



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 05:08 AM UTC

PDB ID : 2XAN / pdb_00002xan
Title : inositol 1,3,4,5,6-pentakisphosphate 2-kinase from *A. thaliana* in complex with AMP PNP and IP5
Authors : Gonzalez, B.; Banos-Sanz, J.I.; Villate, M.; Brearley, C.A.; Sanz-Aparicio, J.
Deposited on : 2010-03-31
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

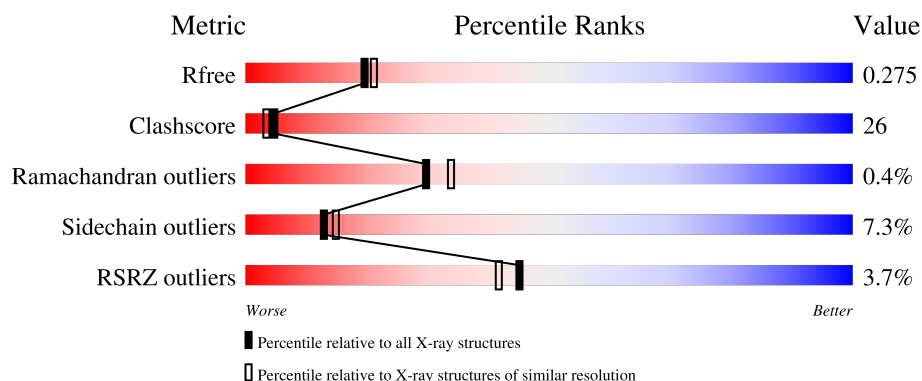
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	451	3% 63% 25% 8%
1	B	451	4% 61% 25% 6% 8%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6979 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.

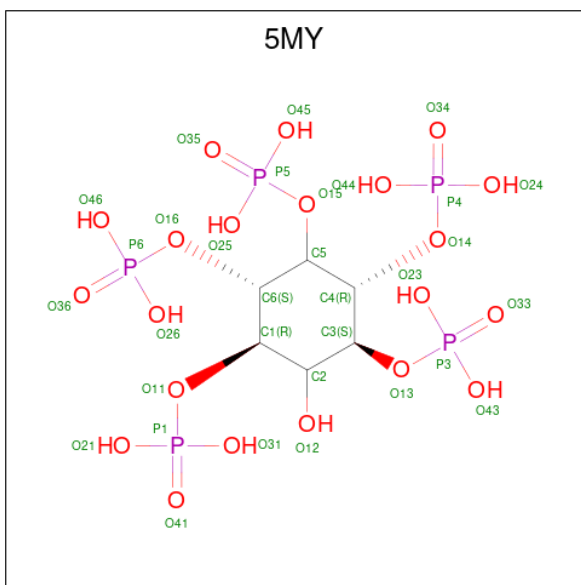
- Molecule 1 is a protein called INOSITOL-PENTAKISPHOSPHATE 2-KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	0	0
			3287	2090	554	630	13			
1	B	417	Total	C	N	O	S	0	0	0
			3303	2101	557	632	13			

There are 16 discrepancies between the modelled and reference sequences:

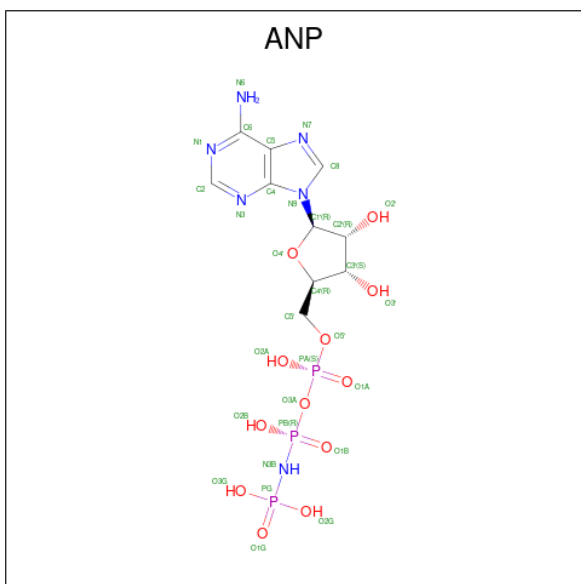
Chain	Residue	Modelled	Actual	Comment	Reference
A	54	SER	ALA	conflict	UNP Q93YN9
A	90	GLN	LYS	conflict	UNP Q93YN9
A	157	THR	SER	SEE REMARK 999	UNP Q93YN9
A	204	ILE	ASN	conflict	UNP Q93YN9
A	224	ARG	SER	conflict	UNP Q93YN9
A	321	CYS	SER	conflict	UNP Q93YN9
A	325	ILE	LEU	conflict	UNP Q93YN9
A	337	ARG	LYS	SEE REMARK 999	UNP Q93YN9
B	54	SER	ALA	conflict	UNP Q93YN9
B	90	GLN	LYS	conflict	UNP Q93YN9
B	157	THR	SER	SEE REMARK 999	UNP Q93YN9
B	204	ILE	ASN	conflict	UNP Q93YN9
B	224	ARG	SER	conflict	UNP Q93YN9
B	321	CYS	SER	conflict	UNP Q93YN9
B	325	ILE	LEU	conflict	UNP Q93YN9
B	337	ARG	LYS	conflict	UNP Q93YN9

- Molecule 2 is MYO-INOSITOL-(1,3,4,5,6)-PENTAKISPHOSPHATE (CCD ID: 5MY) (formula: C₆H₁₇O₂₁P₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 32	C 6	O 21	P 5	0	0
2	B	1	Total 32	C 6	O 21	P 5	0	0

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{12}\text{P}_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 10	N 6	O 12	P 3	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	B	1	Total	Mg	0	0
			1	1		

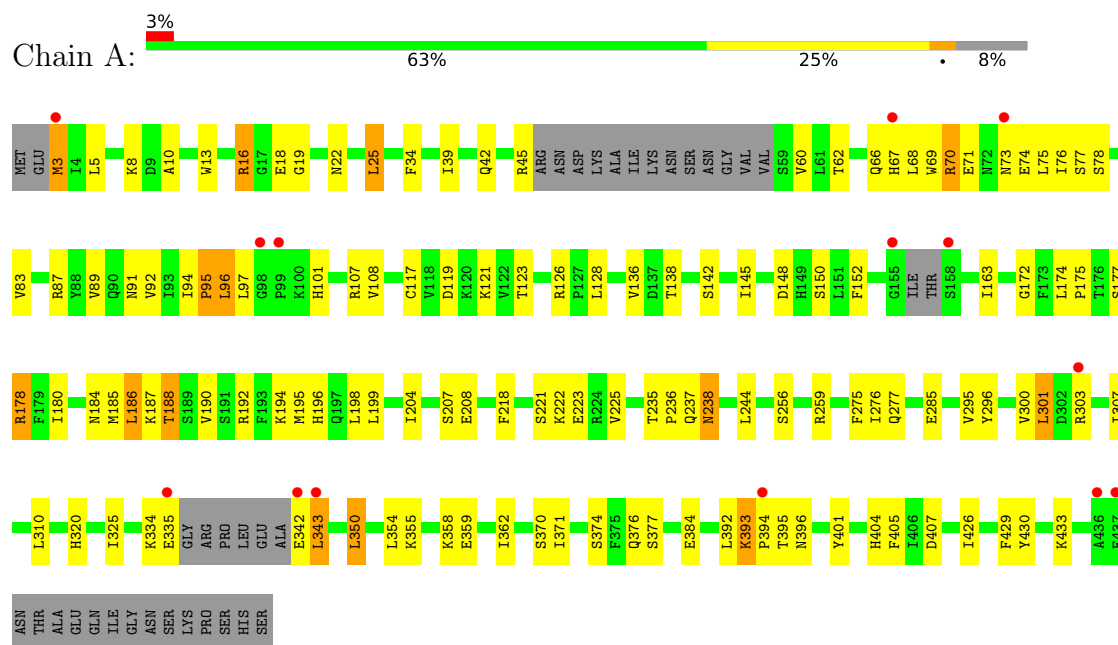
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	122	Total	O	0	0
			122	122		
6	B	137	Total	O	0	0
			137	137		

