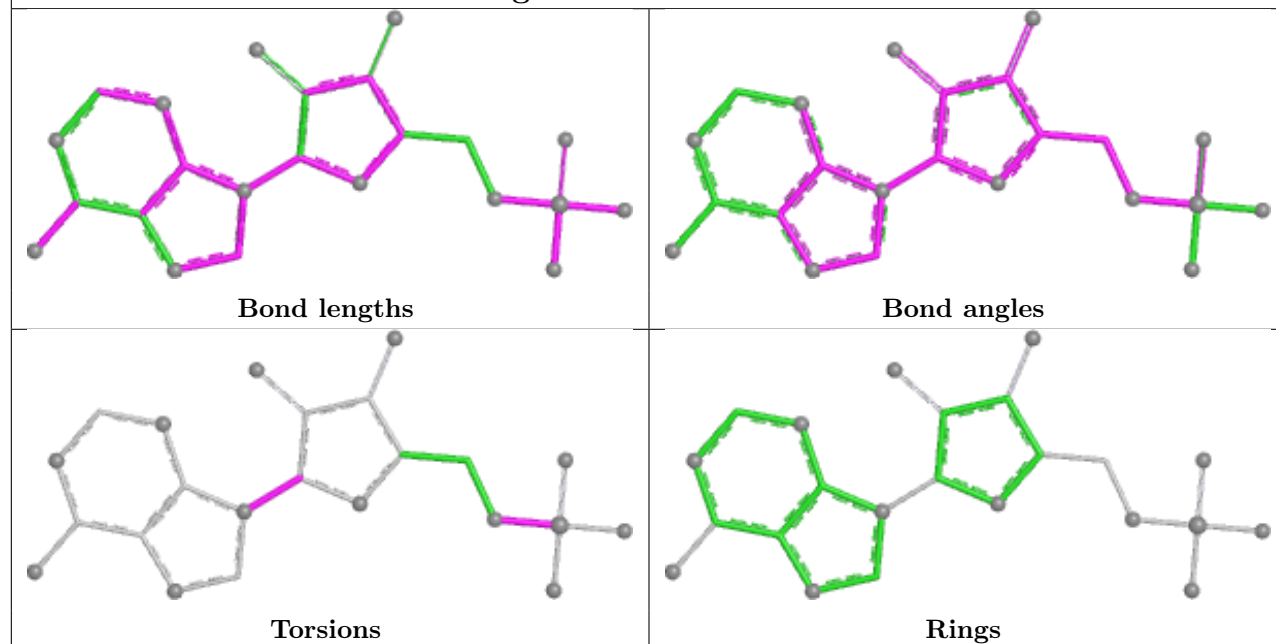
Ligand AMP Q 7507



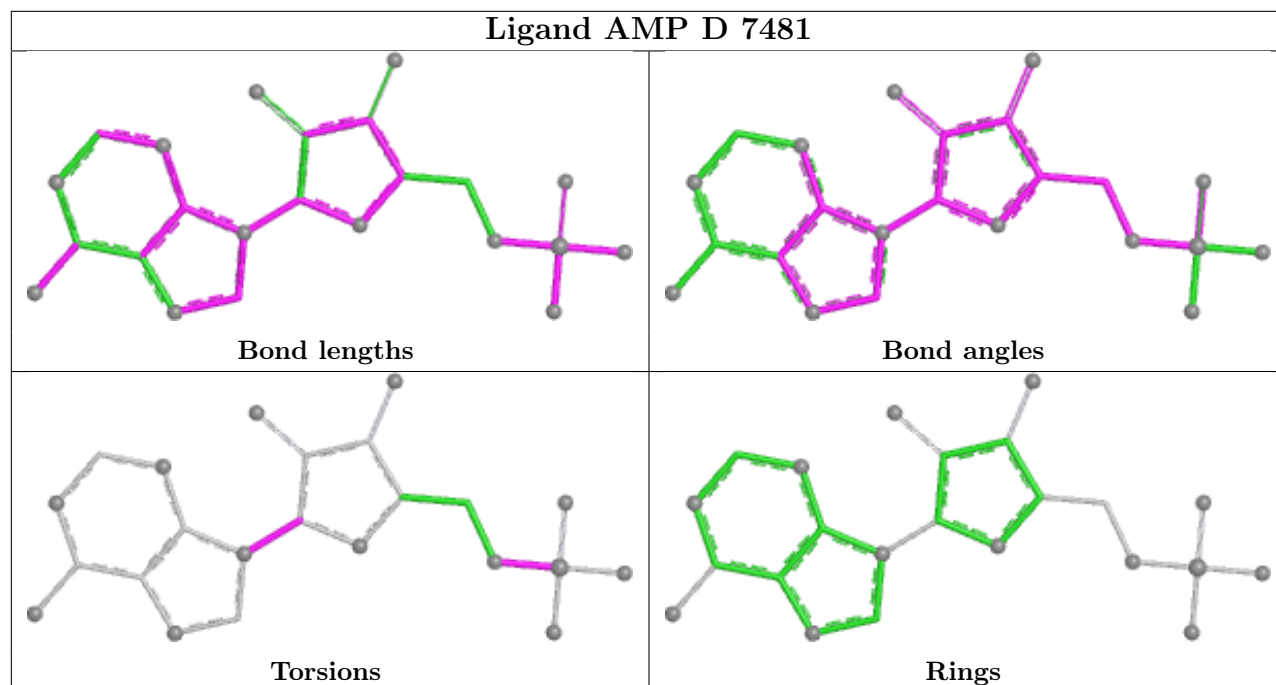
Ligand AMP P 7505



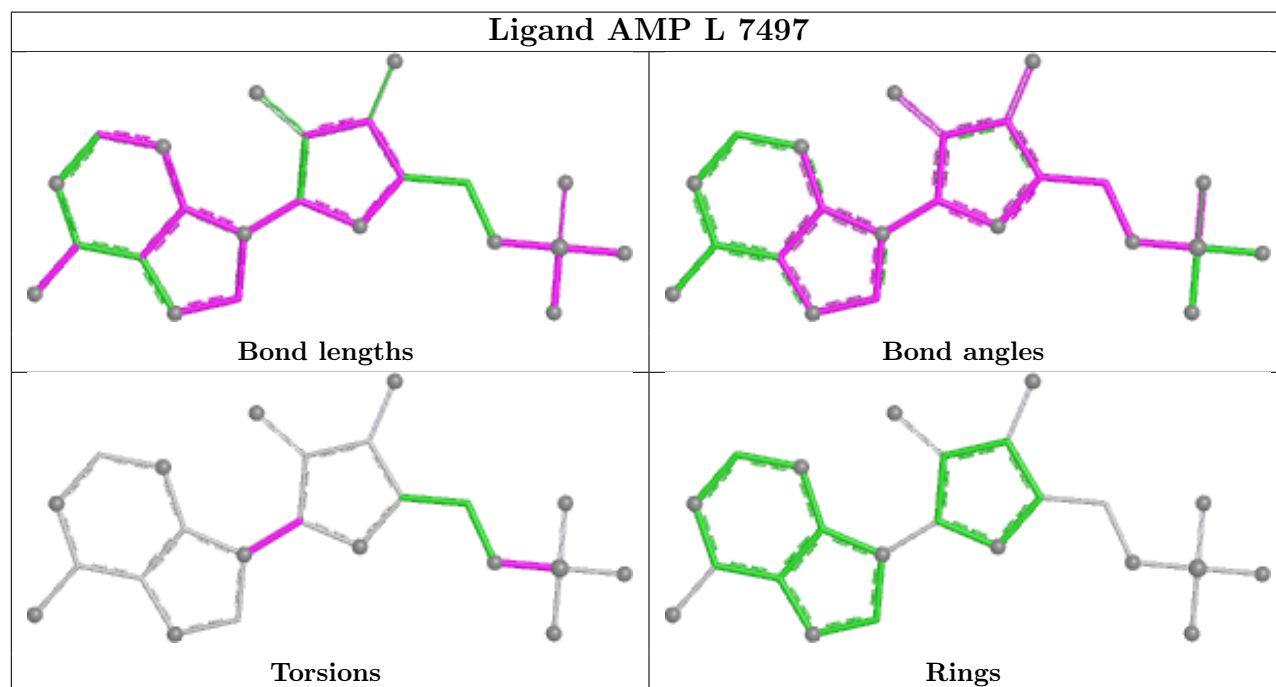
Ligand AMP W 7519



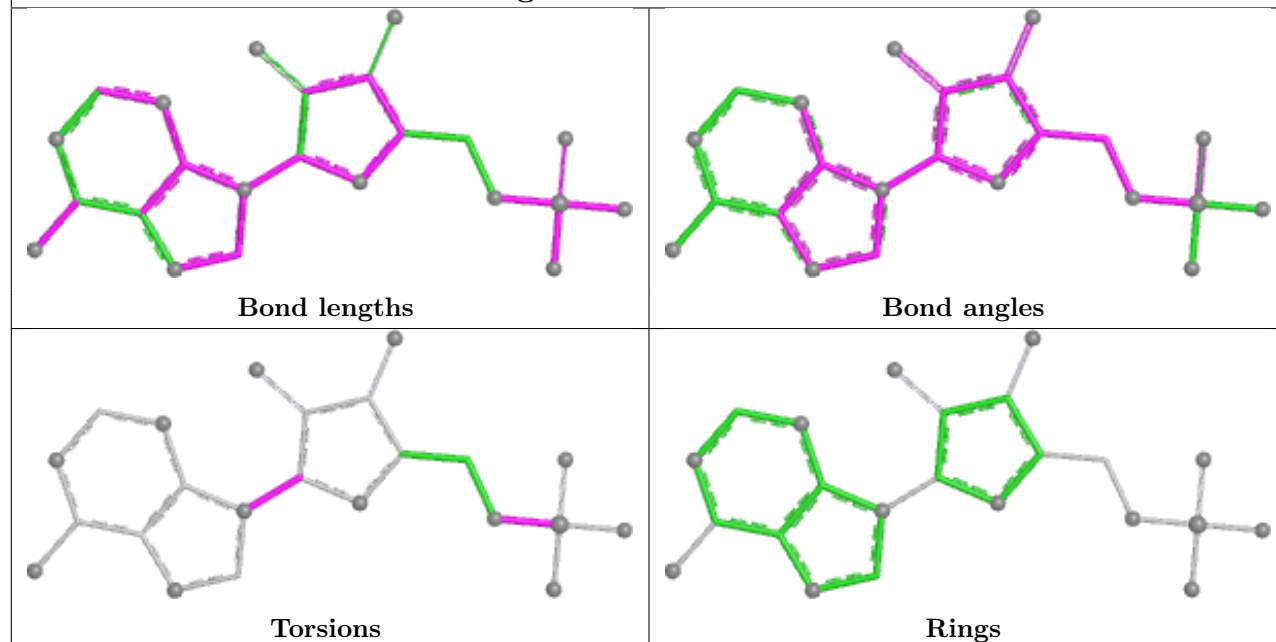
Ligand AMP D 7481



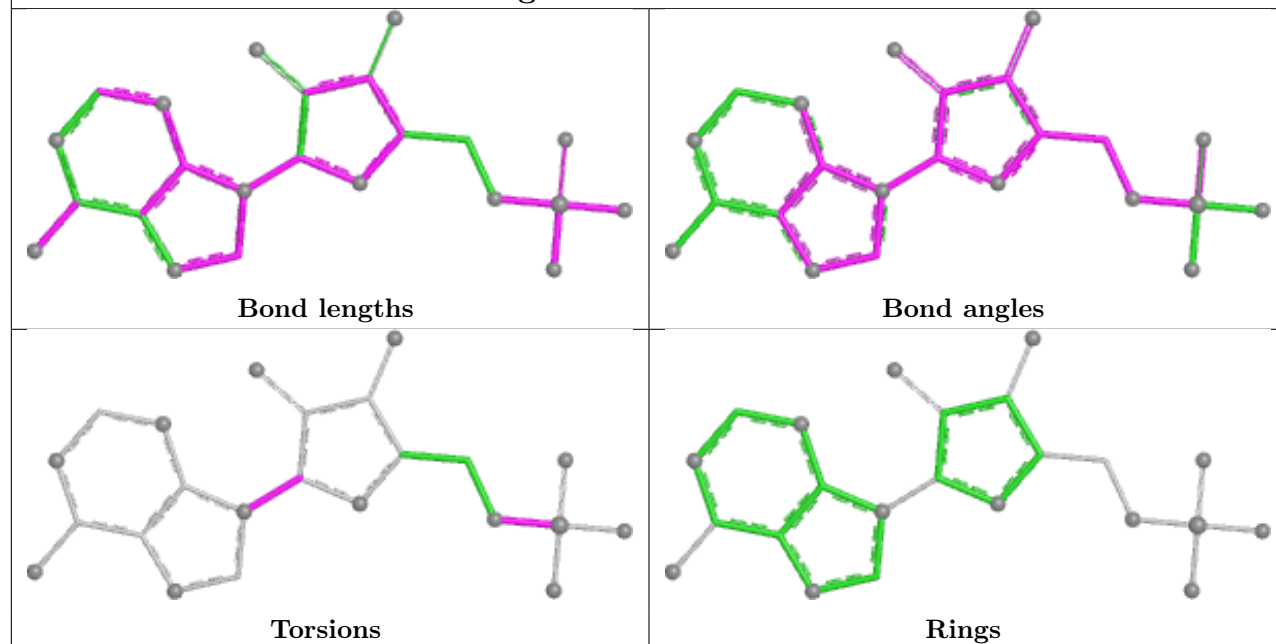
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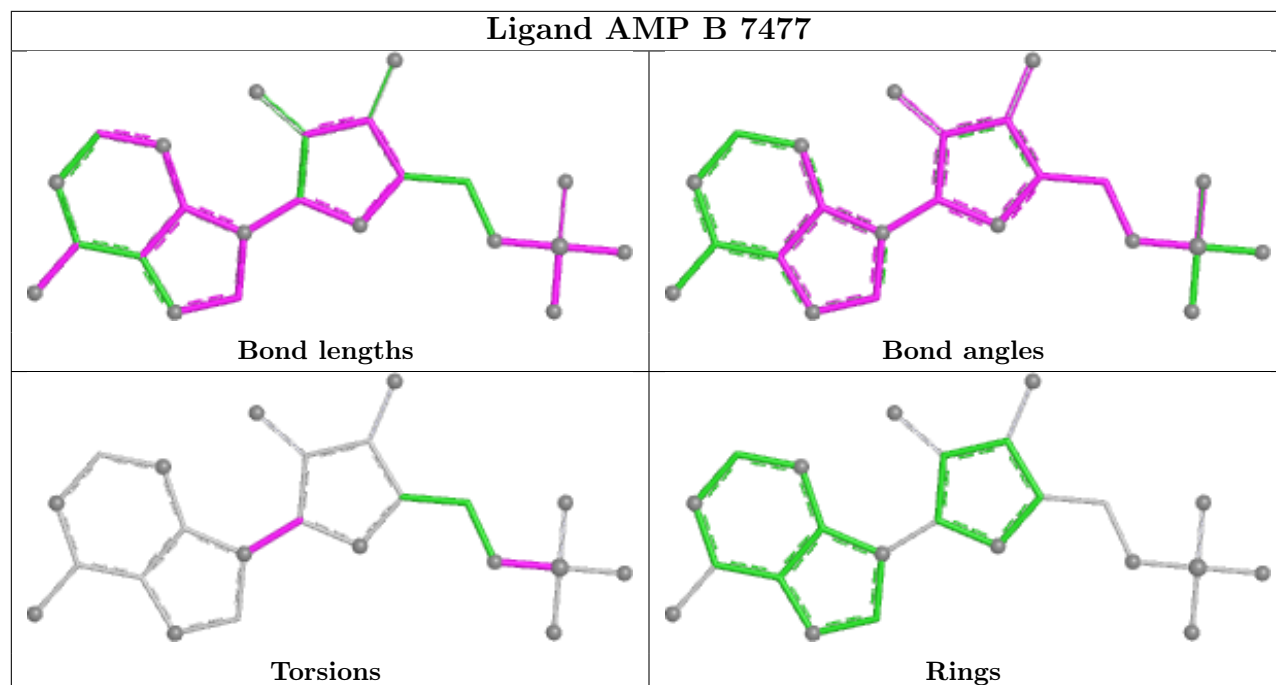
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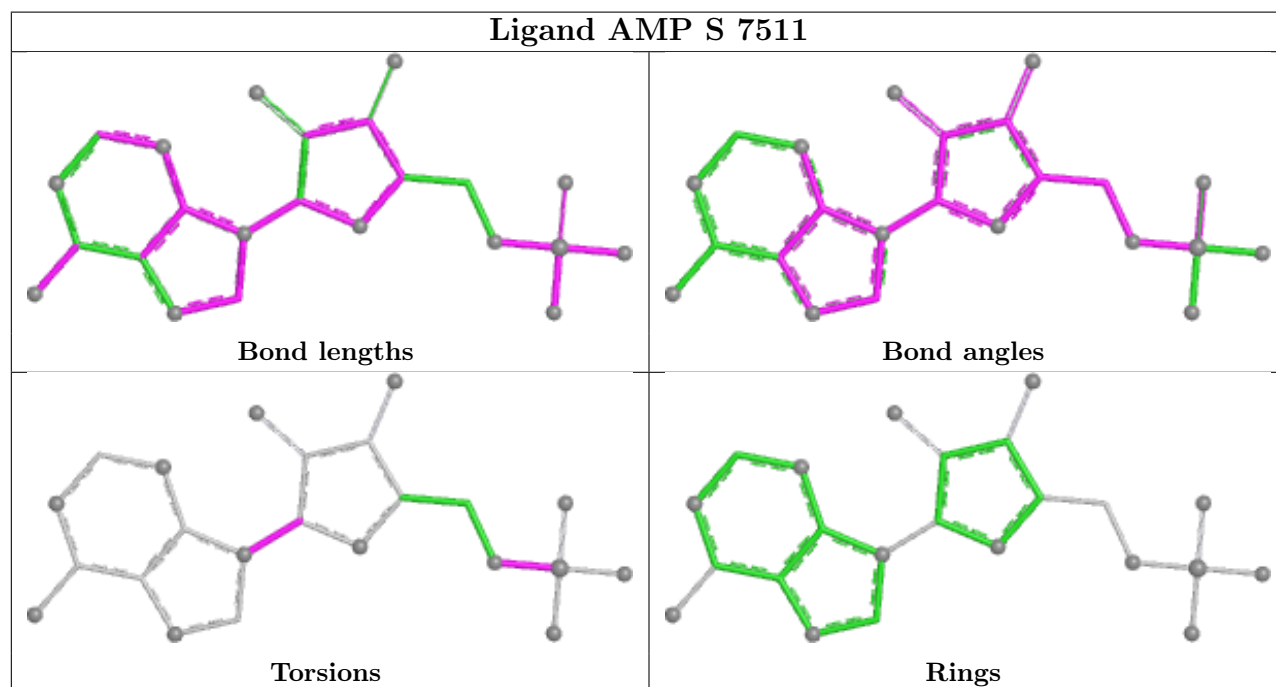
Ligand AMP T 7513