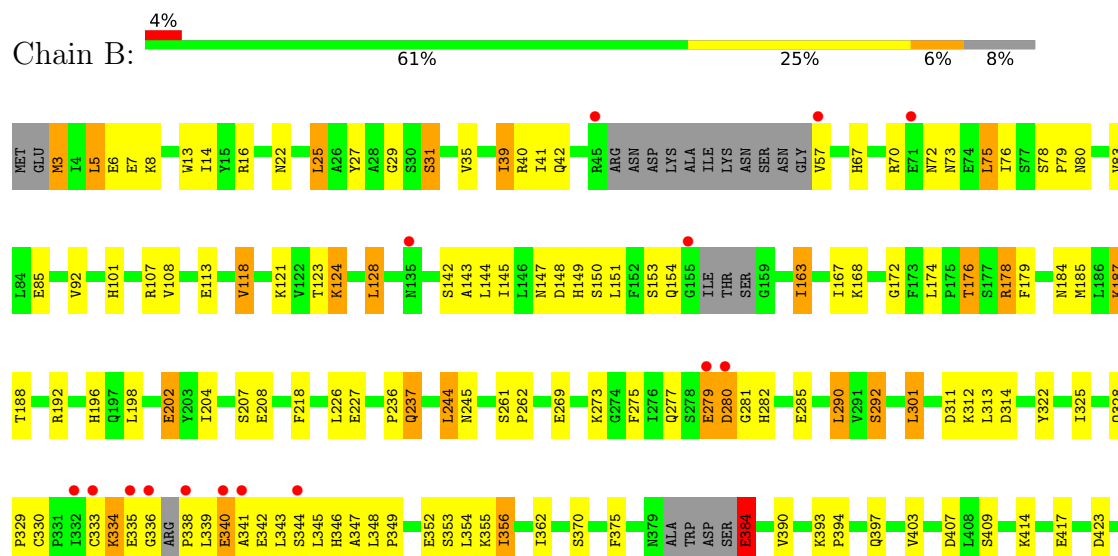
3 Residue-property plots [i](#)

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: INOSITOL-PENTAKISPHOSPHATE 2-KINASE



• Molecule 1: INOSITOL-PENTAKISPHOSPHATE 2-KINASE



F429	
K433	
Q434	
K435	
A436	
E437	
N438	
THR	
ALA	
GLU	
GLN	
ILE	
GLY	
ASN	
SER	
LYS	
PRO	
SER	
HIS	
SER	

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.42Å 113.43Å 140.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	140.03 – 2.20 88.25 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (140.03-2.20) 99.5 (88.25-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.97 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.224 , 0.277 0.223 , 0.275	Depositor DCC
R_{free} test set	2387 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6979	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ANP, 5MY, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/3348	0.78	4/4513 (0.1%)
1	B	0.48	1/3362 (0.0%)	0.77	2/4530 (0.0%)
All	All	0.46	1/6710 (0.0%)	0.77	6/9043 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	346	HIS	CD2-NE2	-7.56	1.29	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	384	GLU	CA-C-N	5.90	126.36	120.52
1	B	384	GLU	C-N-CA	5.90	126.36	120.52
1	A	384	GLU	CA-C-N	5.64	125.97	119.93
1	A	384	GLU	C-N-CA	5.64	125.97	119.93
1	A	235	THR	CA-C-N	5.48	125.00	119.19
1	A	235	THR	C-N-CA	5.48	125.00	119.19

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3287	0	3289	146	0
1	B	3303	0	3315	201	1
2	A	32	0	7	1	0
2	B	32	0	7	1	0
3	A	31	0	13	3	0
3	B	31	0	13	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	122	0	0	11	0
6	B	137	0	0	11	0
All	All	6979	0	6644	343	1

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 26.