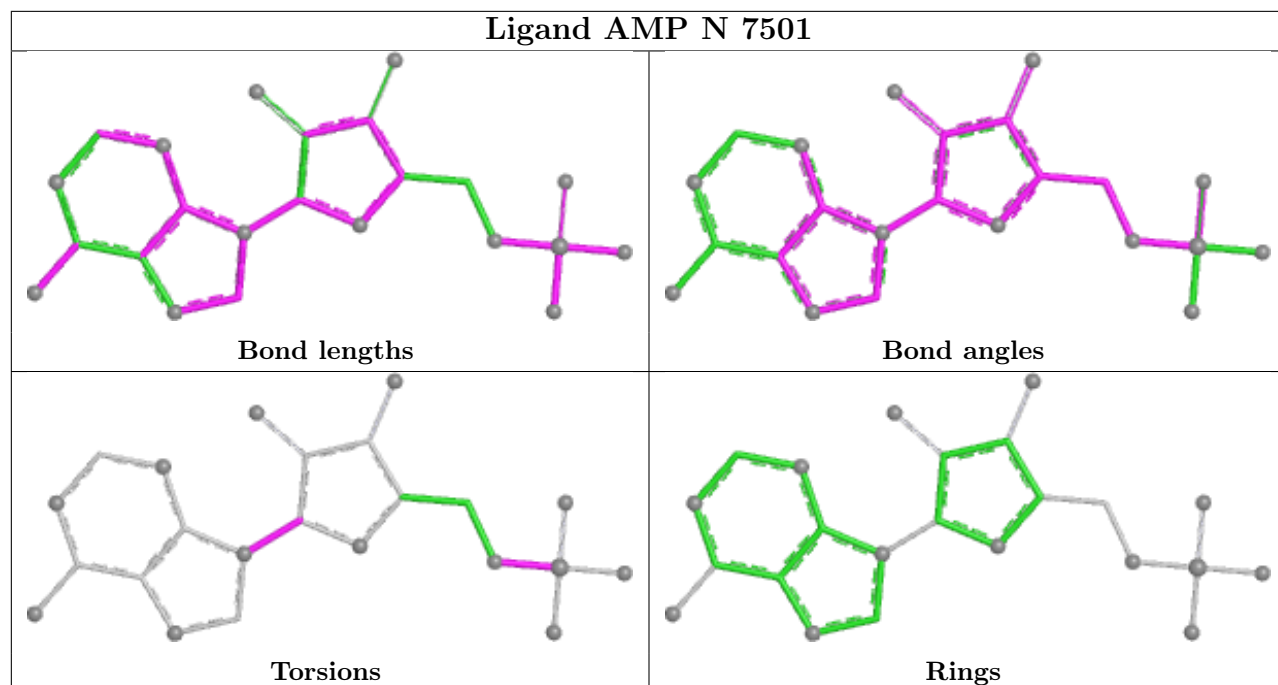
Ligand AMP B 7477



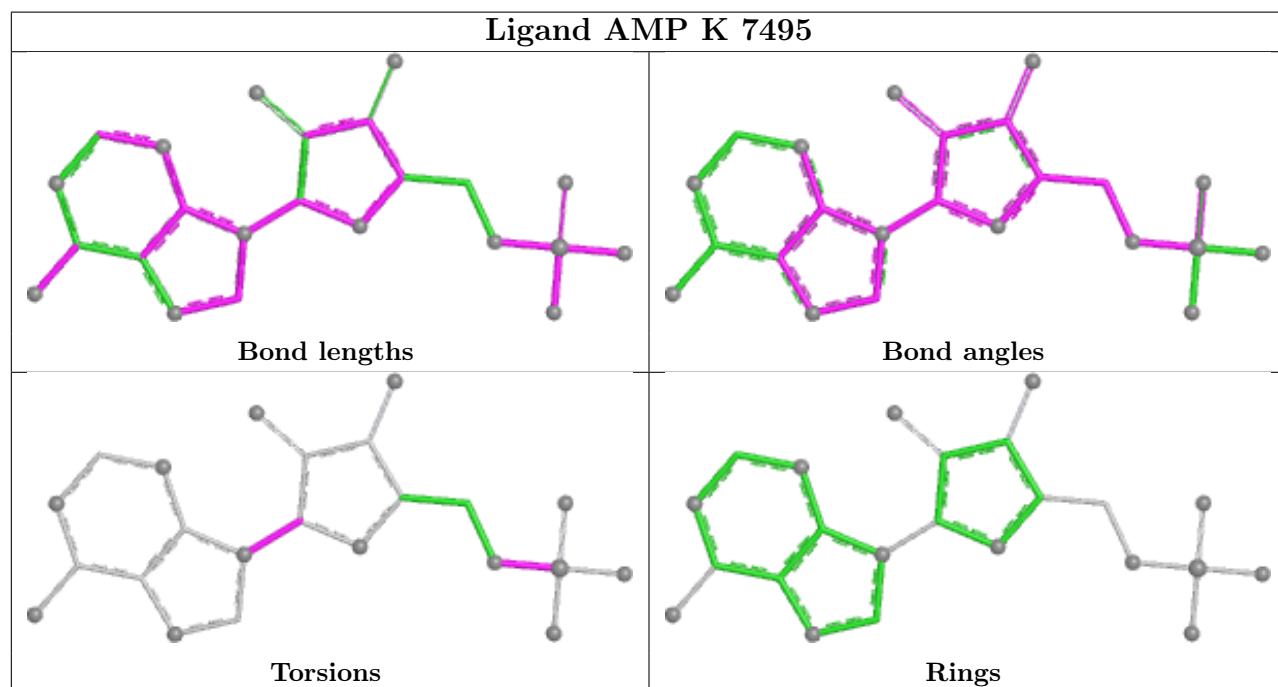
Ligand AMP S 7511



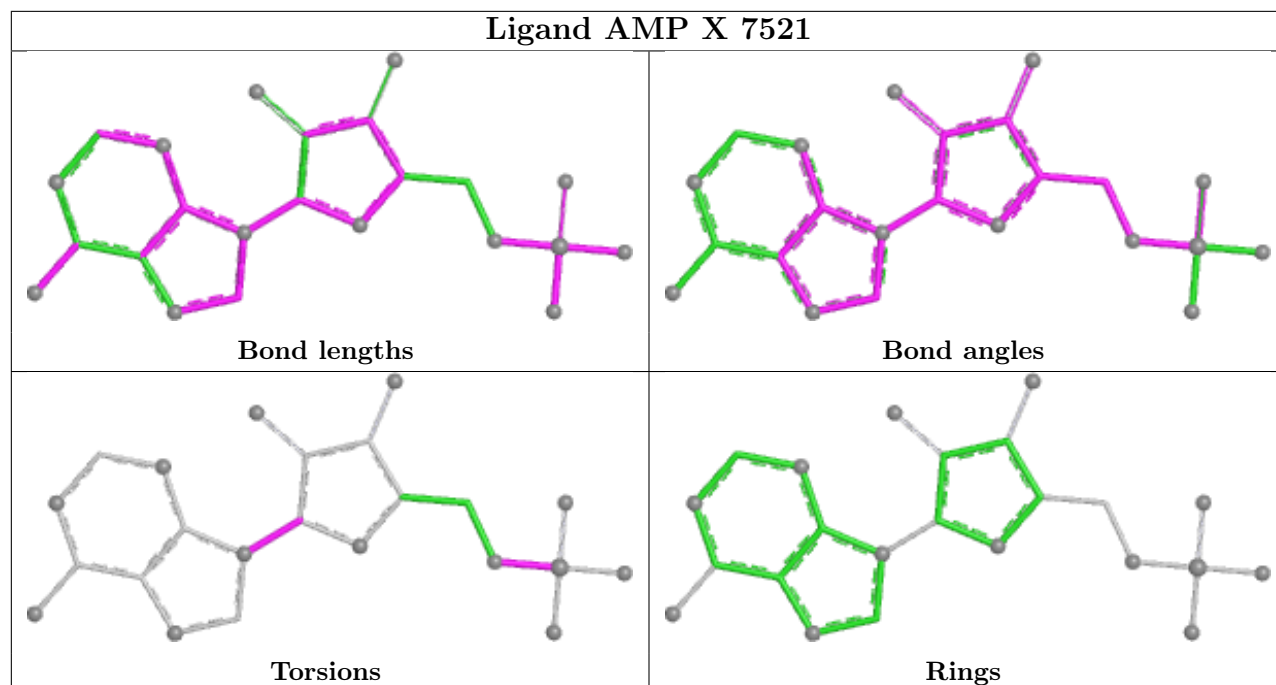
Ligand AMP N 7501



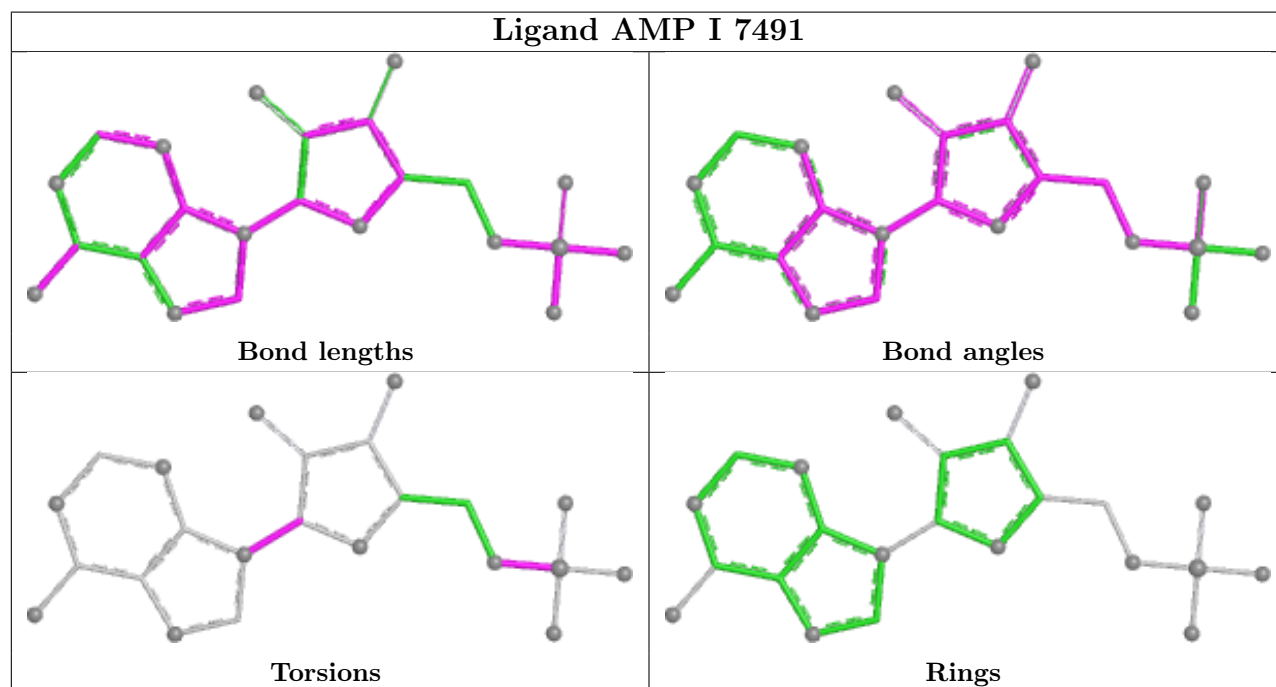
Ligand AMP K 7495



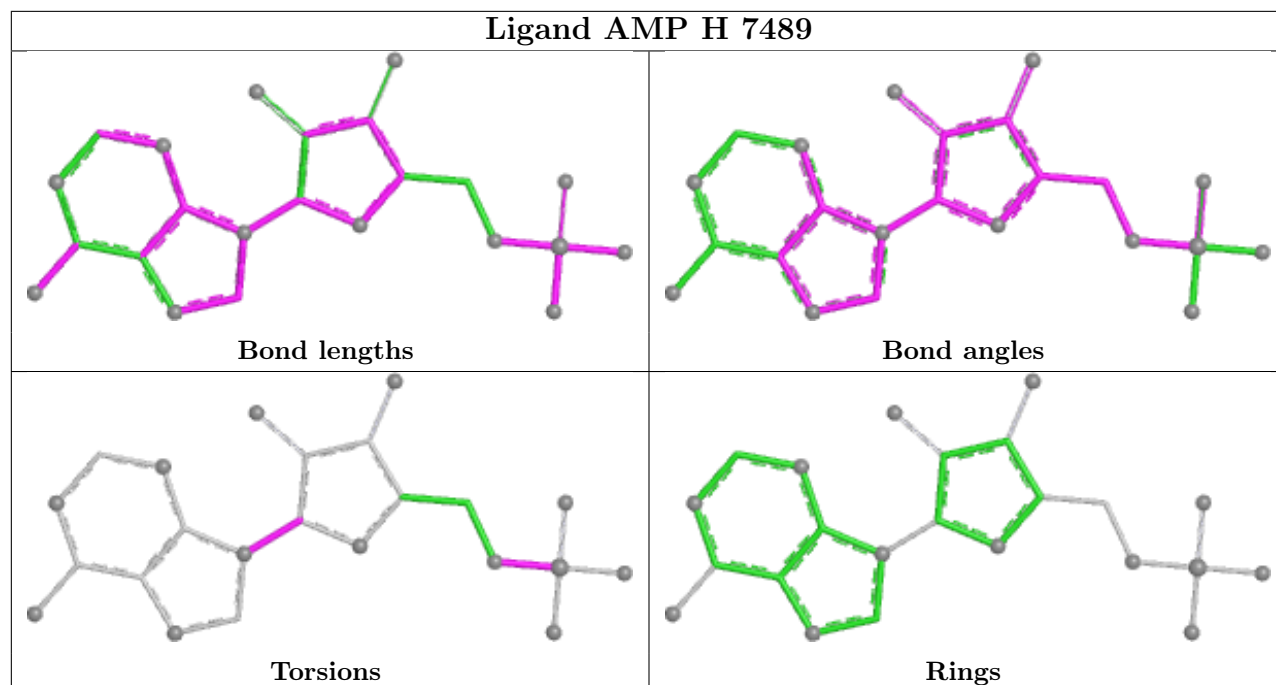