All (343) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:LYS:HE2	1:A:393:LYS:CA	1.45	1.39
1:B:185:MET:O	1:B:188:THR:HG22	1.28	1.27
1:A:393:LYS:HA	1:A:393:LYS:CE	1.49	1.24
1:B:384:GLU:N	1:B:384:GLU:OE2	1.70	1.24
6:A:2051:HOH:O	1:B:312:LYS:HE3	1.43	1.18
1:B:3:MET:O	1:B:3:MET:HE2	1.40	1.16
1:B:290:LEU:CD1	1:B:390:VAL:HG21	1.74	1.15
1:B:14:ILE:HD12	6:B:2005:HOH:O	1.43	1.15
1:B:79:PRO:HD2	1:B:83:VAL:HG11	1.32	1.11
1:B:163:ILE:HD13	1:B:275:PHE:CG	1.86	1.10
1:B:3:MET:HE2	1:B:3:MET:C	1.77	1.09
1:B:348:LEU:HD12	1:B:349:PRO:CD	1.84	1.06
1:A:178:ARG:HH11	1:A:178:ARG:CG	1.68	1.06
1:B:178:ARG:HG3	1:B:178:ARG:HH11	1.19	1.05
1:A:178:ARG:HH11	1:A:178:ARG:HG3	1.19	1.04
1:B:348:LEU:CD2	1:B:352:GLU:HG2	1.89	1.03
1:B:204:ILE:O	1:B:204:ILE:HG22	1.54	1.03
1:B:290:LEU:HD13	1:B:390:VAL:CG2	1.89	1.01
1:B:178:ARG:HH11	1:B:178:ARG:CG	1.75	1.00
1:B:348:LEU:HD12	1:B:349:PRO:HD3	1.41	0.99
1:B:39:ILE:HD11	1:B:143:ALA:HB1	1.45	0.98
1:B:290:LEU:HD13	1:B:390:VAL:HG21	1.43	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:ILE:O	1:B:204:ILE:CG2	2.13	0.95
1:B:384:GLU:OE2	1:B:384:GLU:CA	2.17	0.93
1:B:340:GLU:HA	1:B:340:GLU:OE1	1.67	0.93
1:A:404:HIS:HD2	6:A:2102:HOH:O	1.51	0.92
1:B:124:LYS:O	1:B:124:LYS:HD3	1.68	0.92
1:A:94:ILE:HB	1:A:95:PRO:HD3	1.51	0.91
1:B:279:GLU:O	1:B:281:GLY:N	2.04	0.91
1:A:199:LEU:HD22	1:A:426:ILE:HD13	1.50	0.91
1:B:39:ILE:HD12	1:B:41:ILE:HG13	1.54	0.90
1:A:18:GLU:OE1	1:A:126:ARG:HG2	1.72	0.90
1:B:280:ASP:HB3	1:B:282:HIS:HD2	1.37	0.89
1:B:290:LEU:CD1	1:B:390:VAL:CG2	2.46	0.89
1:A:301:LEU:HD11	1:A:371:ILE:CD1	2.04	0.88
1:B:178:ARG:HG3	1:B:178:ARG:NH1	1.84	0.88
1:B:325:ILE:HD12	1:B:354:LEU:HD23	1.57	0.87
1:A:204:ILE:HD12	1:B:345:LEU:HD21	1.54	0.87
1:B:39:ILE:HD13	1:B:40:ARG:N	1.90	0.87
1:B:290:LEU:HD12	1:B:390:VAL:HG21	1.57	0.85
1:B:163:ILE:CD1	1:B:275:PHE:CG	2.58	0.85
1:B:79:PRO:CD	1:B:83:VAL:HG11	2.06	0.85
1:B:348:LEU:HD12	1:B:349:PRO:HD2	1.58	0.85
1:B:148:ASP:HB3	1:B:151:LEU:HD21	1.59	0.84
1:B:149:HIS:HE1	6:B:2025:HOH:O	1.58	0.84
1:B:13:TRP:O	1:B:121:LYS:HE2	1.77	0.83
1:B:185:MET:O	1:B:188:THR:CG2	2.22	0.83
1:B:184:ASN:O	1:B:187:LYS:HG2	1.78	0.83
1:A:301:LEU:HD11	1:A:371:ILE:HD11	1.60	0.82
1:A:429:PHE:CZ	1:A:433:LYS:HE2	2.13	0.82
1:A:74:GLU:N	1:A:74:GLU:OE1	2.13	0.82
1:A:128:LEU:HD12	1:B:338:PRO:O	1.80	0.82
1:B:348:LEU:HD23	1:B:352:GLU:HG2	1.63	0.80
1:A:204:ILE:HD12	1:B:345:LEU:CD2	2.12	0.80
1:B:348:LEU:CD1	1:B:349:PRO:HD2	2.13	0.79
1:A:301:LEU:CD1	1:A:371:ILE:HD11	2.12	0.79
1:B:148:ASP:HB3	1:B:151:LEU:CD2	2.13	0.78
1:A:275:PHE:HD1	1:A:276:ILE:HD12	1.49	0.78
1:B:39:ILE:HD11	1:B:143:ALA:CB	2.14	0.77
1:B:280:ASP:HB3	1:B:282:HIS:CD2	2.21	0.76
1:B:290:LEU:HD13	1:B:390:VAL:HG23	1.67	0.76
1:A:350:LEU:CD1	1:A:354:LEU:HD11	2.15	0.76
1:A:89:VAL:O	1:A:94:ILE:HG12	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:SER:HB3	1:B:83:VAL:HG13	1.67	0.75
1:A:301:LEU:CD1	1:A:371:ILE:CD1	2.66	0.74
1:A:178:ARG:HG3	1:A:178:ARG:NH1	1.95	0.74
1:B:437:GLU:OE1	1:B:438:ASN:N	2.21	0.74
1:B:163:ILE:HD13	1:B:275:PHE:CD2	2.23	0.73
1:A:25:LEU:N	1:A:25:LEU:HD22	2.04	0.73
1:A:204:ILE:CD1	1:B:345:LEU:CD2	2.65	0.73
1:B:348:LEU:CG	1:B:352:GLU:HG2	2.17	0.73
1:B:3:MET:C	1:B:3:MET:CE	2.60	0.73
1:B:163:ILE:CD1	1:B:275:PHE:CD1	2.71	0.72
1:A:94:ILE:HB	1:A:95:PRO:CD	2.19	0.72
1:A:192:ARG:NH2	6:A:2044:HOH:O	2.22	0.71
1:B:163:ILE:HD13	1:B:275:PHE:CD1	2.24	0.71
1:A:142:SER:HB3	6:A:2013:HOH:O	1.89	0.71
1:A:108:VAL:HG11	1:A:145:ILE:HD11	1.72	0.70
1:A:94:ILE:O	1:A:96:LEU:N	2.25	0.70
1:B:147:ASN:ND2	1:B:154:GLN:OE1	2.24	0.70
1:A:94:ILE:C	1:A:96:LEU:H	2.00	0.69
6:A:2051:HOH:O	1:B:312:LYS:CE	2.16	0.69
1:A:128:LEU:CD1	1:B:338:PRO:O	2.41	0.69
1:B:40:ARG:NH2	1:B:85:GLU:OE2	2.26	0.69
1:A:393:LYS:HB2	1:A:394:PRO:CD	2.22	0.68
1:B:348:LEU:HG	1:B:352:GLU:HG2	1.73	0.68
1:B:429:PHE:CZ	1:B:433:LYS:HD2	2.27	0.68
1:A:204:ILE:HD13	1:B:345:LEU:HD23	1.75	0.68
1:B:437:GLU:OE1	1:B:437:GLU:N	2.26	0.68
1:B:348:LEU:CD1	1:B:349:PRO:CD	2.67	0.68
1:B:437:GLU:OE1	1:B:437:GLU:C	2.37	0.68
1:B:325:ILE:HD12	1:B:354:LEU:CD2	2.24	0.68
1:A:108:VAL:HB	1:A:145:ILE:HD12	1.76	0.67
1:A:350:LEU:HD13	1:A:354:LEU:CD1	2.24	0.67
1:B:202:GLU:OE2	6:B:2050:HOH:O	2.13	0.67
1:B:79:PRO:HD2	1:B:83:VAL:CG1	2.19	0.66
1:A:238:ASN:HD22	1:A:238:ASN:H	1.43	0.65
1:B:108:VAL:HG11	1:B:145:ILE:CD1	2.26	0.65
1:A:350:LEU:HD13	1:A:354:LEU:HD11	1.78	0.65
1:B:226:LEU:HA	1:B:292:SER:OG	1.96	0.65
1:B:273:LYS:HE2	6:B:2087:HOH:O	1.96	0.64
1:A:204:ILE:CD1	1:B:345:LEU:HD23	2.27	0.64
1:B:178:ARG:HH11	1:B:178:ARG:CB	2.09	0.64
1:A:13:TRP:O	1:A:121:LYS:HE2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ARG:HG3	6:A:2072:HOH:O	1.97	0.64
1:A:393:LYS:CB	1:A:394:PRO:CD	2.76	0.64
1:B:437:GLU:OE1	1:B:437:GLU:CA	2.46	0.63
1:A:76:ILE:C	1:A:76:ILE:HD12	2.23	0.63
1:A:16:ARG:NH2	1:A:148:ASP:OD1	2.30	0.63
1:B:107:ARG:NH1	1:B:142:SER:OG	2.32	0.63
1:B:279:GLU:C	1:B:281:GLY:H	2.05	0.63
1:A:3:MET:HA	1:A:3:MET:CE	2.30	0.62
1:B:196:HIS:HD2	6:B:2132:HOH:O	1.81	0.62