Ligand AMP X 7521



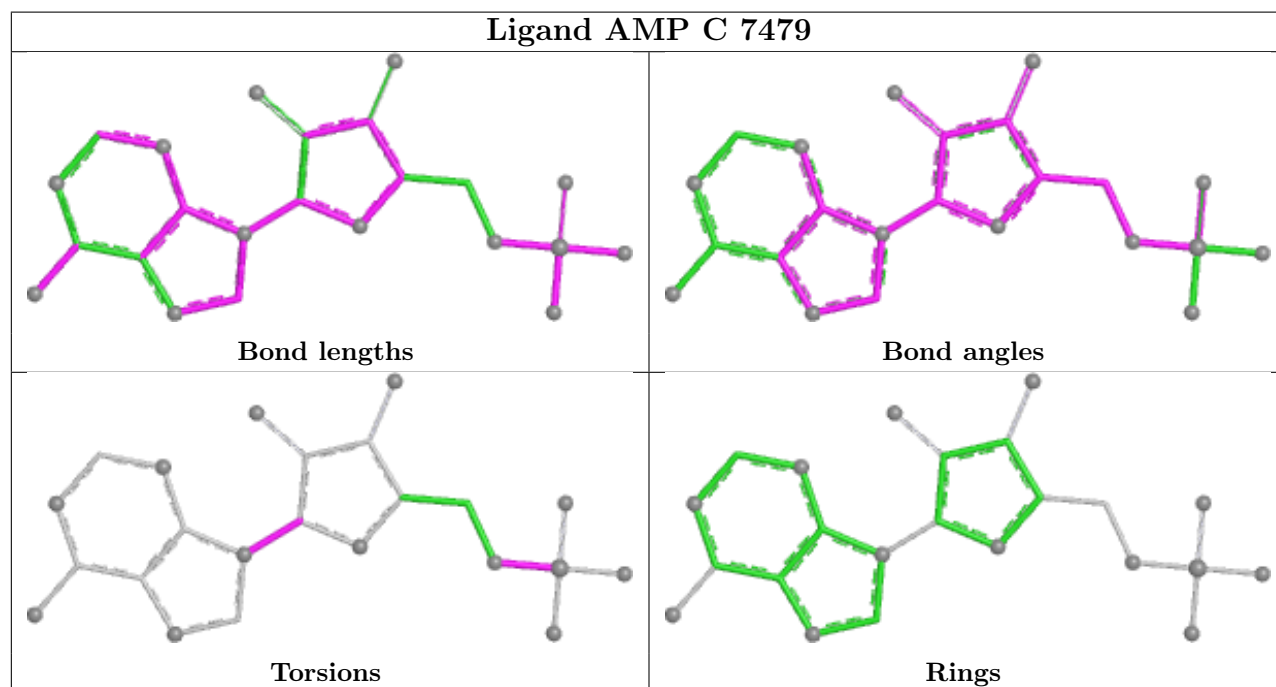
Ligand AMP I 7491



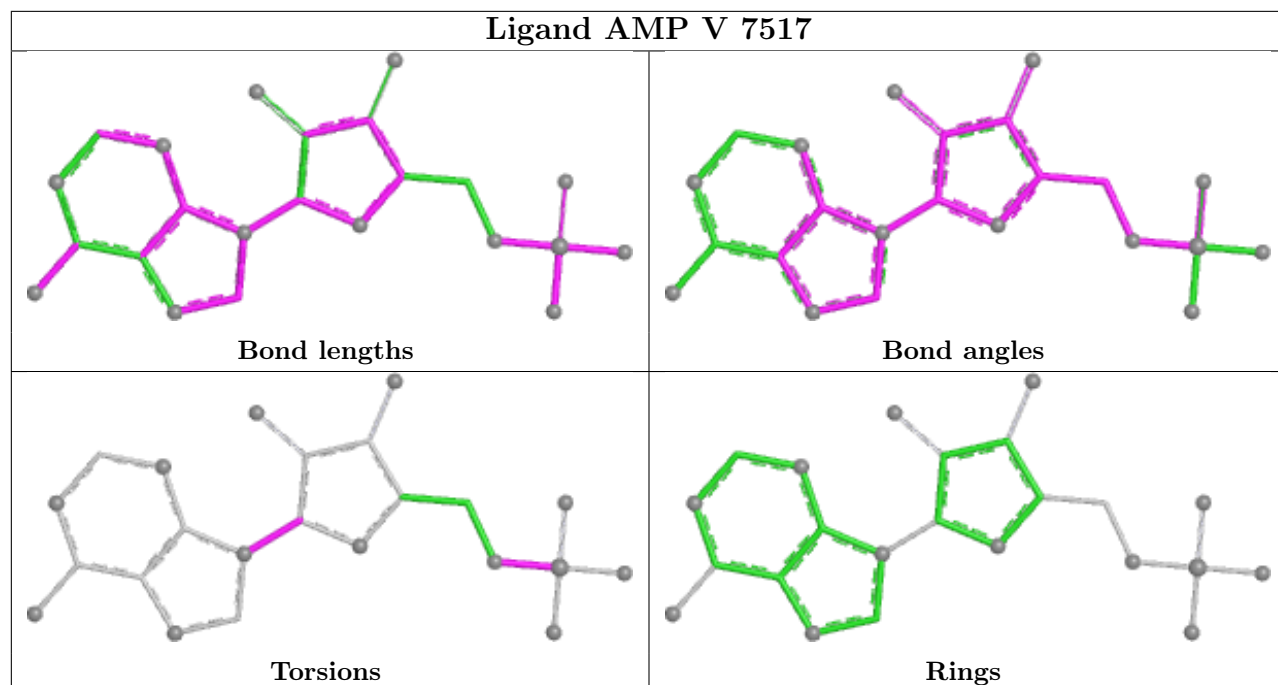
Ligand AMP H 7489



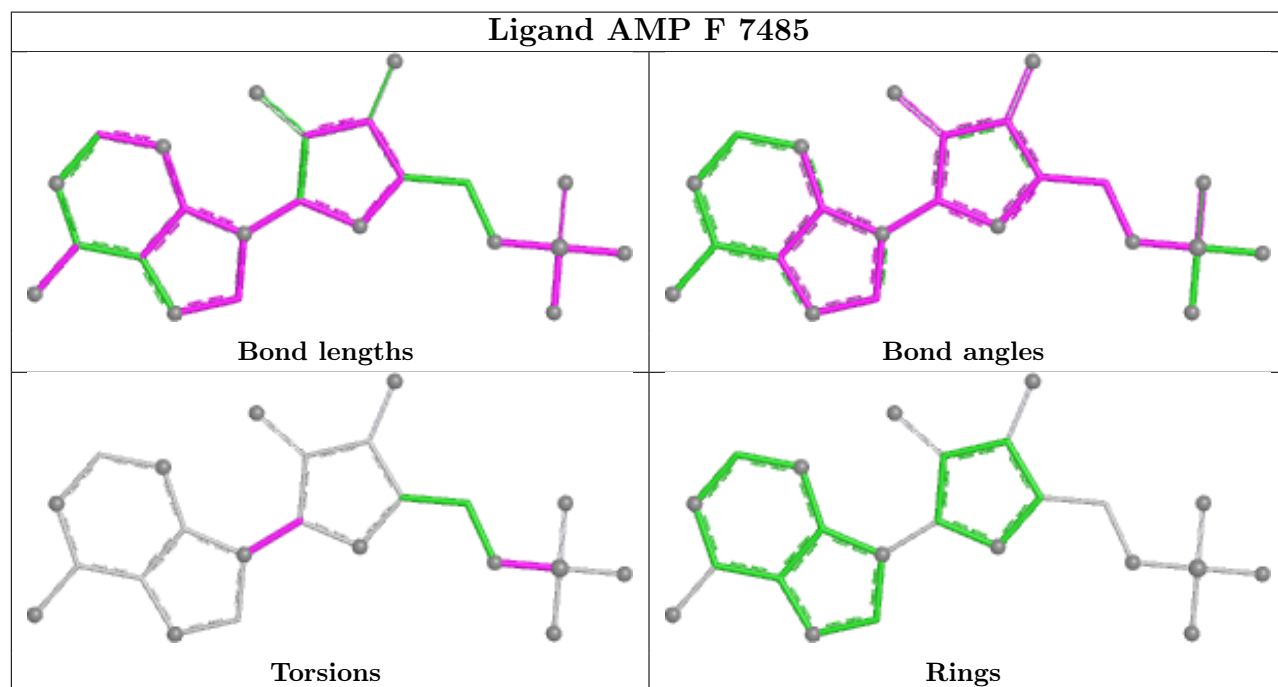
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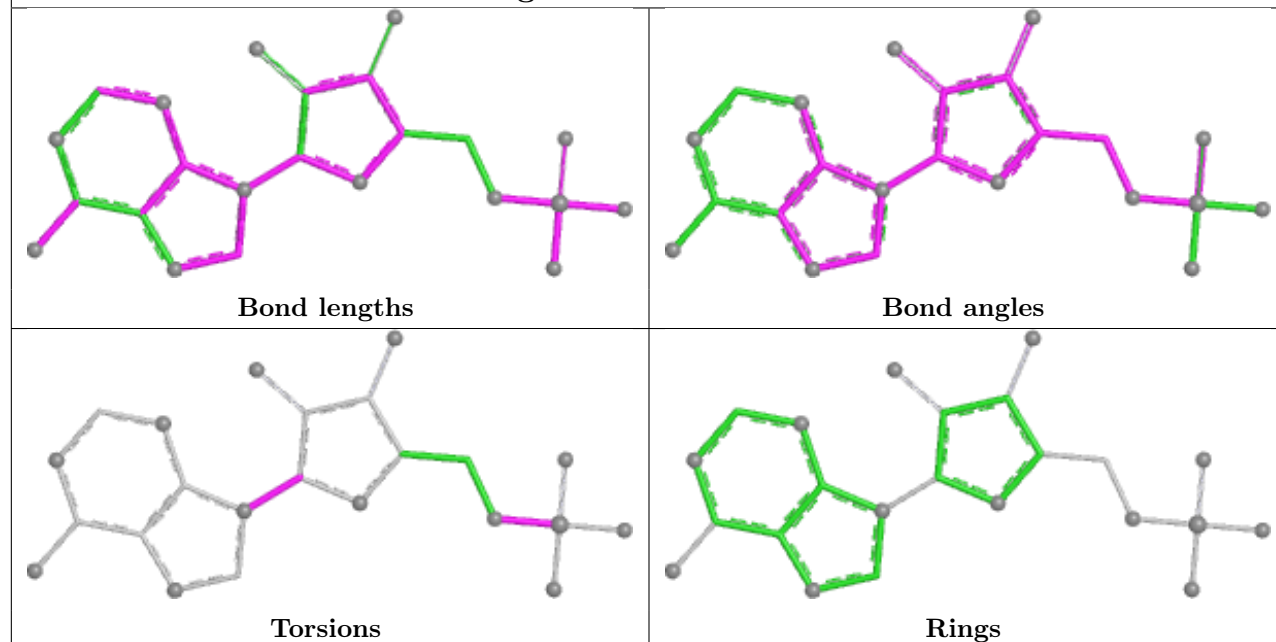
Ligand AMP V 7517



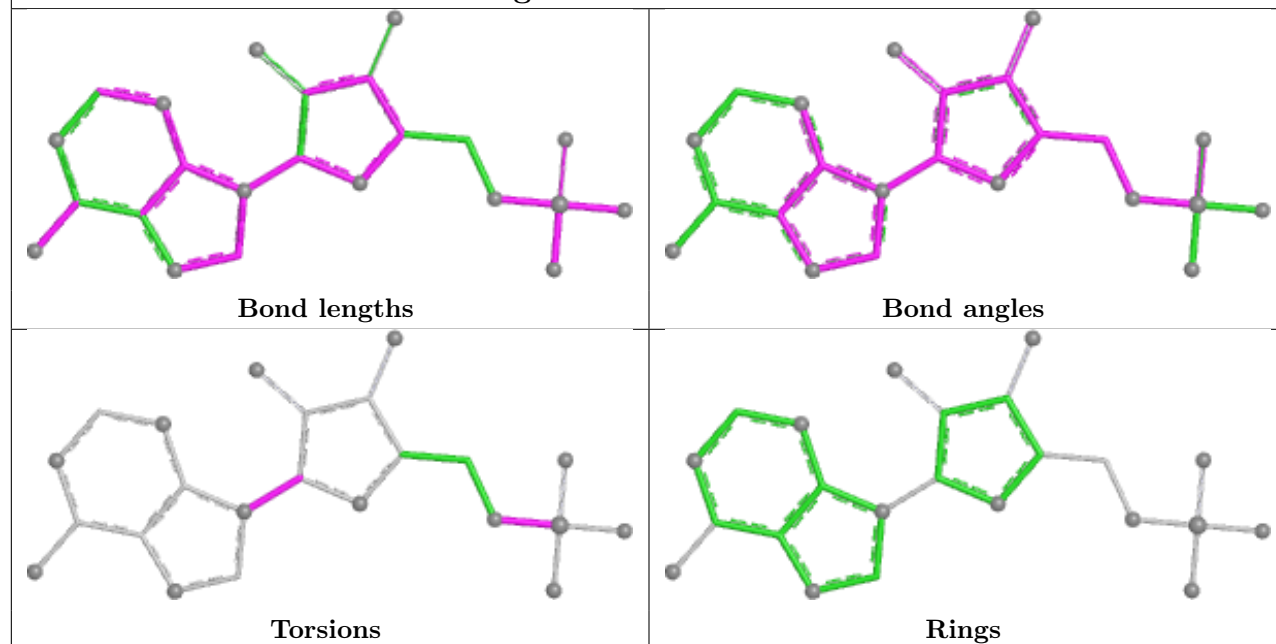
Ligand AMP F 7485



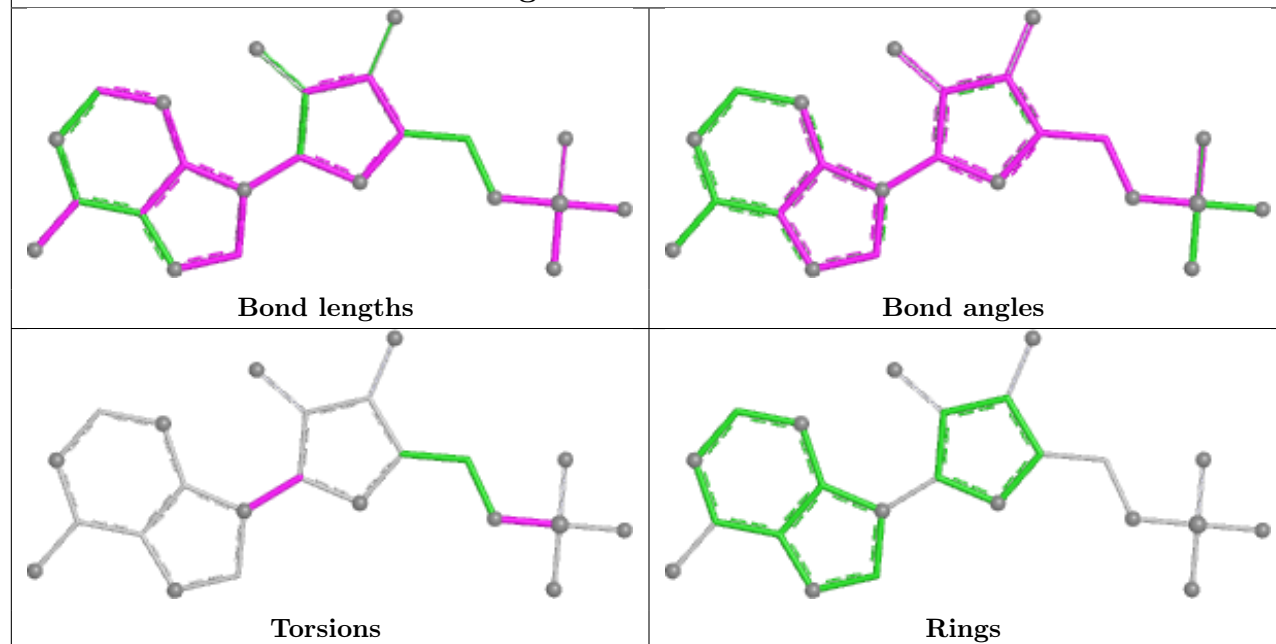
Ligand AMP R 7509



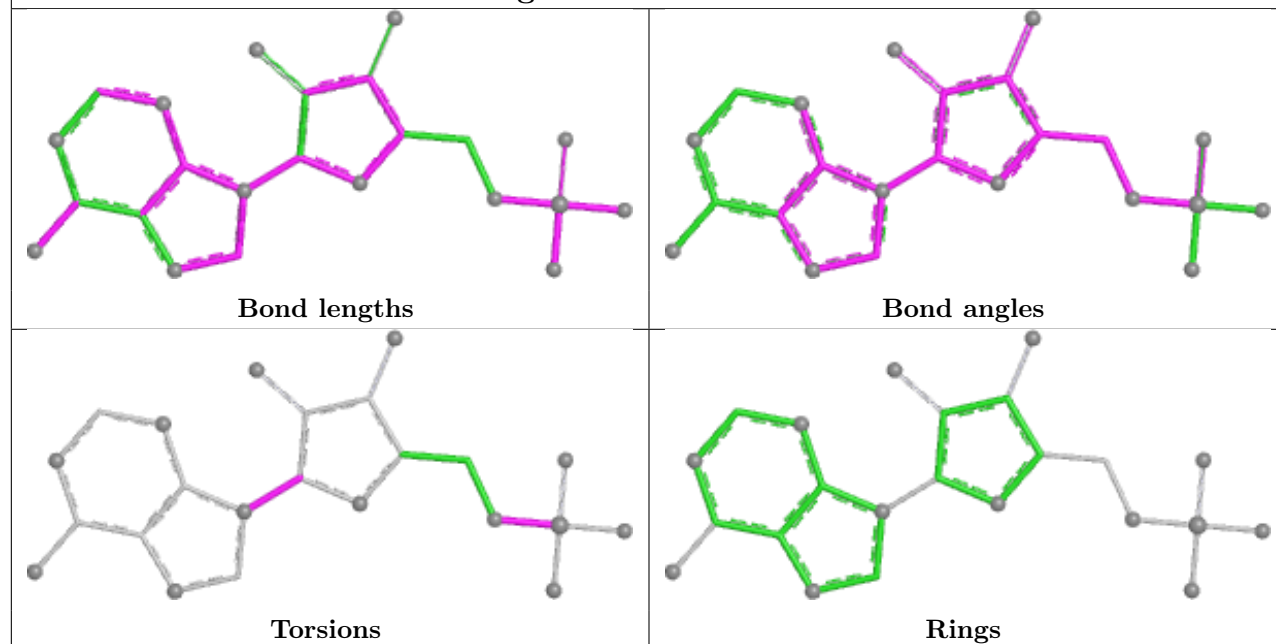
Ligand AMP M 7499

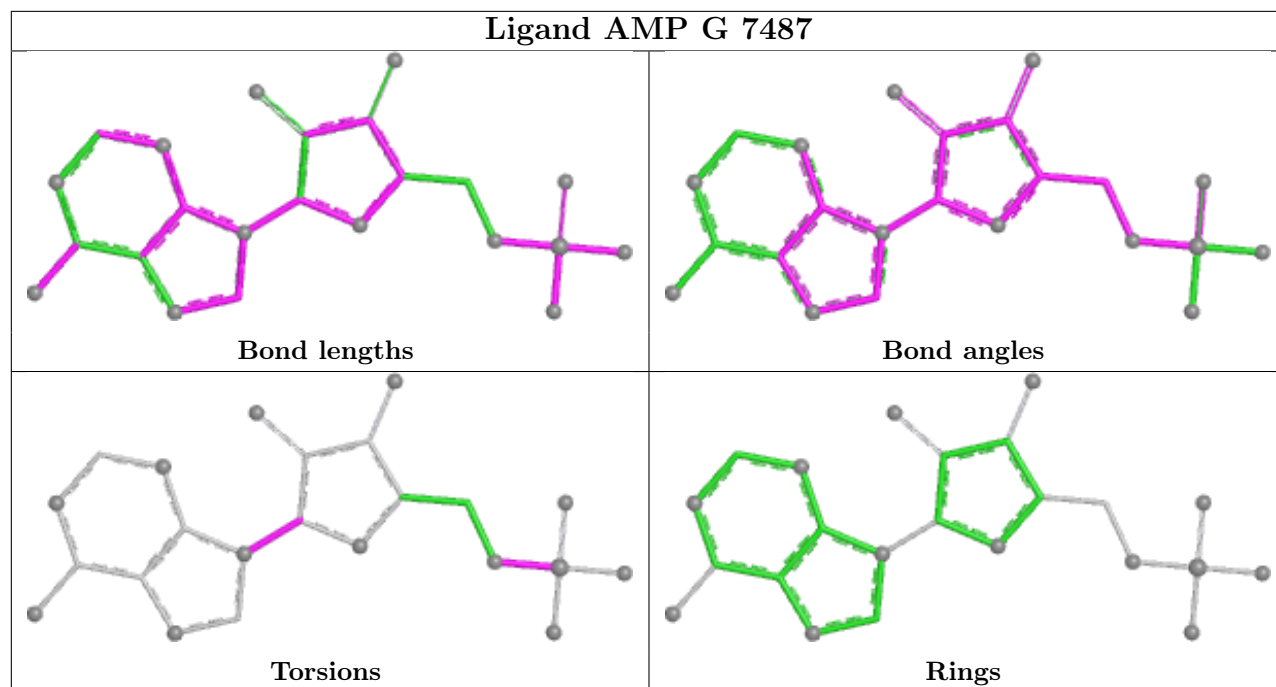


Ligand AMP E 7483



Ligand AMP O 7503





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	1-A	477/477 (100%)	2.41	203 (42%) 0 0	1, 2, 4, 5	477 (100%)
1	1-B	477/477 (100%)	2.40	202 (42%) 0 0	1, 2, 4, 5	477 (100%)
1	1-C	477/477 (100%)	2.17	190 (39%) 1 0	1, 2, 4, 5	477 (100%)
1	1-D	477/477 (100%)	2.50	214 (44%) 0 0	1, 2, 4, 5	477 (100%)
1	1-E	477/477 (100%)	2.37	210 (44%) 0 0	1, 2, 4, 5	477 (100%)
1	1-F	477/477 (100%)	2.63	230 (48%) 0 0	1, 2, 4, 5	477 (100%)
1	1-G	477/477 (100%)	2.76	235 (49%) 0 0	1, 2, 4, 5	477 (100%)
1	1-H	477/477 (100%)	2.33	203 (42%) 0 0	1, 2, 4, 5	477 (100%)
1	1-I	477/477 (100%)	2.19	188 (39%) 1 0	1, 2, 4, 5	477 (100%)
1	1-J	477/477 (100%)	2.35	197 (41%) 0 0	1, 2, 4, 5	477 (100%)
1	1-K	477/477 (100%)	2.42	212 (44%) 0 0	1, 2, 4, 5	477 (100%)
1	1-L	477/477 (100%)	2.75	251 (52%) 0 0	1, 2, 4, 5	477 (100%)
1	1-M	477/477 (100%)	2.36	206 (43%) 0 0	1, 2, 4, 5	477 (100%)
1	1-N	477/477 (100%)	2.43	209 (43%) 0 0	1, 2, 4, 5	477 (100%)
1	1-O	477/477 (100%)	2.19	193 (40%) 0 0	1, 2, 4, 5	477 (100%)
1	1-P	477/477 (100%)	2.62	229 (48%) 0 0	1, 2, 4, 5	477 (100%)
1	1-Q	477/477 (100%)	2.46	214 (44%) 0 0	1, 2, 4, 5	477 (100%)
1	1-R	477/477 (100%)	2.64	229 (48%) 0 0	1, 2, 4, 5	477 (100%)
1	1-S	477/477 (100%)	2.77	229 (48%) 0 0	1, 2, 4, 5	477 (100%)
1	1-T	477/477 (100%)	2.37	207 (43%) 0 0	1, 2, 4, 5	477 (100%)
1	1-U	477/477 (100%)	2.20	203 (42%) 0 0	1, 2, 4, 5	477 (100%)
1	1-V	477/477 (100%)	2.30	196 (41%) 0 0	1, 2, 4, 5	477 (100%)
1	1-W	477/477 (100%)	2.43	203 (42%) 0 0	1, 2, 4, 5	477 (100%)
1	1-X	477/477 (100%)	2.58	219 (45%) 0 0	1, 2, 4, 5	477 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	2-A	0/477	-	-	-	-
1	2-B	0/477	-	-	-	-
1	2-C	0/477	-	-	-	-
1	2-D	0/477	-	-	-	-
1	2-E	0/477	-	-	-	-
1	2-F	0/477	-	-	-	-
1	2-G	0/477	-	-	-	-
1	2-H	0/477	-	-	-	-
1	2-I	0/477	-	-	-	-
1	2-J	0/477	-	-	-	-
1	2-K	0/477	-	-	-	-
1	2-L	0/477	-	-	-	-
1	2-M	0/477	-	-	-	-
1	2-N	0/477	-	-	-	-
1	2-O	0/477	-	-	-	-
1	2-P	0/477	-	-	-	-
1	2-Q	0/477	-	-	-	-
1	2-R	0/477	-	-	-	-
1	2-S	0/477	-	-	-	-
1	2-T	0/477	-	-	-	-
1	2-U	0/477	-	-	-	-
1	2-V	0/477	-	-	-	-
1	2-W	0/477	-	-	-	-
1	2-X	0/477	-	-	-	-
1	3-A	0/477	-	-	-	-
1	3-B	0/477	-	-	-	-
1	3-C	0/477	-	-	-	-
1	3-D	0/477	-	-	-	-
1	3-E	0/477	-	-	-	-
1	3-F	0/477	-	-	-	-
1	3-G	0/477	-	-	-	-
1	3-H	0/477	-	-	-	-
1	3-I	0/477	-	-	-	-
1	3-J	0/477	-	-	-	-
1	3-K	0/477	-	-	-	-
1	3-L	0/477	-	-	-	-
1	3-M	0/477	-	-	-	-
1	3-N	0/477	-	-	-	-
1	3-O	0/477	-	-	-	-
1	3-P	0/477	-	-	-	-
1	3-Q	0/477	-	-	-	-
1	3-R	0/477	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	3-S	0/477	-	-	-	-
1	3-T	0/477	-	-	-	-
1	3-U	0/477	-	-	-	-
1	3-V	0/477	-	-	-	-
1	3-W	0/477	-	-	-	-
1	3-X	0/477	-	-	-	-
1	4-A	0/477	-	-	-	-
1	4-B	0/477	-	-	-	-
1	4-C	0/477	-	-	-	-
1	4-D	0/477	-	-	-	-
1	4-E	0/477	-	-	-	-
1	4-F	0/477	-	-	-	-
1	4-G	0/477	-	-	-	-
1	4-H	0/477	-	-	-	-
1	4-I	0/477	-	-	-	-
1	4-J	0/477	-	-	-	-
1	4-K	0/477	-	-	-	-
1	4-L	0/477	-	-	-	-
1	4-M	0/477	-	-	-	-
1	4-N	0/477	-	-	-	-
1	4-O	0/477	-	-	-	-
1	4-P	0/477	-	-	-	-
1	4-Q	0/477	-	-	-	-
1	4-R	0/477	-	-	-	-
1	4-S	0/477	-	-	-	-
1	4-T	0/477	-	-	-	-
1	4-U	0/477	-	-	-	-
1	4-V	0/477	-	-	-	-
1	4-W	0/477	-	-	-	-
1	4-X	0/477	-	-	-	-
1	5-A	0/477	-	-	-	-
1	5-B	0/477	-	-	-	-
1	5-C	0/477	-	-	-	-
1	5-D	0/477	-	-	-	-
1	5-E	0/477	-	-	-	-
1	5-F	0/477	-	-	-	-
1	5-G	0/477	-	-	-	-
1	5-H	0/477	-	-	-	-
1	5-I	0/477	-	-	-	-
1	5-J	0/477	-	-	-	-
1	5-K	0/477	-	-	-	-
1	5-L	0/477	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	5-M	0/477	-	-	-	-
1	5-N	0/477	-	-	-	-
1	5-O	0/477	-	-	-	-
1	5-P	0/477	-	-	-	-
1	5-Q	0/477	-	-	-	-
1	5-R	0/477	-	-	-	-
1	5-S	0/477	-	-	-	-
1	5-T	0/477	-	-	-	-
1	5-U	0/477	-	-	-	-
1	5-V	0/477	-	-	-	-
1	5-W	0/477	-	-	-	-
1	5-X	0/477	-	-	-	-
1	6-A	0/477	-	-	-	-
1	6-B	0/477	-	-	-	-
1	6-C	0/477	-	-	-	-
1	6-D	0/477	-	-	-	-
1	6-E	0/477	-	-	-	-
1	6-F	0/477	-	-	-	-
1	6-G	0/477	-	-	-	-
1	6-H	0/477	-	-	-	-
1	6-I	0/477	-	-	-	-
1	6-J	0/477	-	-	-	-
1	6-K	0/477	-	-	-	-
1	6-L	0/477	-	-	-	-
1	6-M	0/477	-	-	-	-
1	6-N	0/477	-	-	-	-
1	6-O	0/477	-	-	-	-
1	6-P	0/477	-	-	-	-
1	6-Q	0/477	-	-	-	-
1	6-R	0/477	-	-	-	-
1	6-S	0/477	-	-	-	-
1	6-T	0/477	-	-	-	-
1	6-U	0/477	-	-	-	-
1	6-V	0/477	-	-	-	-
1	6-W	0/477	-	-	-	-
1	6-X	0/477	-	-	-	-
1	7-A	0/477	-	-	-	-
1	7-B	0/477	-	-	-	-
1	7-C	0/477	-	-	-	-
1	7-D	0/477	-	-	-	-
1	7-E	0/477	-	-	-	-
1	7-F	0/477	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	7-G	0/477	-	-	-	-
1	7-H	0/477	-	-	-	-
1	7-I	0/477	-	-	-	-
1	7-J	0/477	-	-	-	-
1	7-K	0/477	-	-	-	-
1	7-L	0/477	-	-	-	-
1	7-M	0/477	-	-	-	-
1	7-N	0/477	-	-	-	-
1	7-O	0/477	-	-	-	-
1	7-P	0/477	-	-	-	-
1	7-Q	0/477	-	-	-	-
1	7-R	0/477	-	-	-	-
1	7-S	0/477	-	-	-	-
1	7-T	0/477	-	-	-	-
1	7-U	0/477	-	-	-	-
1	7-V	0/477	-	-	-	-
1	7-W	0/477	-	-	-	-
1	7-X	0/477	-	-	-	-
1	8-A	0/477	-	-	-	-
1	8-B	0/477	-	-	-	-
1	8-C	0/477	-	-	-	-
1	8-D	0/477	-	-	-	-
1	8-E	0/477	-	-	-	-
1	8-F	0/477	-	-	-	-
1	8-G	0/477	-	-	-	-
1	8-H	0/477	-	-	-	-
1	8-I	0/477	-	-	-	-
1	8-J	0/477	-	-	-	-
1	8-K	0/477	-	-	-	-
1	8-L	0/477	-	-	-	-
1	8-M	0/477	-	-	-	-
1	8-N	0/477	-	-	-	-
1	8-O	0/477	-	-	-	-
1	8-P	0/477	-	-	-	-
1	8-Q	0/477	-	-	-	-
1	8-R	0/477	-	-	-	-
1	8-S	0/477	-	-	-	-
1	8-T	0/477	-	-	-	-
1	8-U	0/477	-	-	-	-
1	8-V	0/477	-	-	-	-
1	8-W	0/477	-	-	-	-
1	8-X	0/477	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	9-A	0/477	-	-	-	-
1	9-B	0/477	-	-	-	-
1	9-C	0/477	-	-	-	-
1	9-D	0/477	-	-	-	-
1	9-E	0/477	-	-	-	-
1	9-F	0/477	-	-	-	-
1	9-G	0/477	-	-	-	-
1	9-H	0/477	-	-	-	-
1	9-I	0/477	-	-	-	-
1	9-J	0/477	-	-	-	-
1	9-K	0/477	-	-	-	-
1	9-L	0/477	-	-	-	-
1	9-M	0/477	-	-	-	-
1	9-N	0/477	-	-	-	-
1	9-O	0/477	-	-	-	-
1	9-P	0/477	-	-	-	-
1	9-Q	0/477	-	-	-	-
1	9-R	0/477	-	-	-	-
1	9-S	0/477	-	-	-	-
1	9-T	0/477	-	-	-	-
1	9-U	0/477	-	-	-	-
1	9-V	0/477	-	-	-	-
1	9-W	0/477	-	-	-	-
1	9-X	0/477	-	-	-	-
1	10-A	0/477	-	-	-	-
1	10-B	0/477	-	-	-	-
1	10-C	0/477	-	-	-	-
1	10-D	0/477	-	-	-	-
1	10-E	0/477	-	-	-	-
1	10-F	0/477	-	-	-	-
1	10-G	0/477	-	-	-	-
1	10-H	0/477	-	-	-	-
1	10-I	0/477	-	-	-	-
1	10-J	0/477	-	-	-	-
1	10-K	0/477	-	-	-	-
1	10-L	0/477	-	-	-	-
1	10-M	0/477	-	-	-	-
1	10-N	0/477	-	-	-	-
1	10-O	0/477	-	-	-	-
1	10-P	0/477	-	-	-	-
1	10-Q	0/477	-	-	-	-
1	10-R	0/477	-	-	-	-

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	10-S	0/477	-	-	-	-
1	10-T	0/477	-	-	-	-
1	10-U	0/477	-	-	-	-
1	10-V	0/477	-	-	-	-
1	10-W	0/477	-	-	-	-
1	10-X	0/477	-	-	-	-
All	All	11448/114480 (10%)	2.44	5072 (44%) 0 0	1, 2, 4, 5	11448 (100%)

The worst 5 of 5072 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	325	GLY	15.9
1	1-P	328	ALA	15.6
1	1-R	166	ALA	14.8
1	1-X	64	ASP	14.8
1	1-A	60	ILE	14.4