1:B:179:PHE:CE2	1:B:341:ALA:HB3	2.33	0.62
1:B:92:VAL:HG11	1:B:362:ILE:HD11	1.81	0.62
1:B:434:GLN:O	1:B:438:ASN:HB3	1.99	0.62
1:A:276:ILE:HD12	1:A:276:ILE:N	2.15	0.62
1:B:244:LEU:HD23	1:B:244:LEU:C	2.24	0.62
1:A:70:ARG:HG2	1:A:71:GLU:N	2.12	0.62
1:A:199:LEU:CD2	1:A:426:ILE:HD13	2.27	0.61
1:A:67:HIS:HD2	1:A:354:LEU:HD21	1.64	0.61
1:B:179:PHE:HE2	1:B:341:ALA:HB3	1.65	0.61
1:B:280:ASP:O	1:B:282:HIS:CD2	2.53	0.61
1:B:179:PHE:CE2	1:B:341:ALA:CB	2.83	0.61
1:B:16:ARG:NH2	1:B:148:ASP:OD1	2.34	0.61
1:B:280:ASP:CB	1:B:282:HIS:HD2	2.13	0.61
1:B:108:VAL:CG1	1:B:145:ILE:HD13	2.31	0.61
1:A:185:MET:O	1:A:188:THR:HB	2.01	0.60
1:A:275:PHE:HD1	1:A:276:ILE:CD1	2.14	0.60
1:A:25:LEU:HD23	1:A:39:ILE:HG23	1.83	0.60
1:B:168:LYS:HA	1:B:370:SER:HB3	1.82	0.60
1:B:290:LEU:HD11	1:B:375:PHE:CE2	2.36	0.60
1:A:259:ARG:CG	6:A:2072:HOH:O	2.50	0.60
1:A:393:LYS:HB2	1:A:394:PRO:HD3	1.83	0.59
1:A:190:VAL:HB	1:A:195:MET:HE3	1.83	0.59
1:A:208:GLU:OE1	1:A:259:ARG:NE	2.36	0.59
1:B:176:THR:O	1:B:176:THR:CG2	2.50	0.59
1:A:407:ASP:OD2	3:A:600:ANP:O3G	2.20	0.59
1:B:39:ILE:HD13	1:B:40:ARG:H	1.67	0.59
1:A:101:HIS:HD2	1:A:303:ARG:NH2	2.01	0.58
1:A:74:GLU:O	1:A:87:ARG:HD3	2.03	0.58
1:B:192:ARG:NH2	6:B:2048:HOH:O	2.36	0.58
1:B:202:GLU:HA	1:B:202:GLU:OE1	2.04	0.58
1:A:18:GLU:OE1	1:A:126:ARG:CG	2.47	0.58
1:A:83:VAL:CG2	1:A:107:ARG:NE	2.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:VAL:HG11	1:A:145:ILE:CD1	2.34	0.58
1:B:39:ILE:HD12	1:B:41:ILE:CG1	2.32	0.58
1:A:73:ASN:O	1:A:76:ILE:HG13	2.04	0.57
1:A:178:ARG:HH11	1:A:178:ARG:HG2	1.64	0.57
1:B:179:PHE:HE2	1:B:341:ALA:CB	2.18	0.57
1:B:384:GLU:OE2	1:B:384:GLU:HA	2.03	0.57
1:B:237:GLN:HE21	1:B:237:GLN:HA	1.69	0.56
1:B:149:HIS:CE1	6:B:2025:HOH:O	2.42	0.56
1:B:328:GLN:O	1:B:329:PRO:C	2.49	0.56
1:B:40:ARG:NH2	1:B:85:GLU:CD	2.64	0.56
1:B:348:LEU:CG	1:B:349:PRO:HD2	2.35	0.56
1:A:163:ILE:HG13	1:A:275:PHE:CD1	2.40	0.56
1:B:163:ILE:HD12	1:B:275:PHE:CD1	2.40	0.56
1:B:244:LEU:C	1:B:244:LEU:CD2	2.79	0.56
1:A:83:VAL:HG22	1:A:107:ARG:NE	2.20	0.56
1:A:395:THR:O	1:A:396:ASN:HB2	2.06	0.55
1:B:340:GLU:OE1	1:B:340:GLU:CA	2.47	0.55
1:A:60:VAL:HG21	1:A:78:SER:O	2.07	0.54
1:A:194:LYS:HE3	6:A:2115:HOH:O	2.06	0.54
1:A:238:ASN:HD22	1:A:238:ASN:N	2.04	0.54
1:B:178:ARG:HH11	1:B:178:ARG:HB2	1.72	0.54
1:B:330:CYS:O	1:B:334:LYS:HG2	2.08	0.54
1:A:74:GLU:N	1:A:74:GLU:CD	2.65	0.54
1:A:393:LYS:CA	1:A:393:LYS:CE	2.33	0.54
1:B:108:VAL:CG1	1:B:145:ILE:CD1	2.86	0.54
1:A:76:ILE:HD12	1:A:77:SER:N	2.23	0.53
1:B:335:GLU:HG3	1:B:335:GLU:O	2.08	0.53
1:B:3:MET:HE1	1:B:5:LEU:HD13	1.90	0.53
1:A:94:ILE:CB	1:A:95:PRO:CD	2.87	0.53
1:B:290:LEU:HD11	1:B:375:PHE:CD2	2.43	0.53
1:A:22:ASN:HD21	1:A:42:GLN:HG2	1.72	0.53
1:A:178:ARG:CG	1:A:178:ARG:NH1	2.41	0.53
1:B:16:ARG:NH2	1:B:150:SER:OG	2.42	0.53
1:A:94:ILE:C	1:A:96:LEU:N	2.59	0.53
1:B:167:ILE:O	1:B:370:SER:HB2	2.08	0.52
1:B:144:LEU:HD12	6:B:2020:HOH:O	2.08	0.52
1:B:7:GLU:HG3	1:B:113:GLU:HB3	1.91	0.52
1:B:244:LEU:CD2	1:B:245:ASN:ND2	2.73	0.52
1:B:348:LEU:HG	1:B:349:PRO:HD2	1.92	0.52
1:A:172:GLY:HA3	1:A:218:PHE:CD2	2.44	0.52
1:B:172:GLY:HA3	1:B:218:PHE:CD2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:ASN:C	1:A:75:LEU:H	2.16	0.52
1:B:27:TYR:CZ	1:B:29:GLY:HA3	2.45	0.51
1:A:73:ASN:C	1:A:75:LEU:N	2.64	0.51
1:B:25:LEU:HB2	1:B:39:ILE:HG22	1.92	0.51
1:B:348:LEU:HD21	1:B:352:GLU:HG2	1.87	0.51
1:A:236:PRO:O	1:A:237:GLN:C	2.53	0.51
1:B:92:VAL:HG11	1:B:362:ILE:CD1	2.40	0.51
1:B:167:ILE:O	1:B:370:SER:CB	2.59	0.51
1:B:325:ILE:HD11	1:B:354:LEU:HA	1.92	0.51
1:B:16:ARG:NH2	1:B:150:SER:HB3	2.25	0.51
2:B:500:5MY:O43	3:B:600:ANP:O1G	2.29	0.51
1:A:62:THR:O	1:A:66:GLN:HG3	2.11	0.51
1:B:176:THR:O	1:B:176:THR:HG23	2.11	0.51
1:B:57:VAL:HG12	1:B:57:VAL:O	2.11	0.50
1:B:73:ASN:HA	1:B:76:ILE:HG12	1.92	0.50
1:B:101:HIS:CE1	1:B:403:VAL:HG22	2.46	0.50
1:A:295:VAL:HG13	1:A:301:LEU:HD22	1.93	0.50
1:B:3:MET:HE1	1:B:5:LEU:CD1	2.42	0.50
1:B:39:ILE:HD13	1:B:39:ILE:C	2.34	0.50
1:A:198:LEU:HD12	1:A:430:TYR:CD1	2.46	0.50
1:A:325:ILE:HD11	1:A:354:LEU:HA	1.93	0.50
1:B:333:CYS:O	1:B:335:GLU:N	2.45	0.50
1:B:108:VAL:HG11	1:B:145:ILE:HD11	1.94	0.50
1:A:275:PHE:CD1	1:A:276:ILE:HD12	2.38	0.49
1:B:67:HIS:CE1	1:B:70:ARG:HH21	2.30	0.49
1:A:97:LEU:HG	1:A:307:ILE:HD11	1.95	0.49
1:B:269:GLU:OE2	1:B:281:GLY:HA2	2.12	0.49
1:B:25:LEU:HD21	1:B:118:VAL:HG13	1.94	0.49
1:B:80:ASN:O	1:B:83:VAL:HG12	2.12	0.49
1:B:407:ASP:OD2	3:B:600:ANP:O3G	2.31	0.49
1:B:429:PHE:CE2	1:B:433:LYS:HD2	2.48	0.49
1:B:236:PRO:O	1:B:237:GLN:C	2.56	0.49
1:B:343:LEU:O	1:B:347:ALA:N	2.38	0.48
1:A:19:GLY:HA3	3:A:600:ANP:N3B	2.28	0.48
1:A:25:LEU:N	1:A:25:LEU:CD2	2.75	0.48
1:B:163:ILE:CD1	1:B:275:PHE:CB	2.91	0.48
1:B:179:PHE:CZ	1:B:341:ALA:HB1	2.48	0.48
1:B:198:LEU:HD13	1:B:433:LYS:HD3	1.96	0.48
1:A:300:VAL:HG22	1:A:405:PHE:CZ	2.49	0.48
1:B:336:GLY:O	1:B:338:PRO:N	2.46	0.47
1:A:152:PHE:CD1	1:A:376:GLN:HG2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:PHE:CE1	1:B:301:LEU:HG	2.48	0.47