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(Å ²)	Q<0.9
3	AMP	1-D	7481	23/23	0.40	0.20	24,24,24,24	23
2	MN	2-A	470	1/1	-	-	24,24,24,24	1
2	MN	3-A	470	1/1	-	-	24,24,24,24	1
2	MN	4-A	470	1/1	-	-	24,24,24,24	1
2	MN	5-A	470	1/1	-	-	24,24,24,24	1
2	MN	6-A	470	1/1	-	-	24,24,24,24	1
2	MN	7-A	470	1/1	-	-	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	8-A	470	1/1	-	-	24,24,24,24	1
2	MN	9-A	470	1/1	-	-	24,24,24,24	1
2	MN	10-A	470	1/1	-	-	24,24,24,24	1
3	AMP	1-K	7495	23/23	0.40	0.20	24,24,24,24	23
2	MN	2-B	470	1/1	-	-	24,24,24,24	1
2	MN	3-B	470	1/1	-	-	24,24,24,24	1
2	MN	4-B	470	1/1	-	-	24,24,24,24	1
2	MN	5-B	470	1/1	-	-	24,24,24,24	1
2	MN	6-B	470	1/1	-	-	24,24,24,24	1
2	MN	7-B	470	1/1	-	-	24,24,24,24	1
2	MN	8-B	470	1/1	-	-	24,24,24,24	1
2	MN	9-B	470	1/1	-	-	24,24,24,24	1
2	MN	10-B	470	1/1	-	-	24,24,24,24	1
4	CIT	1-E	7484	13/13	0.41	0.31	24,24,24,24	13
2	MN	2-C	470	1/1	-	-	24,24,24,24	1
2	MN	3-C	470	1/1	-	-	24,24,24,24	1
2	MN	4-C	470	1/1	-	-	24,24,24,24	1
2	MN	5-C	470	1/1	-	-	24,24,24,24	1
2	MN	6-C	470	1/1	-	-	24,24,24,24	1
2	MN	7-C	470	1/1	-	-	24,24,24,24	1
2	MN	8-C	470	1/1	-	-	24,24,24,24	1
2	MN	9-C	470	1/1	-	-	24,24,24,24	1
2	MN	10-C	470	1/1	-	-	24,24,24,24	1
3	AMP	1-I	7491	23/23	0.43	0.19	24,24,24,24	23
2	MN	2-D	470	1/1	-	-	24,24,24,24	1
2	MN	3-D	470	1/1	-	-	24,24,24,24	1
2	MN	4-D	470	1/1	-	-	24,24,24,24	1
2	MN	5-D	470	1/1	-	-	24,24,24,24	1
2	MN	6-D	470	1/1	-	-	24,24,24,24	1
2	MN	7-D	470	1/1	-	-	24,24,24,24	1
2	MN	8-D	470	1/1	-	-	24,24,24,24	1
2	MN	9-D	470	1/1	-	-	24,24,24,24	1
2	MN	10-D	470	1/1	-	-	24,24,24,24	1
3	AMP	1-N	7501	23/23	0.45	0.19	24,24,24,24	23
2	MN	2-E	470	1/1	-	-	24,24,24,24	1
2	MN	3-E	470	1/1	-	-	24,24,24,24	1
2	MN	4-E	470	1/1	-	-	24,24,24,24	1
2	MN	5-E	470	1/1	-	-	24,24,24,24	1
2	MN	6-E	470	1/1	-	-	24,24,24,24	1
2	MN	7-E	470	1/1	-	-	24,24,24,24	1
2	MN	8-E	470	1/1	-	-	24,24,24,24	1
2	MN	9-E	470	1/1	-	-	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	10-E	470	1/1	-	-	24,24,24,24	1
3	AMP	1-P	7505	23/23	0.45	0.19	24,24,24,24	23
2	MN	2-F	470	1/1	-	-	24,24,24,24	1
2	MN	3-F	470	1/1	-	-	24,24,24,24	1
2	MN	4-F	470	1/1	-	-	24,24,24,24	1
2	MN	5-F	470	1/1	-	-	24,24,24,24	1
2	MN	6-F	470	1/1	-	-	24,24,24,24	1
2	MN	7-F	470	1/1	-	-	24,24,24,24	1
2	MN	8-F	470	1/1	-	-	24,24,24,24	1
2	MN	9-F	470	1/1	-	-	24,24,24,24	1
2	MN	10-F	470	1/1	-	-	24,24,24,24	1
3	AMP	1-J	7493	23/23	0.45	0.20	24,24,24,24	23
2	MN	2-G	470	1/1	-	-	24,24,24,24	1
2	MN	3-G	470	1/1	-	-	24,24,24,24	1
2	MN	4-G	470	1/1	-	-	24,24,24,24	1
2	MN	5-G	470	1/1	-	-	24,24,24,24	1
2	MN	6-G	470	1/1	-	-	24,24,24,24	1
2	MN	7-G	470	1/1	-	-	24,24,24,24	1
2	MN	8-G	470	1/1	-	-	24,24,24,24	1
2	MN	9-G	470	1/1	-	-	24,24,24,24	1
2	MN	10-G	470	1/1	-	-	24,24,24,24	1
3	AMP	1-A	7475	23/23	0.46	0.19	24,24,24,24	23
2	MN	2-H	470	1/1	-	-	24,24,24,24	1
2	MN	3-H	470	1/1	-	-	24,24,24,24	1
2	MN	4-H	470	1/1	-	-	24,24,24,24	1
2	MN	5-H	470	1/1	-	-	24,24,24,24	1
2	MN	6-H	470	1/1	-	-	24,24,24,24	1
2	MN	7-H	470	1/1	-	-	24,24,24,24	1
2	MN	8-H	470	1/1	-	-	24,24,24,24	1
2	MN	9-H	470	1/1	-	-	24,24,24,24	1
2	MN	10-H	470	1/1	-	-	24,24,24,24	1
3	AMP	1-H	7489	23/23	0.46	0.20	24,24,24,24	23
2	MN	2-I	470	1/1	-	-	24,24,24,24	1
2	MN	3-I	470	1/1	-	-	24,24,24,24	1
2	MN	4-I	470	1/1	-	-	24,24,24,24	1
2	MN	5-I	470	1/1	-	-	24,24,24,24	1
2	MN	6-I	470	1/1	-	-	24,24,24,24	1
2	MN	7-I	470	1/1	-	-	24,24,24,24	1
2	MN	8-I	470	1/1	-	-	24,24,24,24	1
2	MN	9-I	470	1/1	-	-	24,24,24,24	1
2	MN	10-I	470	1/1	-	-	24,24,24,24	1
3	AMP	1-V	7517	23/23	0.48	0.18	24,24,24,24	23

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	2-J	470	1/1	-	-	24,24,24,24	1
2	MN	3-J	470	1/1	-	-	24,24,24,24	1
2	MN	4-J	470	1/1	-	-	24,24,24,24	1
2	MN	5-J	470	1/1	-	-	24,24,24,24	1
2	MN	6-J	470	1/1	-	-	24,24,24,24	1
2	MN	7-J	470	1/1	-	-	24,24,24,24	1
2	MN	8-J	470	1/1	-	-	24,24,24,24	1
2	MN	9-J	470	1/1	-	-	24,24,24,24	1
2	MN	10-J	470	1/1	-	-	24,24,24,24	1
3	AMP	1-F	7485	23/23	0.51	0.18	24,24,24,24	23
2	MN	2-K	470	1/1	-	-	24,24,24,24	1
2	MN	3-K	470	1/1	-	-	24,24,24,24	1
2	MN	4-K	470	1/1	-	-	24,24,24,24	1
2	MN	5-K	470	1/1	-	-	24,24,24,24	1
2	MN	6-K	470	1/1	-	-	24,24,24,24	1
2	MN	7-K	470	1/1	-	-	24,24,24,24	1
2	MN	8-K	470	1/1	-	-	24,24,24,24	1
2	MN	9-K	470	1/1	-	-	24,24,24,24	1
2	MN	10-K	470	1/1	-	-	24,24,24,24	1
3	AMP	1-R	7509	23/23	0.51	0.20	24,24,24,24	23
2	MN	2-L	470	1/1	-	-	24,24,24,24	1
2	MN	3-L	470	1/1	-	-	24,24,24,24	1
2	MN	4-L	470	1/1	-	-	24,24,24,24	1
2	MN	5-L	470	1/1	-	-	24,24,24,24	1
2	MN	6-L	470	1/1	-	-	24,24,24,24	1
2	MN	7-L	470	1/1	-	-	24,24,24,24	1
2	MN	8-L	470	1/1	-	-	24,24,24,24	1
2	MN	9-L	470	1/1	-	-	24,24,24,24	1
2	MN	10-L	470	1/1	-	-	24,24,24,24	1
3	AMP	1-G	7487	23/23	0.52	0.17	24,24,24,24	23
2	MN	2-M	470	1/1	-	-	24,24,24,24	1
2	MN	3-M	470	1/1	-	-	24,24,24,24	1
2	MN	4-M	470	1/1	-	-	24,24,24,24	1
2	MN	5-M	470	1/1	-	-	24,24,24,24	1
2	MN	6-M	470	1/1	-	-	24,24,24,24	1
2	MN	7-M	470	1/1	-	-	24,24,24,24	1
2	MN	8-M	470	1/1	-	-	24,24,24,24	1
2	MN	9-M	470	1/1	-	-	24,24,24,24	1
2	MN	10-M	470	1/1	-	-	24,24,24,24	1
4	CIT	1-B	7478	13/13	0.52	0.27	24,24,24,24	13
2	MN	2-N	470	1/1	-	-	24,24,24,24	1
2	MN	3-N	470	1/1	-	-	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	4-N	470	1/1	-	-	24,24,24,24	1
2	MN	5-N	470	1/1	-	-	24,24,24,24	1
2	MN	6-N	470	1/1	-	-	24,24,24,24	1
2	MN	7-N	470	1/1	-	-	24,24,24,24	1
2	MN	8-N	470	1/1	-	-	24,24,24,24	1
2	MN	9-N	470	1/1	-	-	24,24,24,24	1
2	MN	10-N	470	1/1	-	-	24,24,24,24	1
3	AMP	1-B	7477	23/23	0.52	0.17	24,24,24,24	23
2	MN	2-O	470	1/1	-	-	24,24,24,24	1
2	MN	3-O	470	1/1	-	-	24,24,24,24	1
2	MN	4-O	470	1/1	-	-	24,24,24,24	1
2	MN	5-O	470	1/1	-	-	24,24,24,24	1
2	MN	6-O	470	1/1	-	-	24,24,24,24	1
2	MN	7-O	470	1/1	-	-	24,24,24,24	1
2	MN	8-O	470	1/1	-	-	24,24,24,24	1
2	MN	9-O	470	1/1	-	-	24,24,24,24	1
2	MN	10-O	470	1/1	-	-	24,24,24,24	1
4	CIT	1-T	7514	13/13	0.52	0.26	24,24,24,24	13
2	MN	2-P	470	1/1	-	-	24,24,24,24	1
2	MN	3-P	470	1/1	-	-	24,24,24,24	1
2	MN	4-P	470	1/1	-	-	24,24,24,24	1
2	MN	5-P	470	1/1	-	-	24,24,24,24	1
2	MN	6-P	470	1/1	-	-	24,24,24,24	1
2	MN	7-P	470	1/1	-	-	24,24,24,24	1
2	MN	8-P	470	1/1	-	-	24,24,24,24	1
2	MN	9-P	470	1/1	-	-	24,24,24,24	1
2	MN	10-P	470	1/1	-	-	24,24,24,24	1
3	AMP	1-E	7483	23/23	0.53	0.17	24,24,24,24	23
2	MN	2-Q	470	1/1	-	-	24,24,24,24	1
2	MN	3-Q	470	1/1	-	-	24,24,24,24	1
2	MN	4-Q	470	1/1	-	-	24,24,24,24	1
2	MN	5-Q	470	1/1	-	-	24,24,24,24	1
2	MN	6-Q	470	1/1	-	-	24,24,24,24	1
2	MN	7-Q	470	1/1	-	-	24,24,24,24	1
2	MN	8-Q	470	1/1	-	-	24,24,24,24	1
2	MN	9-Q	470	1/1	-	-	24,24,24,24	1
2	MN	10-Q	470	1/1	-	-	24,24,24,24	1
3	AMP	1-U	7515	23/23	0.53	0.17	24,24,24,24	23
2	MN	2-R	470	1/1	-	-	24,24,24,24	1
2	MN	3-R	470	1/1	-	-	24,24,24,24	1
2	MN	4-R	470	1/1	-	-	24,24,24,24	1
2	MN	5-R	470	1/1	-	-	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	6-R	470	1/1	-	-	24,24,24,24	1
2	MN	7-R	470	1/1	-	-	24,24,24,24	1
2	MN	8-R	470	1/1	-	-	24,24,24,24	1
2	MN	9-R	470	1/1	-	-	24,24,24,24	1
2	MN	10-R	470	1/1	-	-	24,24,24,24	1
3	AMP	1-O	7503	23/23	0.54	0.17	24,24,24,24	23
2	MN	2-S	470	1/1	-	-	24,24,24,24	1
2	MN	3-S	470	1/1	-	-	24,24,24,24	1
2	MN	4-S	470	1/1	-	-	24,24,24,24	1
2	MN	5-S	470	1/1	-	-	24,24,24,24	1
2	MN	6-S	470	1/1	-	-	24,24,24,24	1
2	MN	7-S	470	1/1	-	-	24,24,24,24	1
2	MN	8-S	470	1/1	-	-	24,24,24,24	1
2	MN	9-S	470	1/1	-	-	24,24,24,24	1
2	MN	10-S	470	1/1	-	-	24,24,24,24	1
3	AMP	1-W	7519	23/23	0.54	0.18	24,24,24,24	23
2	MN	2-T	470	1/1	-	-	24,24,24,24	1
2	MN	3-T	470	1/1	-	-	24,24,24,24	1
2	MN	4-T	470	1/1	-	-	24,24,24,24	1
2	MN	5-T	470	1/1	-	-	24,24,24,24	1
2	MN	6-T	470	1/1	-	-	24,24,24,24	1
2	MN	7-T	470	1/1	-	-	24,24,24,24	1
2	MN	8-T	470	1/1	-	-	24,24,24,24	1
2	MN	9-T	470	1/1	-	-	24,24,24,24	1
2	MN	10-T	470	1/1	-	-	24,24,24,24	1
3	AMP	1-L	7497	23/23	0.54	0.19	24,24,24,24	23
2	MN	2-U	470	1/1	-	-	24,24,24,24	1
2	MN	3-U	470	1/1	-	-	24,24,24,24	1
2	MN	4-U	470	1/1	-	-	24,24,24,24	1
2	MN	5-U	470	1/1	-	-	24,24,24,24	1
2	MN	6-U	470	1/1	-	-	24,24,24,24	1
2	MN	7-U	470	1/1	-	-	24,24,24,24	1
2	MN	8-U	470	1/1	-	-	24,24,24,24	1
2	MN	9-U	470	1/1	-	-	24,24,24,24	1
2	MN	10-U	470	1/1	-	-	24,24,24,24	1
3	AMP	1-M	7499	23/23	0.54	0.17	24,24,24,24	23
2	MN	2-V	470	1/1	-	-	24,24,24,24	1
2	MN	3-V	470	1/1	-	-	24,24,24,24	1
2	MN	4-V	470	1/1	-	-	24,24,24,24	1
2	MN	5-V	470	1/1	-	-	24,24,24,24	1
2	MN	6-V	470	1/1	-	-	24,24,24,24	1
2	MN	7-V	470	1/1	-	-	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	8-V	470	1/1	-	-	24,24,24,24	1
2	MN	9-V	470	1/1	-	-	24,24,24,24	1
2	MN	10-V	470	1/1	-	-	24,24,24,24	1
4	CIT	1-I	7492	13/13	0.54	0.25	24,24,24,24	13
2	MN	2-W	470	1/1	-	-	24,24,24,24	1
2	MN	3-W	470	1/1	-	-	24,24,24,24	1
2	MN	4-W	470	1/1	-	-	24,24,24,24	1
2	MN	5-W	470	1/1	-	-	24,24,24,24	1
2	MN	6-W	470	1/1	-	-	24,24,24,24	1
2	MN	7-W	470	1/1	-	-	24,24,24,24	1
2	MN	8-W	470	1/1	-	-	24,24,24,24	1
2	MN	9-W	470	1/1	-	-	24,24,24,24	1
2	MN	10-W	470	1/1	-	-	24,24,24,24	1
3	AMP	1-C	7479	23/23	0.54	0.18	24,24,24,24	23
2	MN	2-X	470	1/1	-	-	24,24,24,24	1
2	MN	3-X	470	1/1	-	-	24,24,24,24	1
2	MN	4-X	470	1/1	-	-	24,24,24,24	1
2	MN	5-X	470	1/1	-	-	24,24,24,24	1
2	MN	6-X	470	1/1	-	-	24,24,24,24	1
2	MN	7-X	470	1/1	-	-	24,24,24,24	1
2	MN	8-X	470	1/1	-	-	24,24,24,24	1
2	MN	9-X	470	1/1	-	-	24,24,24,24	1
2	MN	10-X	470	1/1	-	-	24,24,24,24	1
4	CIT	1-L	7498	13/13	0.55	0.26	24,24,24,24	13
3	AMP	2-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	3-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	4-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	5-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	6-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	7-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	8-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	9-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	10-A	7475	23/23	-	-	24,24,24,24	23
3	AMP	1-Q	7507	23/23	0.56	0.16	24,24,24,24	23
3	AMP	2-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	3-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	4-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	5-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	6-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	7-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	8-B	7477	23/23	-	-	24,24,24,24	23
3	AMP	9-B	7477	23/23	-	-	24,24,24,24	23

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AMP	10-B	7477	23/23	-	-	24,24,24,24	23
4	CIT	1-N	7502	13/13	0.56	0.23	24,24,24,24	13
3	AMP	2-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	3-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	4-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	5-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	6-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	7-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	8-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	9-C	7479	23/23	-	-	24,24,24,24	23
3	AMP	10-C	7479	23/23	-	-	24,24,24,24	23
4	CIT	1-Q	7508	13/13	0.56	0.27	24,24,24,24	13
3	AMP	2-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	3-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	4-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	5-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	6-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	7-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	8-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	9-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	10-D	7481	23/23	-	-	24,24,24,24	23
3	AMP	1-S	7511	23/23	0.56	0.17	24,24,24,24	23
3	AMP	2-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	3-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	4-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	5-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	6-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	7-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	8-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	9-E	7483	23/23	-	-	24,24,24,24	23
3	AMP	10-E	7483	23/23	-	-	24,24,24,24	23
4	CIT	1-F	7486	13/13	0.57	0.29	24,24,24,24	13
3	AMP	2-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	3-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	4-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	5-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	6-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	7-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	8-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	9-F	7485	23/23	-	-	24,24,24,24	23
3	AMP	10-F	7485	23/23	-	-	24,24,24,24	23
4	CIT	1-O	7504	13/13	0.58	0.26	24,24,24,24	13

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AMP	2-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	3-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	4-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	5-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	6-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	7-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	8-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	9-G	7487	23/23	-	-	24,24,24,24	23
3	AMP	10-G	7487	23/23	-	-	24,24,24,24	23
4	CIT	1-C	7480	13/13	0.58	0.28	24,24,24,24	13
3	AMP	2-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	3-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	4-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	5-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	6-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	7-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	8-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	9-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	10-H	7489	23/23	-	-	24,24,24,24	23
3	AMP	1-T	7513	23/23	0.58	0.18	24,24,24,24	23
3	AMP	2-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	3-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	4-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	5-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	6-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	7-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	8-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	9-I	7491	23/23	-	-	24,24,24,24	23
3	AMP	10-I	7491	23/23	-	-	24,24,24,24	23
4	CIT	1-S	7512	13/13	0.59	0.24	24,24,24,24	13
3	AMP	2-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	3-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	4-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	5-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	6-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	7-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	8-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	9-J	7493	23/23	-	-	24,24,24,24	23
3	AMP	10-J	7493	23/23	-	-	24,24,24,24	23
4	CIT	1-H	7490	13/13	0.63	0.23	24,24,24,24	13
3	AMP	2-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	3-K	7495	23/23	-	-	24,24,24,24	23

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AMP	4-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	5-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	6-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	7-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	8-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	9-K	7495	23/23	-	-	24,24,24,24	23
3	AMP	10-K	7495	23/23	-	-	24,24,24,24	23
4	CIT	1-G	7488	13/13	0.63	0.24	24,24,24,24	13
3	AMP	2-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	3-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	4-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	5-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	6-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	7-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	8-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	9-L	7497	23/23	-	-	24,24,24,24	23
3	AMP	10-L	7497	23/23	-	-	24,24,24,24	23
4	CIT	1-V	7518	13/13	0.64	0.20	24,24,24,24	13
3	AMP	2-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	3-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	4-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	5-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	6-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	7-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	8-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	9-M	7499	23/23	-	-	24,24,24,24	23
3	AMP	10-M	7499	23/23	-	-	24,24,24,24	23
4	CIT	1-U	7516	13/13	0.65	0.25	24,24,24,24	13
3	AMP	2-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	3-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	4-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	5-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	6-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	7-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	8-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	9-N	7501	23/23	-	-	24,24,24,24	23
3	AMP	10-N	7501	23/23	-	-	24,24,24,24	23
4	CIT	1-M	7500	13/13	0.65	0.21	24,24,24,24	13
3	AMP	2-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	3-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	4-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	5-O	7503	23/23	-	-	24,24,24,24	23

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AMP	6-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	7-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	8-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	9-O	7503	23/23	-	-	24,24,24,24	23
3	AMP	10-O	7503	23/23	-	-	24,24,24,24	23
4	CIT	1-A	7476	13/13	0.66	0.18	24,24,24,24	13
3	AMP	2-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	3-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	4-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	5-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	6-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	7-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	8-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	9-P	7505	23/23	-	-	24,24,24,24	23
3	AMP	10-P	7505	23/23	-	-	24,24,24,24	23
4	CIT	1-R	7510	13/13	0.66	0.25	24,24,24,24	13
3	AMP	2-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	3-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	4-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	5-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	6-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	7-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	8-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	9-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	10-Q	7507	23/23	-	-	24,24,24,24	23
3	AMP	1-X	7521	23/23	0.66	0.15	24,24,24,24	23
3	AMP	2-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	3-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	4-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	5-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	6-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	7-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	8-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	9-R	7509	23/23	-	-	24,24,24,24	23
3	AMP	10-R	7509	23/23	-	-	24,24,24,24	23
2	MN	1-L	470	1/1	0.68	0.32	24,24,24,24	1
3	AMP	2-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	3-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	4-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	5-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	6-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	7-S	7511	23/23	-	-	24,24,24,24	23

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AMP	8-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	9-S	7511	23/23	-	-	24,24,24,24	23
3	AMP	10-S	7511	23/23	-	-	24,24,24,24	23
2	MN	1-G	470	1/1	0.68	0.46	24,24,24,24	1
3	AMP	2-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	3-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	4-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	5-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	6-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	7-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	8-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	9-T	7513	23/23	-	-	24,24,24,24	23
3	AMP	10-T	7513	23/23	-	-	24,24,24,24	23
4	CIT	1-D	7482	13/13	0.68	0.18	24,24,24,24	13
3	AMP	2-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	3-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	4-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	5-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	6-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	7-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	8-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	9-U	7515	23/23	-	-	24,24,24,24	23
3	AMP	10-U	7515	23/23	-	-	24,24,24,24	23
4	CIT	1-P	7506	13/13	0.69	0.17	24,24,24,24	13
3	AMP	2-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	3-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	4-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	5-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	6-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	7-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	8-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	9-V	7517	23/23	-	-	24,24,24,24	23
3	AMP	10-V	7517	23/23	-	-	24,24,24,24	23
4	CIT	1-W	7520	13/13	0.69	0.21	24,24,24,24	13
3	AMP	2-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	3-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	4-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	5-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	6-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	7-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	8-W	7519	23/23	-	-	24,24,24,24	23
3	AMP	9-W	7519	23/23	-	-	24,24,24,24	23

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AMP	10-W	7519	23/23	-	-	24,24,24,24	23
4	CIT	1-X	7522	13/13	0.69	0.22	24,24,24,24	13
3	AMP	2-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	3-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	4-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	5-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	6-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	7-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	8-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	9-X	7521	23/23	-	-	24,24,24,24	23
3	AMP	10-X	7521	23/23	-	-	24,24,24,24	23
4	CIT	1-J	7494	13/13	0.70	0.18	24,24,24,24	13
4	CIT	2-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	3-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	4-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	5-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	6-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	7-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	8-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	9-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	10-A	7476	13/13	-	-	24,24,24,24	13
4	CIT	1-K	7496	13/13	0.71	0.22	24,24,24,24	13
4	CIT	2-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	3-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	4-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	5-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	6-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	7-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	8-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	9-B	7478	13/13	-	-	24,24,24,24	13
4	CIT	10-B	7478	13/13	-	-	24,24,24,24	13
2	MN	1-D	470	1/1	0.72	0.26	24,24,24,24	1
4	CIT	2-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	3-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	4-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	5-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	6-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	7-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	8-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	9-C	7480	13/13	-	-	24,24,24,24	13
4	CIT	10-C	7480	13/13	-	-	24,24,24,24	13
2	MN	1-E	470	1/1	0.74	0.36	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CIT	2-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	3-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	4-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	5-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	6-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	7-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	8-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	9-D	7482	13/13	-	-	24,24,24,24	13
4	CIT	10-D	7482	13/13	-	-	24,24,24,24	13
2	MN	1-A	470	1/1	0.75	0.32	24,24,24,24	1
4	CIT	2-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	3-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	4-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	5-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	6-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	7-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	8-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	9-E	7484	13/13	-	-	24,24,24,24	13
4	CIT	10-E	7484	13/13	-	-	24,24,24,24	13
2	MN	1-X	470	1/1	0.75	0.35	24,24,24,24	1
4	CIT	2-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	3-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	4-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	5-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	6-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	7-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	8-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	9-F	7486	13/13	-	-	24,24,24,24	13
4	CIT	10-F	7486	13/13	-	-	24,24,24,24	13
2	MN	1-N	470	1/1	0.78	0.29	24,24,24,24	1
4	CIT	2-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	3-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	4-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	5-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	6-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	7-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	8-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	9-G	7488	13/13	-	-	24,24,24,24	13
4	CIT	10-G	7488	13/13	-	-	24,24,24,24	13
2	MN	1-V	470	1/1	0.82	0.30	24,24,24,24	1
4	CIT	2-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	3-H	7490	13/13	-	-	24,24,24,24	13

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CIT	4-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	5-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	6-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	7-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	8-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	9-H	7490	13/13	-	-	24,24,24,24	13
4	CIT	10-H	7490	13/13	-	-	24,24,24,24	13
2	MN	1-O	470	1/1	0.83	0.43	24,24,24,24	1
4	CIT	2-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	3-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	4-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	5-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	6-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	7-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	8-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	9-I	7492	13/13	-	-	24,24,24,24	13
4	CIT	10-I	7492	13/13	-	-	24,24,24,24	13
2	MN	1-H	470	1/1	0.84	0.28	24,24,24,24	1
4	CIT	2-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	3-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	4-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	5-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	6-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	7-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	8-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	9-J	7494	13/13	-	-	24,24,24,24	13
4	CIT	10-J	7494	13/13	-	-	24,24,24,24	13
2	MN	1-M	470	1/1	0.84	0.31	24,24,24,24	1
4	CIT	2-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	3-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	4-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	5-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	6-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	7-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	8-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	9-K	7496	13/13	-	-	24,24,24,24	13
4	CIT	10-K	7496	13/13	-	-	24,24,24,24	13
2	MN	1-I	470	1/1	0.84	0.34	24,24,24,24	1
4	CIT	2-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	3-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	4-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	5-L	7498	13/13	-	-	24,24,24,24	13

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CIT	6-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	7-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	8-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	9-L	7498	13/13	-	-	24,24,24,24	13
4	CIT	10-L	7498	13/13	-	-	24,24,24,24	13
2	MN	1-T	470	1/1	0.85	0.27	24,24,24,24	1
4	CIT	2-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	3-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	4-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	5-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	6-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	7-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	8-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	9-M	7500	13/13	-	-	24,24,24,24	13
4	CIT	10-M	7500	13/13	-	-	24,24,24,24	13
2	MN	1-S	470	1/1	0.86	0.34	24,24,24,24	1
4	CIT	2-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	3-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	4-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	5-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	6-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	7-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	8-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	9-N	7502	13/13	-	-	24,24,24,24	13
4	CIT	10-N	7502	13/13	-	-	24,24,24,24	13
2	MN	1-J	470	1/1	0.86	0.34	24,24,24,24	1
4	CIT	2-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	3-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	4-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	5-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	6-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	7-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	8-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	9-O	7504	13/13	-	-	24,24,24,24	13
4	CIT	10-O	7504	13/13	-	-	24,24,24,24	13
2	MN	1-B	470	1/1	0.88	0.25	24,24,24,24	1
4	CIT	2-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	3-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	4-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	5-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	6-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	7-P	7506	13/13	-	-	24,24,24,24	13

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CIT	8-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	9-P	7506	13/13	-	-	24,24,24,24	13
4	CIT	10-P	7506	13/13	-	-	24,24,24,24	13
2	MN	1-U	470	1/1	0.88	0.40	24,24,24,24	1
4	CIT	2-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	3-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	4-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	5-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	6-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	7-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	8-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	9-Q	7508	13/13	-	-	24,24,24,24	13
4	CIT	10-Q	7508	13/13	-	-	24,24,24,24	13
2	MN	1-W	470	1/1	0.89	0.28	24,24,24,24	1
4	CIT	2-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	3-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	4-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	5-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	6-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	7-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	8-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	9-R	7510	13/13	-	-	24,24,24,24	13
4	CIT	10-R	7510	13/13	-	-	24,24,24,24	13
2	MN	1-C	470	1/1	0.89	0.26	24,24,24,24	1
4	CIT	2-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	3-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	4-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	5-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	6-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	7-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	8-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	9-S	7512	13/13	-	-	24,24,24,24	13
4	CIT	10-S	7512	13/13	-	-	24,24,24,24	13
2	MN	1-R	470	1/1	0.90	0.26	24,24,24,24	1
4	CIT	2-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	3-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	4-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	5-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	6-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	7-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	8-T	7514	13/13	-	-	24,24,24,24	13
4	CIT	9-T	7514	13/13	-	-	24,24,24,24	13

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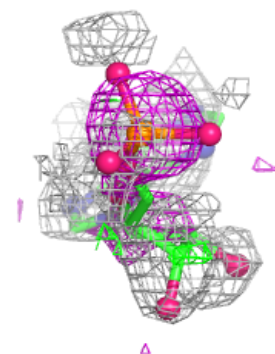
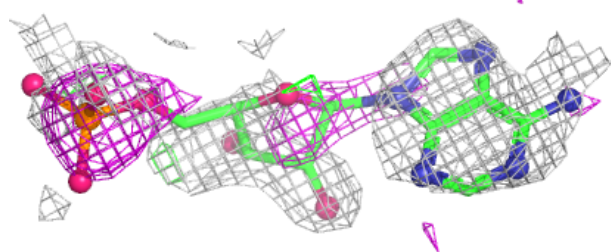
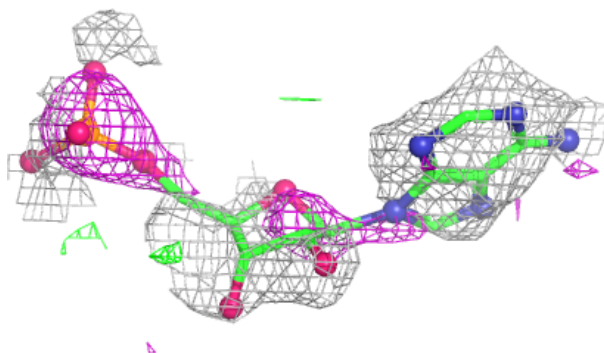
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CIT	10-T	7514	13/13	-	-	24,24,24,24	13
2	MN	1-Q	470	1/1	0.92	0.32	24,24,24,24	1
4	CIT	2-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	3-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	4-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	5-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	6-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	7-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	8-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	9-U	7516	13/13	-	-	24,24,24,24	13
4	CIT	10-U	7516	13/13	-	-	24,24,24,24	13
2	MN	1-K	470	1/1	0.92	0.31	24,24,24,24	1
4	CIT	2-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	3-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	4-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	5-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	6-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	7-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	8-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	9-V	7518	13/13	-	-	24,24,24,24	13
4	CIT	10-V	7518	13/13	-	-	24,24,24,24	13
2	MN	1-P	470	1/1	0.94	0.25	24,24,24,24	1
4	CIT	2-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	3-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	4-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	5-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	6-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	7-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	8-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	9-W	7520	13/13	-	-	24,24,24,24	13
4	CIT	10-W	7520	13/13	-	-	24,24,24,24	13
2	MN	1-F	470	1/1	0.96	0.40	24,24,24,24	1
4	CIT	2-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	3-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	4-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	5-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	6-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	7-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	8-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	9-X	7522	13/13	-	-	24,24,24,24	13
4	CIT	10-X	7522	13/13	-	-	24,24,24,24	13

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.