1:B:393:LYS:HB3	1:B:394:PRO:HD3	1.97	0.47
1:A:3:MET:HA	1:A:3:MET:HE3	1.96	0.47
3:A:600:ANP:O5'	3:A:600:ANP:H8	2.14	0.47
1:B:39:ILE:C	1:B:39:ILE:CD1	2.87	0.47
1:B:16:ARG:NH2	1:B:150:SER:CB	2.77	0.47
1:B:179:PHE:CE2	1:B:341:ALA:HB1	2.49	0.47
1:B:437:GLU:N	1:B:437:GLU:CD	2.73	0.47
1:B:184:ASN:O	1:B:187:LYS:CG	2.59	0.47
1:B:435:LYS:HD2	1:B:435:LYS:N	2.30	0.47
1:B:435:LYS:NZ	1:B:438:ASN:ND2	2.63	0.47
1:A:190:VAL:HB	1:A:195:MET:CE	2.45	0.47
1:A:3:MET:HA	1:A:3:MET:HE2	1.97	0.47
1:A:45:ARG:NH2	2:A:500:5MY:O33	2.48	0.46
1:B:31:SER:O	1:B:35:VAL:HG23	2.15	0.46
1:A:10:ALA:CB	1:A:117:CYS:SG	3.04	0.46
1:A:16:ARG:HH22	1:A:148:ASP:CG	2.24	0.46
1:A:334:LYS:O	1:A:335:GLU:C	2.58	0.46
1:B:101:HIS:ND1	1:B:403:VAL:CG2	2.79	0.46
1:A:285:GLU:CD	6:A:2080:HOH:O	2.57	0.46
1:B:261:SER:HB2	1:B:262:PRO:HD2	1.98	0.46
1:A:177:SER:HB3	1:A:180:ILE:HG13	1.98	0.46
1:A:429:PHE:CZ	1:A:433:LYS:CE	2.93	0.46
1:B:14:ILE:CD1	6:B:2005:HOH:O	2.27	0.46
1:B:403:VAL:HG23	1:B:403:VAL:O	2.14	0.46
1:B:163:ILE:HD11	1:B:275:PHE:HB2	1.98	0.46
1:A:16:ARG:NH2	1:A:150:SER:OG	2.49	0.46
1:A:67:HIS:NE2	1:A:350:LEU:HD11	2.31	0.45
1:B:148:ASP:HB3	1:B:151:LEU:HD23	1.97	0.45
1:B:227:GLU:HG3	6:B:2063:HOH:O	2.15	0.45
1:A:358:LYS:O	1:A:362:ILE:HG13	2.16	0.45
1:A:101:HIS:HD2	1:A:303:ARG:CZ	2.30	0.45
1:B:25:LEU:HB2	1:B:39:ILE:CG2	2.47	0.45
1:A:16:ARG:NH2	1:A:148:ASP:CG	2.74	0.45
1:B:16:ARG:HH21	1:B:150:SER:HB3	1.82	0.45
1:B:290:LEU:HD12	1:B:290:LEU:C	2.42	0.45
1:B:290:LEU:HD12	1:B:290:LEU:O	2.17	0.45
1:A:83:VAL:HG22	1:A:107:ARG:HE	1.82	0.45
1:A:184:ASN:O	1:A:187:LYS:HG3	2.16	0.45
1:A:163:ILE:HG13	1:A:275:PHE:CE1	2.52	0.45
1:A:355:LYS:O	1:A:359:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LEU:HG	1:A:307:ILE:CD1	2.48	0.44
1:A:221:SER:O	1:A:225:VAL:HG23	2.17	0.44
1:B:290:LEU:CD1	1:B:375:PHE:CE2	3.01	0.44
1:A:73:ASN:O	1:A:75:LEU:N	2.51	0.44
1:A:320:HIS:CE1	1:A:342:GLU:OE1	2.70	0.44
1:B:22:ASN:HD21	1:B:42:GLN:HG2	1.82	0.44
1:B:39:ILE:CD1	1:B:40:ARG:N	2.72	0.44
1:B:340:GLU:OE1	1:B:343:LEU:HD12	2.18	0.44
1:A:10:ALA:HB3	1:A:117:CYS:SG	2.58	0.43
1:A:91:ASN:O	1:A:95:PRO:HG2	2.18	0.43
1:A:199:LEU:CD2	1:A:426:ILE:CD1	2.96	0.43
1:B:352:GLU:O	1:B:355:LYS:HB2	2.18	0.43
3:B:600:ANP:H8	3:B:600:ANP:O5'	2.18	0.43
1:B:313:LEU:O	1:B:314:ASP:HB3	2.18	0.43
1:A:119:ASP:CG	1:A:136:VAL:HG22	2.44	0.43
1:A:175:PRO:HB2	1:A:180:ILE:HD11	2.00	0.43
1:B:187:LYS:NZ	1:B:423:ASP:OD2	2.48	0.43
1:A:136:VAL:HG23	1:A:138:THR:HG22	2.01	0.43
1:A:186:LEU:HD12	1:A:186:LEU:HA	1.78	0.43
1:B:72:ASN:O	1:B:75:LEU:HB2	2.19	0.42
1:B:163:ILE:CD1	1:B:275:PHE:HB2	2.49	0.42
1:B:333:CYS:C	1:B:335:GLU:H	2.27	0.42
1:B:108:VAL:HG11	1:B:145:ILE:HD13	1.94	0.42
1:A:393:LYS:HB2	1:A:394:PRO:HD2	2.01	0.42
1:B:348:LEU:HG	1:B:352:GLU:CG	2.45	0.42
1:B:124:LYS:HD3	1:B:124:LYS:C	2.40	0.42
1:B:339:LEU:O	1:B:342:GLU:HB2	2.20	0.42
1:B:344:SER:O	1:B:345:LEU:C	2.62	0.42
1:A:73:ASN:HA	1:A:76:ILE:HG13	2.00	0.42
1:A:222:LYS:HD2	1:A:296:TYR:CE2	2.55	0.42
1:A:68:LEU:HD23	1:A:69:TRP:NE1	2.35	0.42
1:A:94:ILE:O	1:A:95:PRO:C	2.62	0.42
1:B:79:PRO:CG	1:B:83:VAL:HG11	2.47	0.42
1:B:333:CYS:C	1:B:335:GLU:N	2.77	0.42
1:A:18:GLU:OE2	1:A:126:ARG:NH1	2.52	0.42
1:B:6:GLU:O	1:B:7:GLU:C	2.61	0.42
1:B:67:HIS:CE1	1:B:70:ARG:NH2	2.88	0.42
1:B:414:LYS:O	1:B:414:LYS:HG2	2.19	0.42
1:A:75:LEU:HD12	1:A:75:LEU:HA	1.90	0.41
1:B:168:LYS:CA	1:B:370:SER:HB3	2.50	0.41
1:B:198:LEU:HD23	1:B:198:LEU:HA	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ASN:H	1:A:238:ASN:ND2	2.12	0.41
1:A:276:ILE:N	1:A:276:ILE:CD1	2.82	0.41
1:A:277:GLN:O	1:A:395:THR:HG22	2.20	0.41
1:B:261:SER:HB2	1:B:262:PRO:CD	2.49	0.41
1:B:282:HIS:O	1:B:285:GLU:HG2	2.20	0.41
1:A:34:PHE:HE1	1:A:145:ILE:HD13	1.85	0.41
1:A:92:VAL:HA	6:A:2015:HOH:O	2.20	0.41
1:B:322:TYR:CE2	1:B:417:GLU:HG3	2.55	0.41
1:A:108:VAL:CB	1:A:145:ILE:HD12	2.48	0.41
1:A:350:LEU:HD11	1:A:354:LEU:HD11	1.98	0.41
1:B:325:ILE:HD11	1:B:353:SER:C	2.46	0.41
1:B:356:ILE:H	1:B:356:ILE:HG12	1.62	0.41
1:A:370:SER:OG	6:A:2101:HOH:O	2.14	0.41
1:A:22:ASN:ND2	1:A:42:GLN:HG2	2.36	0.41
1:A:392:LEU:HD23	1:A:392:LEU:HA	1.94	0.41
1:A:393:LYS:CB	1:A:394:PRO:HD3	2.45	0.41
1:A:94:ILE:CB	1:A:95:PRO:HD3	2.34	0.41
1:A:196:HIS:CD2	1:A:426:ILE:HD11	2.56	0.41
1:A:374:SER:O	1:A:401:TYR:HA	2.21	0.41
1:A:108:VAL:CG1	1:A:145:ILE:CD1	2.98	0.40
1:A:342:GLU:O	1:A:343:LEU:C	2.64	0.40
1:B:311:ASP:OD1	1:B:311:ASP:C	2.64	0.40
1:B:403:VAL:CG2	1:B:403:VAL:O	2.69	0.40
1:A:152:PHE:CG	1:A:376:GLN:HG2	2.56	0.40
1:B:101:HIS:ND1	1:B:403:VAL:HG22	2.36	0.40
1:B:329:PRO:HB2	6:B:2105:HOH:O	2.21	0.40
1:A:392:LEU:O	1:A:393:LYS:C	2.64	0.40
1:B:92:VAL:CG1	1:B:362:ILE:CD1	3.00	0.40
1:A:393:LYS:HE2	1:A:393:LYS:N	2.23	0.40
1:A:429:PHE:HZ	1:A:433:LYS:HE2	1.80	0.40
1:B:128:LEU:HD12	1:B:128:LEU:HA	1.74	0.40
1:B:277:GLN:H	1:B:397:GLN:HE22	1.70	0.40
1:B:348:LEU:HD12	1:B:348:LEU:HA	1.93	0.40
1:B:352:GLU:O	1:B:356:ILE:HG12	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:ILE:CD1	1:B:394:PRO:O[4_556]	2.04	0.16