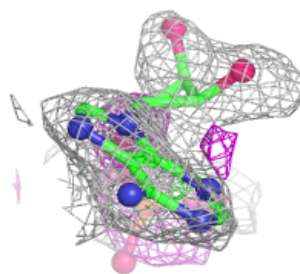
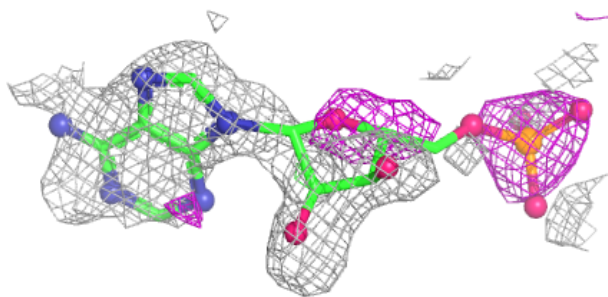
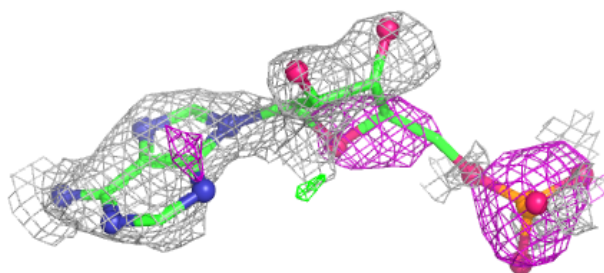
Electron density around AMP D 7481:

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

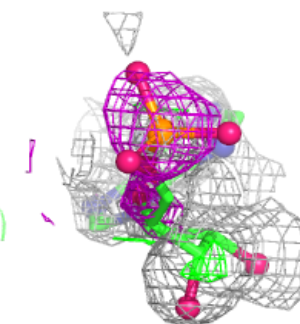
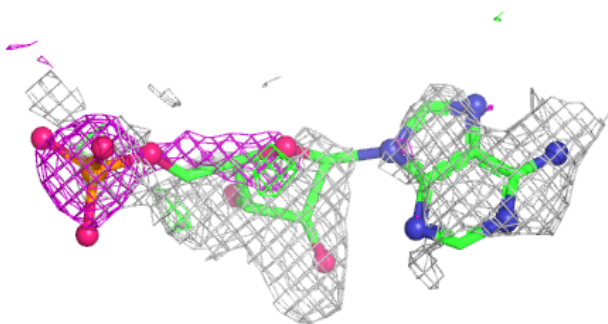
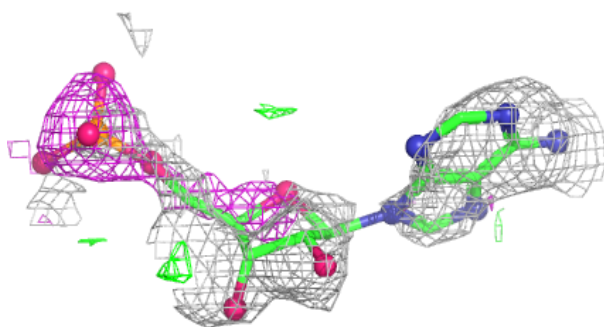


Electron density around AMP K 7495:

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

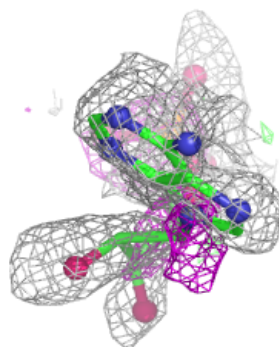
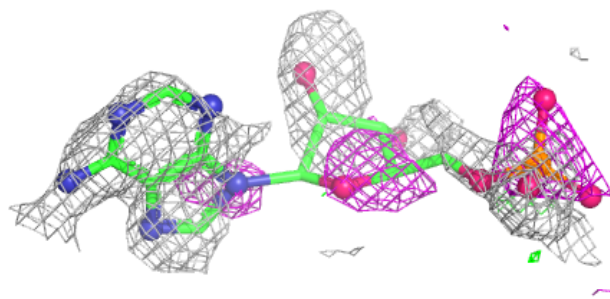
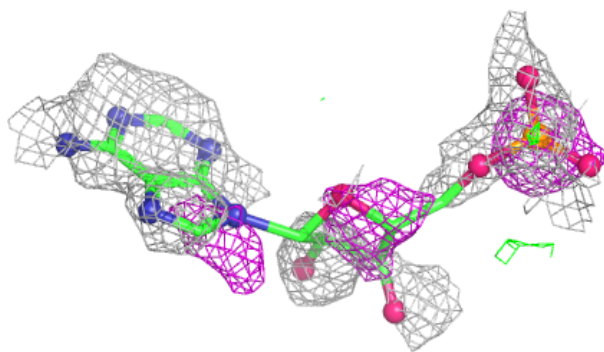
**Electron density around AMP I 7491:**

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

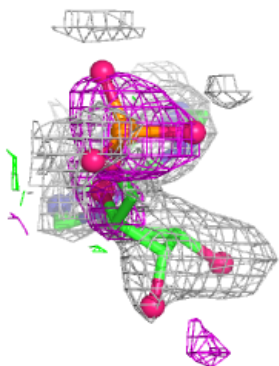
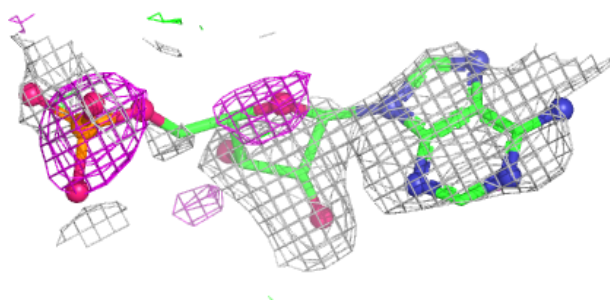
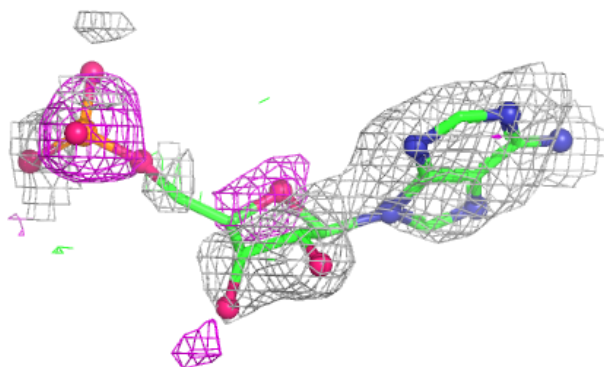


Electron density around AMP N 7501:

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

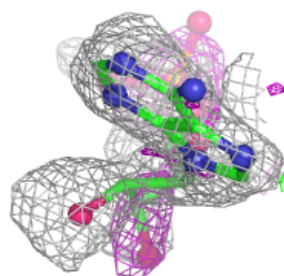
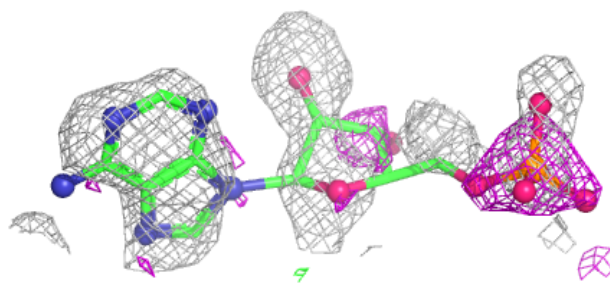
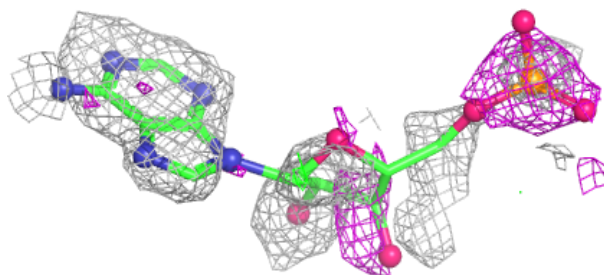
**Electron density around AMP P 7505:**

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

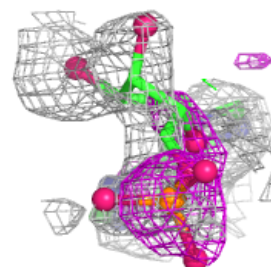
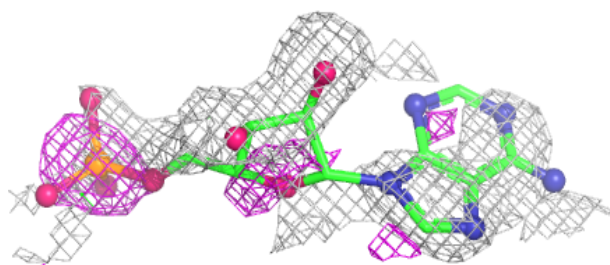
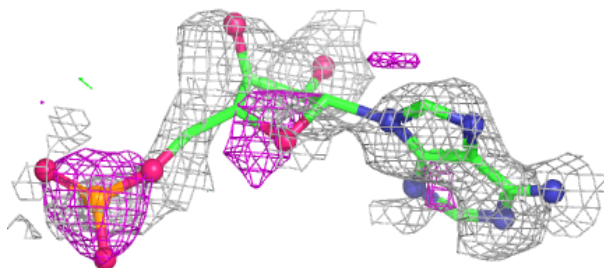


Electron density around AMP J 7493:

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

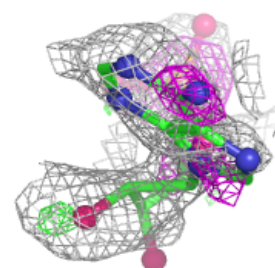
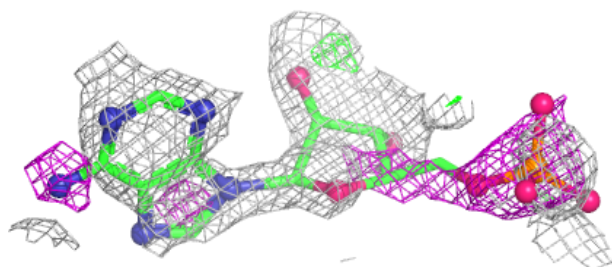
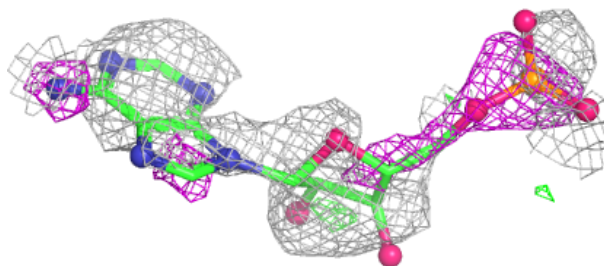
**Electron density around AMP A 7475:**

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

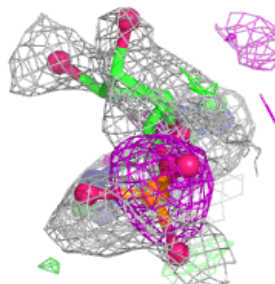
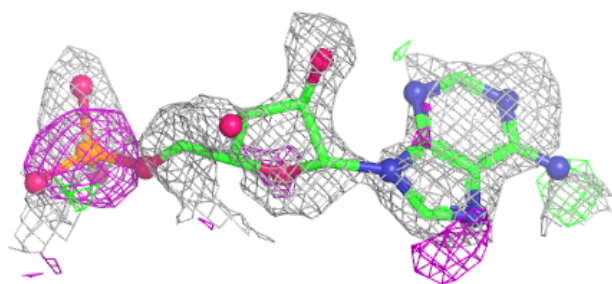
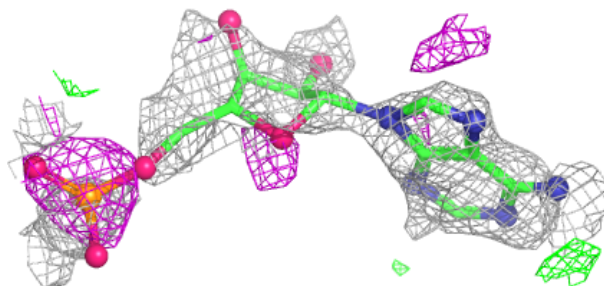


Electron density around AMP H 7489:

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

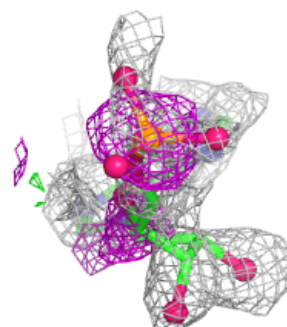
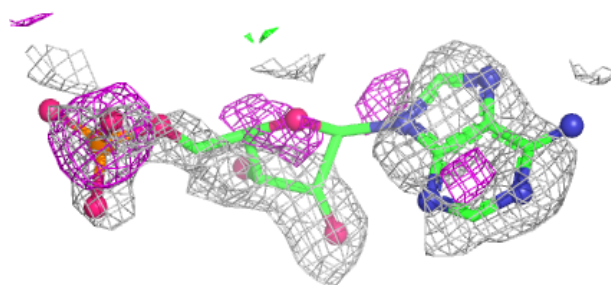
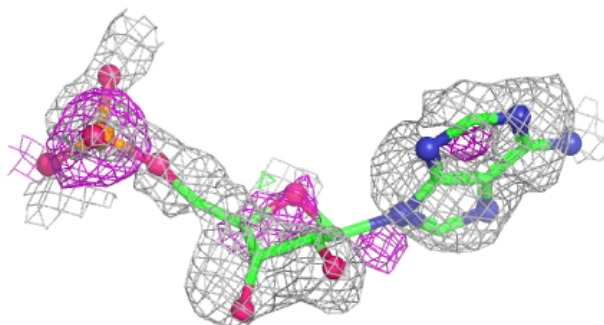
**Electron density around AMP V 7517:**

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

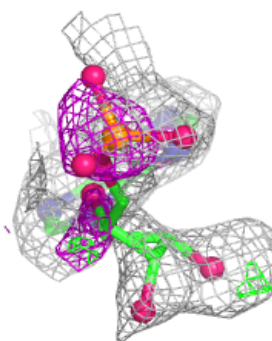
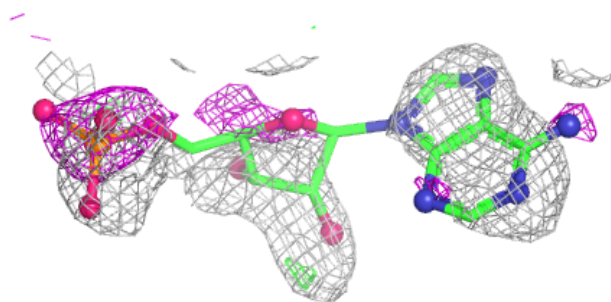
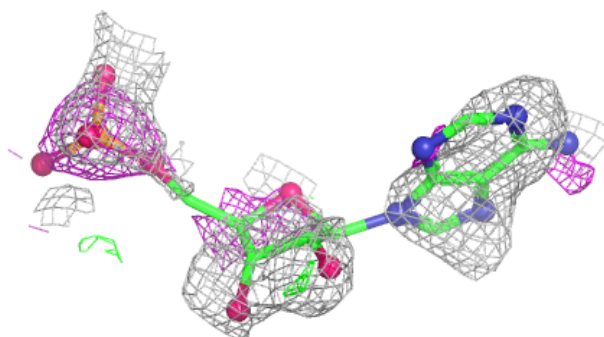


Electron density around AMP F 7485:

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

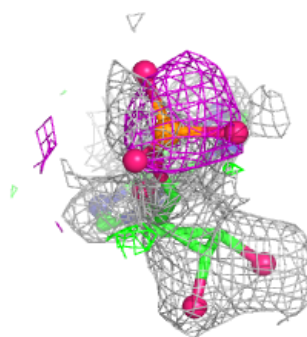
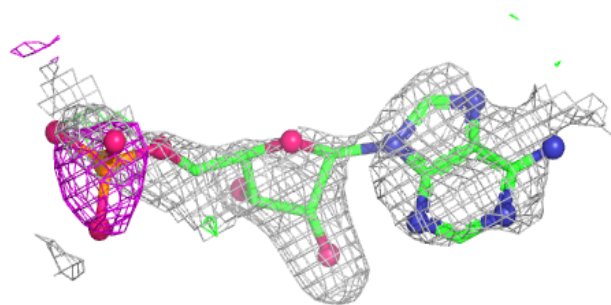
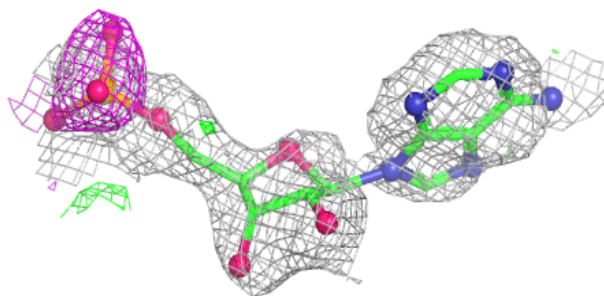
**Electron density around AMP R 7509:**

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

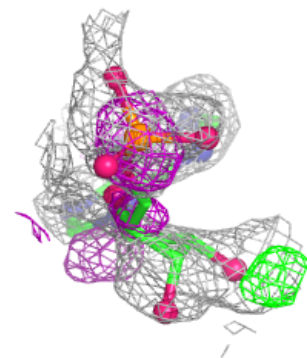
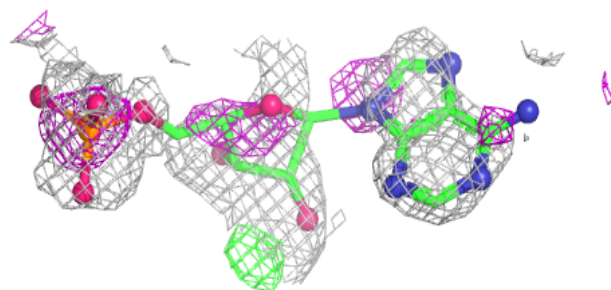
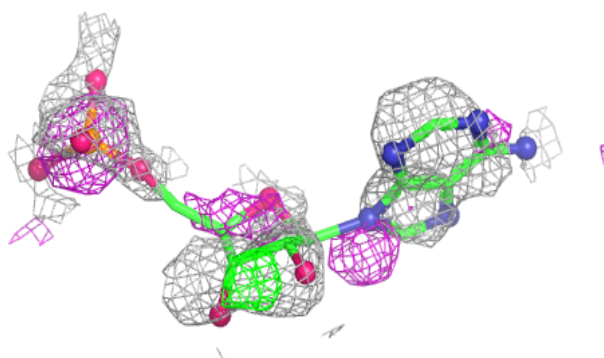


Electron density around AMP G 7487:

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

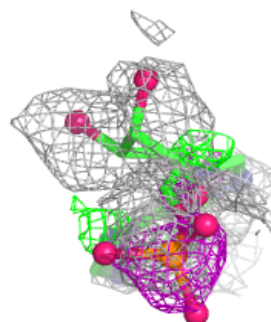
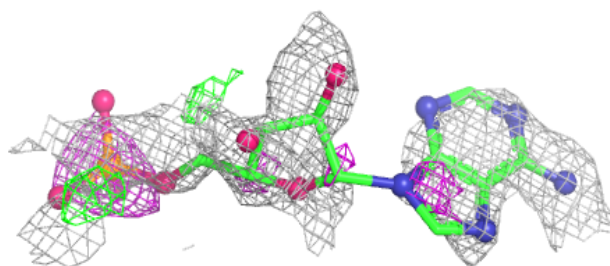
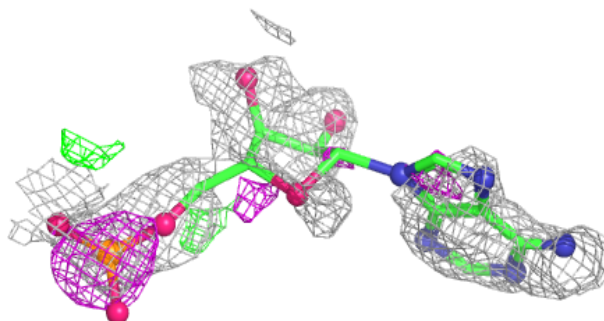
**Electron density around AMP B 7477:**

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

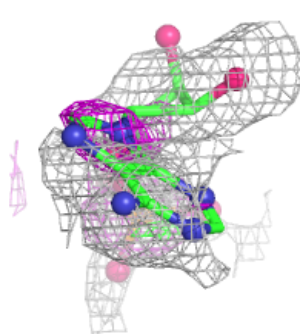
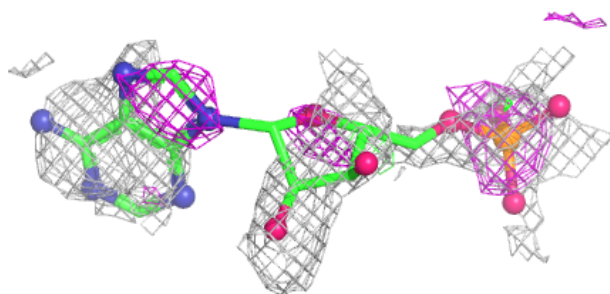
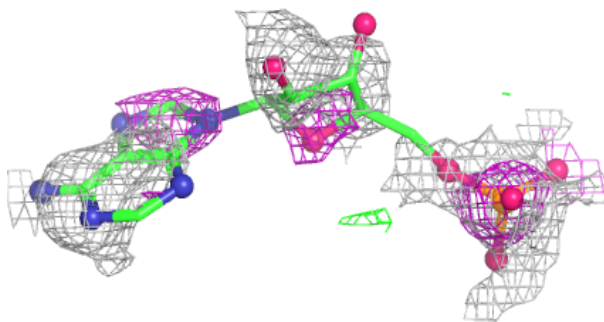


Electron density around AMP E 7483:

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

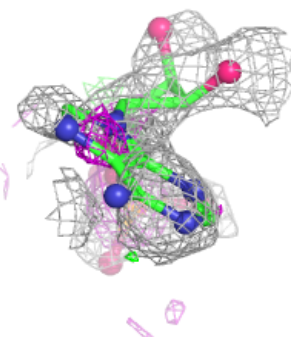
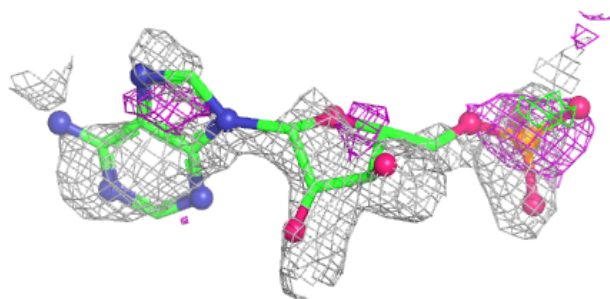
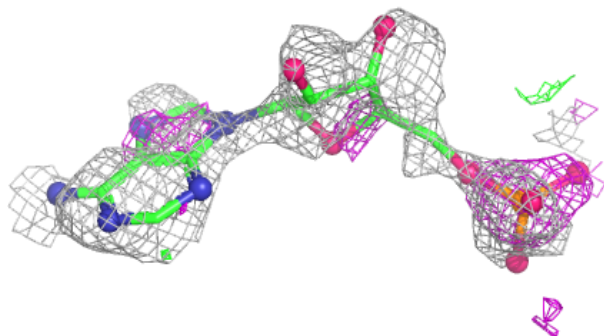
**Electron density around AMP U 7515:**

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

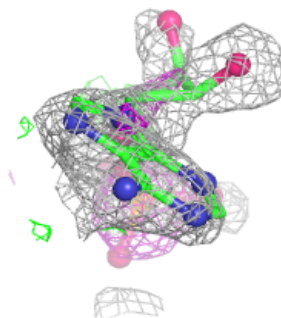
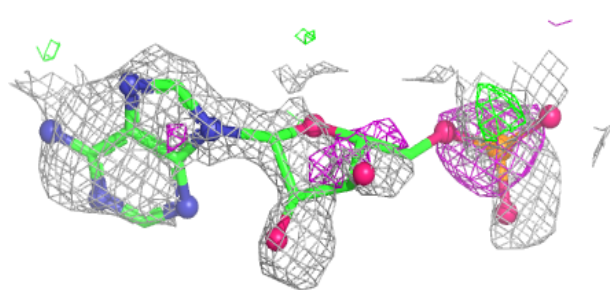
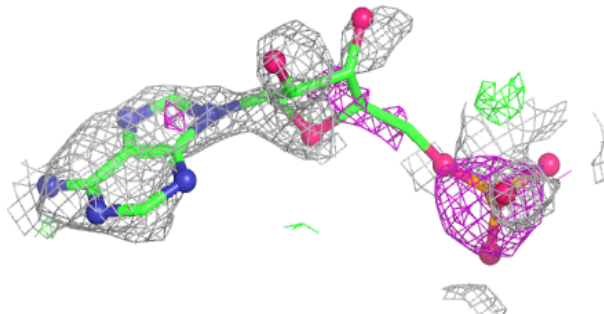


Electron density around AMP O 7503:

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

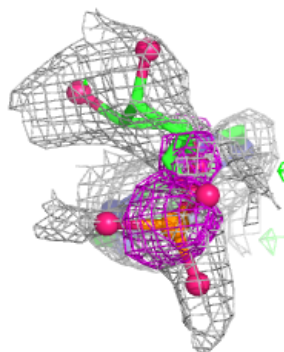
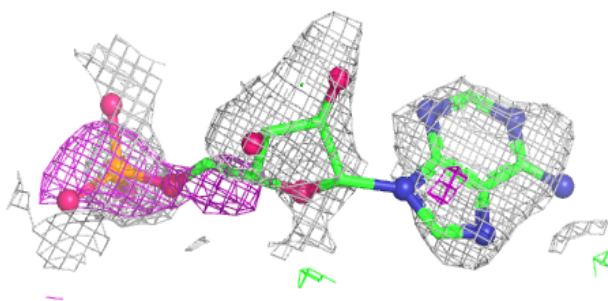
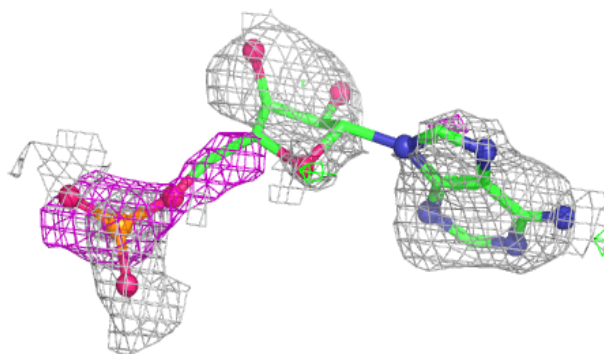
**Electron density around AMP W 7519:**

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

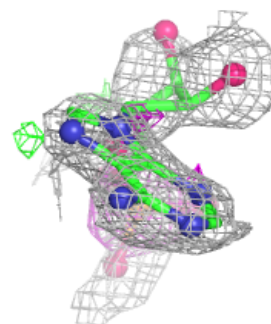
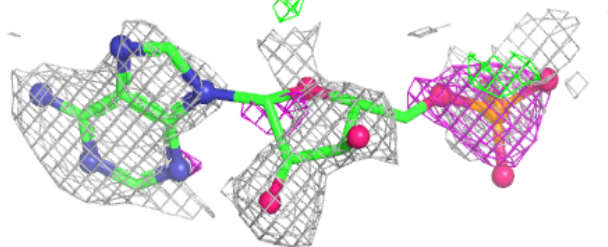
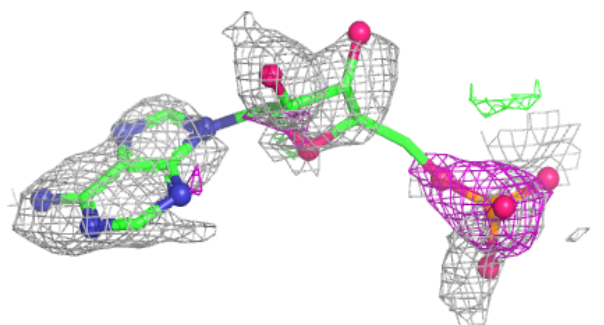


Electron density around AMP L 7497:

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

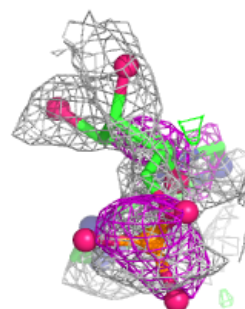
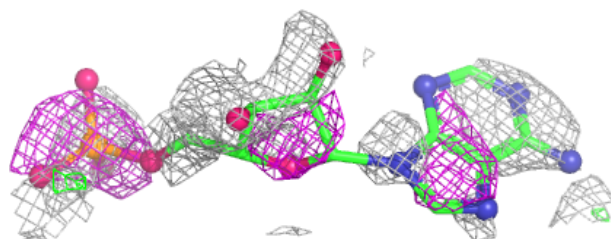
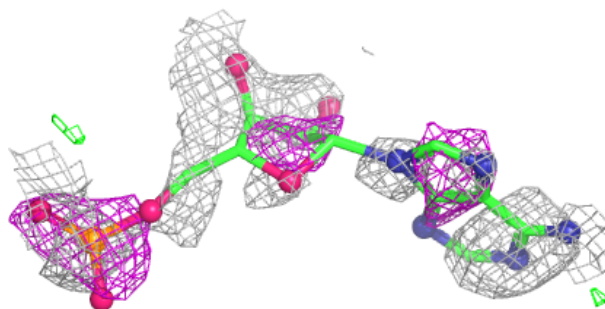
**Electron density around AMP M 7499:**

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

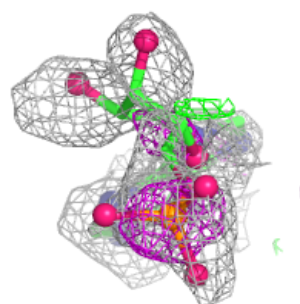
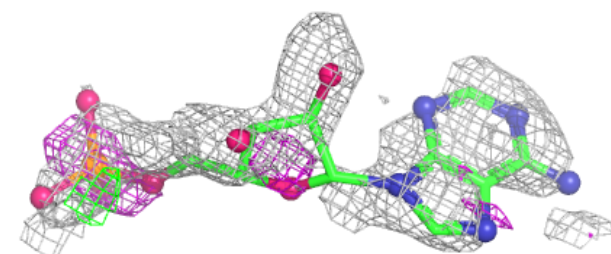
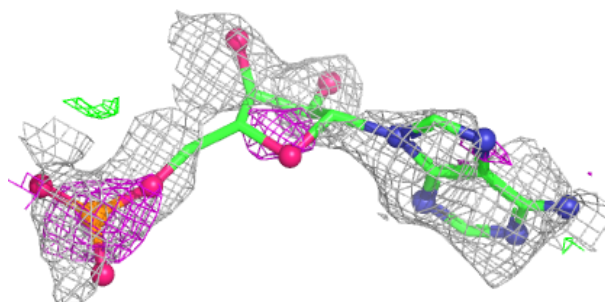


Electron density around AMP C 7479:

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

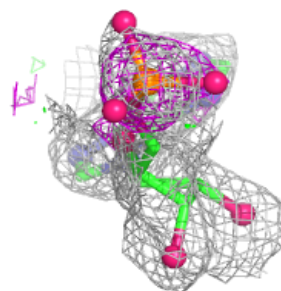
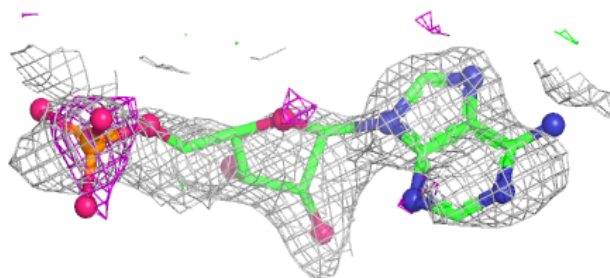
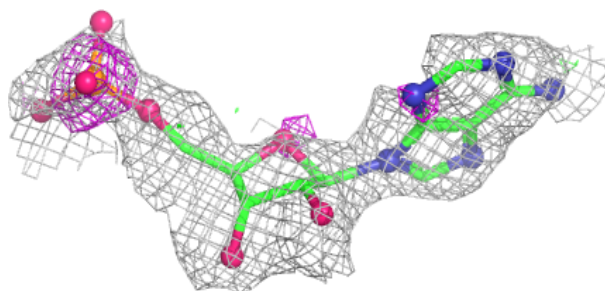
**Electron density around AMP Q 7507:**

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

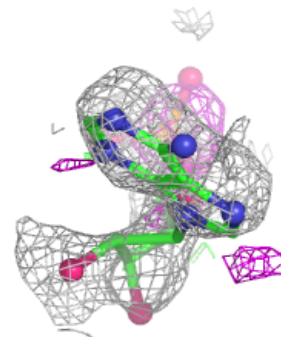
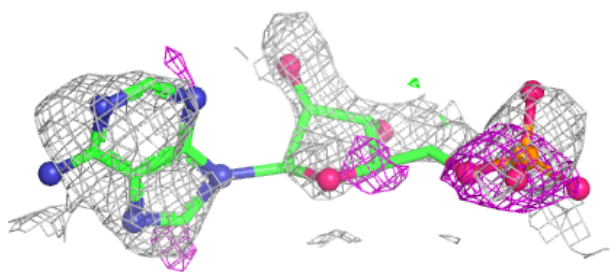
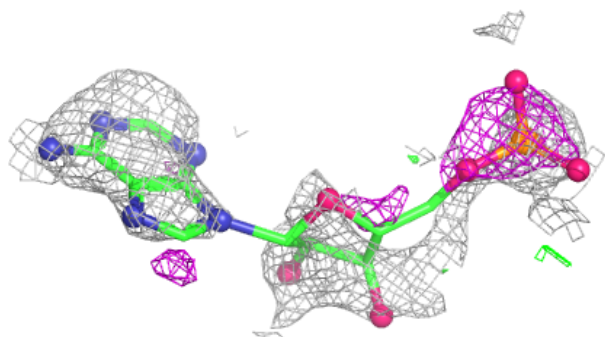


Electron density around AMP S 7511:

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

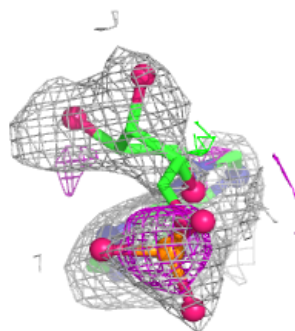
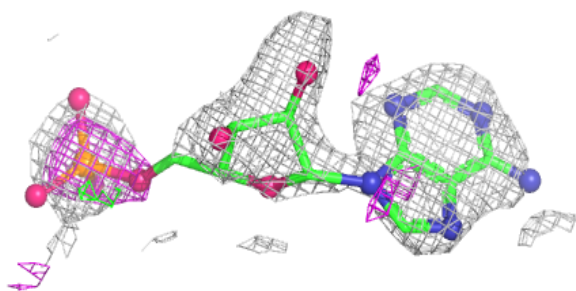
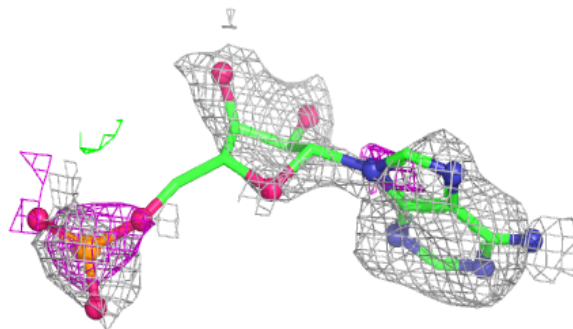
**Electron density around AMP T 7513:**

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



Electron density around AMP X 7521:

$2mF_o-DF_c$ (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.