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	406/451 (90%)	384 (95%)	21 (5%)	1 (0%)	43	51
1	B	407/451 (90%)	390 (96%)	15 (4%)	2 (0%)	24	27
All	All	813/902 (90%)	774 (95%)	36 (4%)	3 (0%)	30	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	280	ASP
1	B	334	LYS
1	A	95	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	368/399 (92%)	345 (94%)	23 (6%)	16	19
1	B	370/399 (93%)	339 (92%)	31 (8%)	10	11
All	All	738/798 (92%)	684 (93%)	54 (7%)	13	15

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	MET
1	A	5	LEU
1	A	8	LYS

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Mol	Chain	Res	Type
1	A	16	ARG
1	A	25	LEU
1	A	70	ARG
1	A	96	LEU
1	A	123	THR
1	A	174	LEU
1	A	178	ARG
1	A	186	LEU
1	A	188	THR
1	A	207	SER
1	A	223	GLU
1	A	238	ASN
1	A	244	LEU
1	A	256	SER
1	A	301	LEU
1	A	310	LEU
1	A	343	LEU
1	A	350	LEU
1	A	377	SER
1	A	393	LYS
1	B	3	MET
1	B	5	LEU
1	B	8	LYS
1	B	25	LEU
1	B	31	SER
1	B	39	ILE
1	B	75	LEU
1	B	118	VAL
1	B	123	THR
1	B	124	LYS
1	B	128	LEU
1	B	153	SER
1	B	163	ILE
1	B	174	LEU
1	B	176	THR
1	B	178	ARG
1	B	187	LYS
1	B	202	GLU
1	B	207	SER
1	B	208	GLU
1	B	237	GLN
1	B	244	LEU

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Mol	Chain	Res	Type
1	B	279	GLU
1	B	290	LEU
1	B	292	SER
1	B	301	LEU
1	B	340	GLU
1	B	356	ILE
1	B	384	GLU
1	B	409	SER
1	B	437	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	66	GLN
1	A	101	HIS
1	A	147	ASN
1	A	149	HIS
1	A	238	ASN
1	A	328	GLN
1	A	376	GLN
1	A	404	HIS
1	B	22	ASN
1	B	67	HIS
1	B	147	ASN
1	B	149	HIS
1	B	154	GLN
1	B	196	HIS
1	B	237	GLN
1	B	282	HIS
1	B	376	GLN
1	B	404	HIS
1	B	438	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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$
2	5MY	A	500	-	32,32,32	0.80	0	53,53,53	0.91	1 (1%)
2	5MY	B	500	-	32,32,32	0.71	0	53,53,53	0.97	2 (3%)
3	ANP	A	600	5	33,33,33	2.06	10 (30%)	45,52,52	1.93	12 (26%)
3	ANP	B	600	5	33,33,33	2.17	12 (36%)	45,52,52	1.96	14 (31%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	5MY	A	500	-	-	1/25/49/49	0/1/1/1
2	5MY	B	500	-	-	1/25/49/49	0/1/1/1
3	ANP	A	600	5	-	2/18/38/38	0/3/3/3
3	ANP	B	600	5	-	2/18/38/38	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	600	ANP	PB-N3B	5.00	1.76	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	600	ANP	PG-N3B	4.70	1.75	1.63
3	A	600	ANP	PB-N3B	4.66	1.75	1.63
3	B	600	ANP	PG-O1G	4.52	1.53	1.46
3	B	600	ANP	C5-C4	4.50	1.47	1.39
3	A	600	ANP	PG-N3B	4.40	1.74	1.63
3	A	600	ANP	C5-C4	4.36	1.46	1.39
3	A	600	ANP	PG-O1G	4.28	1.52	1.46
3	A	600	ANP	PB-O1B	3.48	1.51	1.46
3	B	600	ANP	PB-O1B	3.31	1.51	1.46
3	B	600	ANP	C8-N7	2.71	1.36	1.31
3	A	600	ANP	C5-C6	2.69	1.48	1.41
3	B	600	ANP	PB-O3A	2.69	1.62	1.59
3	B	600	ANP	C5-C6	2.68	1.48	1.41
3	A	600	ANP	C8-N7	2.58	1.36	1.31
3	B	600	ANP	PA-O3A	2.42	1.62	1.59
3	B	600	ANP	PB-O2B	-2.33	1.50	1.56
3	A	600	ANP	PB-O2B	-2.28	1.50	1.56
3	B	600	ANP	PG-O2G	-2.28	1.50	1.56
3	A	600	ANP	PA-O3A	2.17	1.61	1.59
3	A	600	ANP	C4-N9	-2.17	1.33	1.37
3	B	600	ANP	C5-N7	-2.17	1.35	1.39

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	600	ANP	O1G-PG-N3B	-5.21	104.11	111.77
3	A	600	ANP	C5-C4-N3	-5.20	119.55	126.72
3	B	600	ANP	C5-C4-N3	-5.18	119.58	126.72
3	A	600	ANP	O2B-PB-O1B	4.12	118.71	109.87
3	A	600	ANP	O1G-PG-N3B	-4.07	105.78	111.77
3	A	600	ANP	N3-C4-N9	4.05	134.06	127.17
3	B	600	ANP	N3-C4-N9	4.04	134.03	127.17
3	B	600	ANP	O2B-PB-O1B	4.00	118.45	109.87
3	A	600	ANP	C2-N3-C4	3.63	120.70	111.83
3	B	600	ANP	N3-C2-N1	-3.56	123.20	128.58
3	B	600	ANP	C2-N3-C4	3.56	120.52	111.83
3	A	600	ANP	C4-C5-N7	-3.45	106.64	110.58
3	B	600	ANP	C4-C5-N7	-3.42	106.67	110.58
3	A	600	ANP	N3-C2-N1	-3.41	123.41	128.58
3	A	600	ANP	C4-N9-C8	3.25	109.15	105.74
3	B	600	ANP	C4-N9-C8	2.92	108.80	105.74
3	B	600	ANP	C5-N7-C8	2.59	107.52	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	600	ANP	C5-N7-C8	2.52	107.42	103.45
3	A	600	ANP	N9-C8-N7	-2.49	110.40	113.94
3	A	600	ANP	C6-C5-N7	2.41	136.73	132.09
2	B	500	5MY	O46-P6-O26	2.38	116.72	107.80
3	B	600	ANP	N9-C8-N7	-2.33	110.63	113.94
3	B	600	ANP	C2'-C1'-N9	-2.30	107.58	113.30
2	A	500	5MY	O43-P3-O23	2.28	116.37	107.80
3	B	600	ANP	C2-N1-C6	2.27	122.46	118.73
3	B	600	ANP	C6-C5-N7	2.26	136.44	132.09
3	B	600	ANP	O2G-PG-O3G	2.15	113.37	107.59
3	A	600	ANP	C2'-C1'-N9	-2.14	107.98	113.30
2	B	500	5MY	O45-P5-O25	2.03	115.40	107.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	600	ANP	PG-N3B-PB-O1B
3	A	600	ANP	PG-N3B-PB-O3A
3	B	600	ANP	PG-N3B-PB-O1B
3	B	600	ANP	PG-N3B-PB-O3A
2	A	500	5MY	C4-O14-P4-O34
2	B	500	5MY	C3-O13-P3-O23

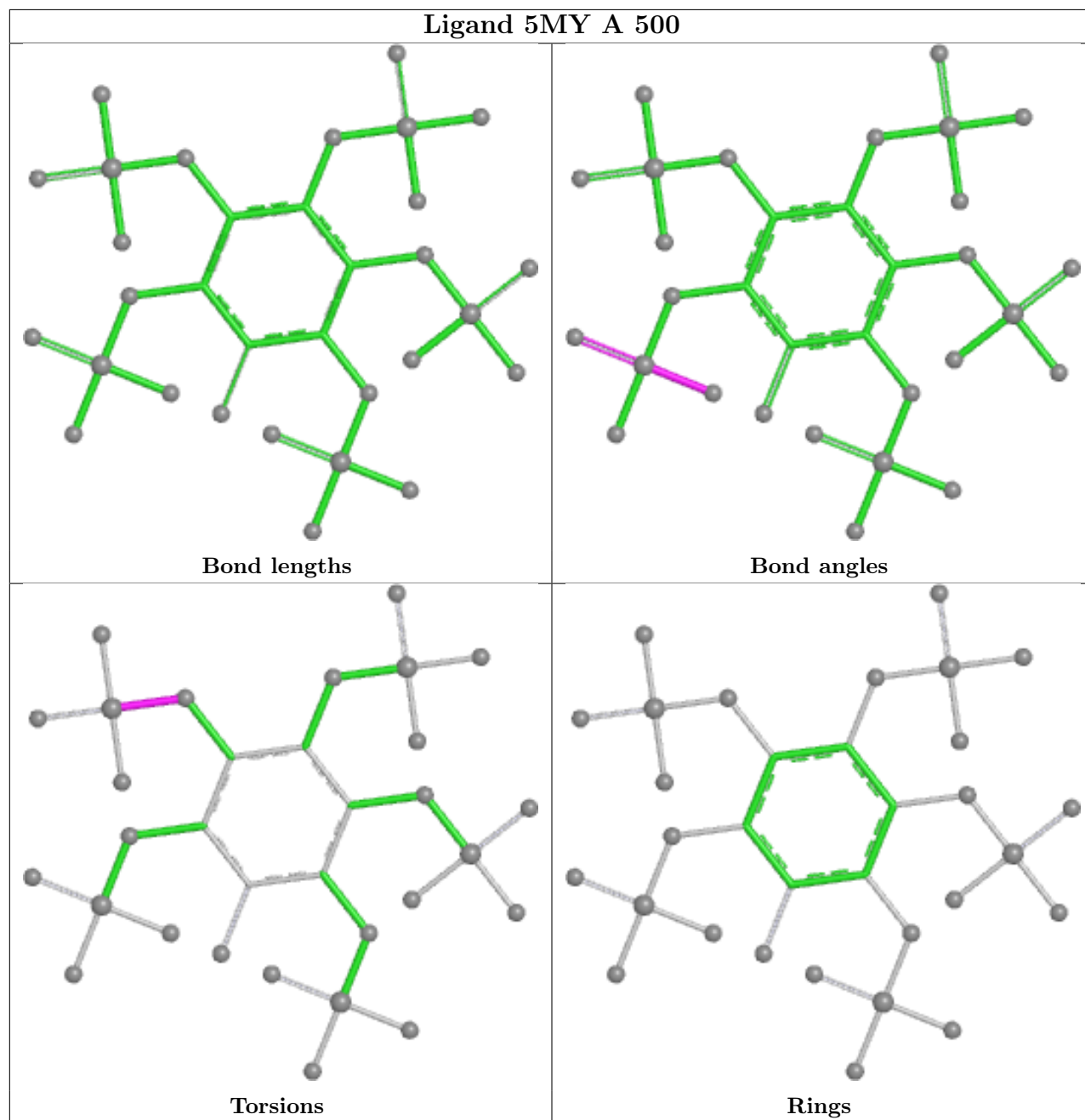
There are no ring outliers.

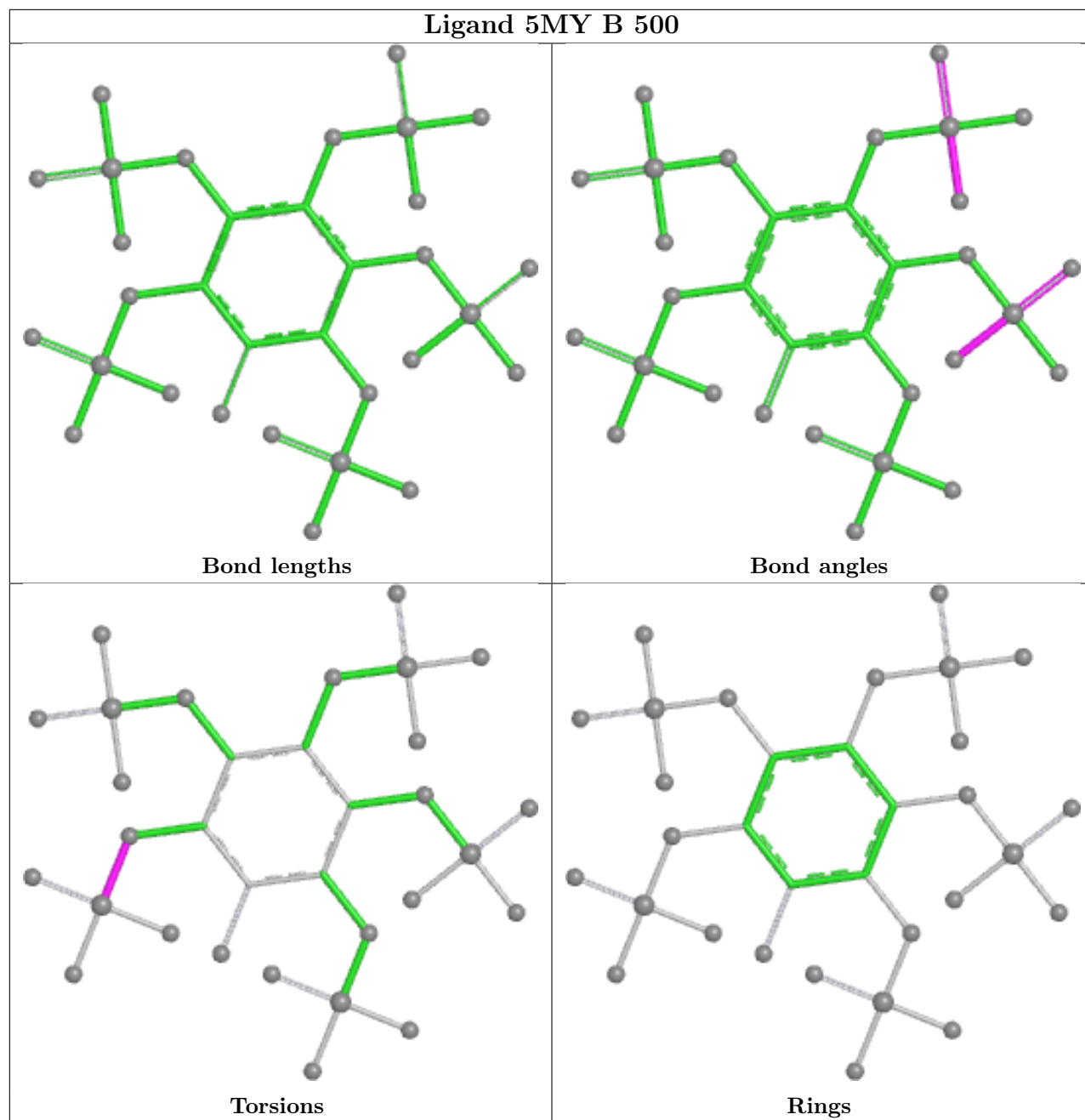
4 monomers are involved in 7 short contacts:

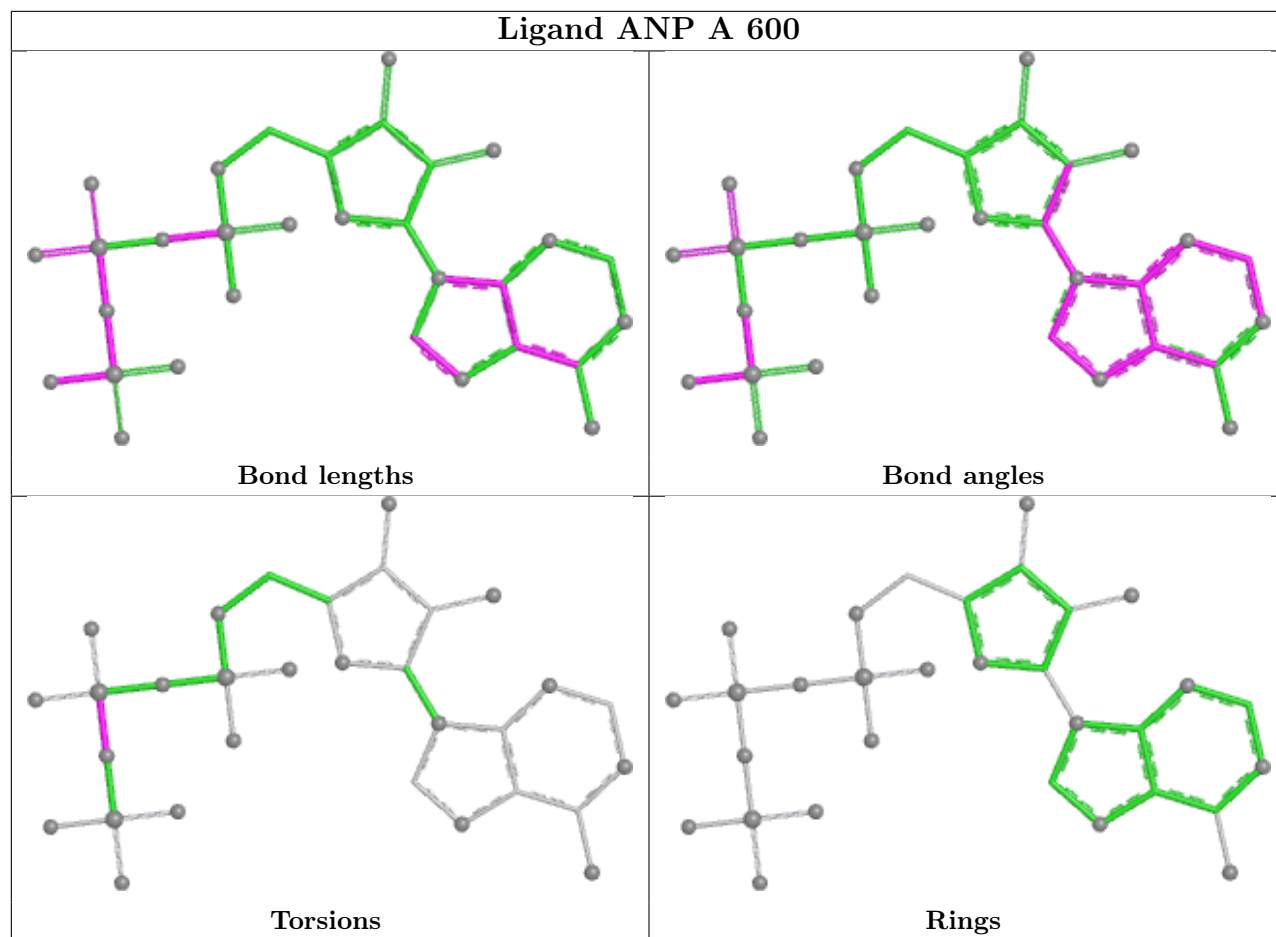
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	5MY	1	0
2	B	500	5MY	1	0
3	A	600	ANP	3	0
3	B	600	ANP	3	0

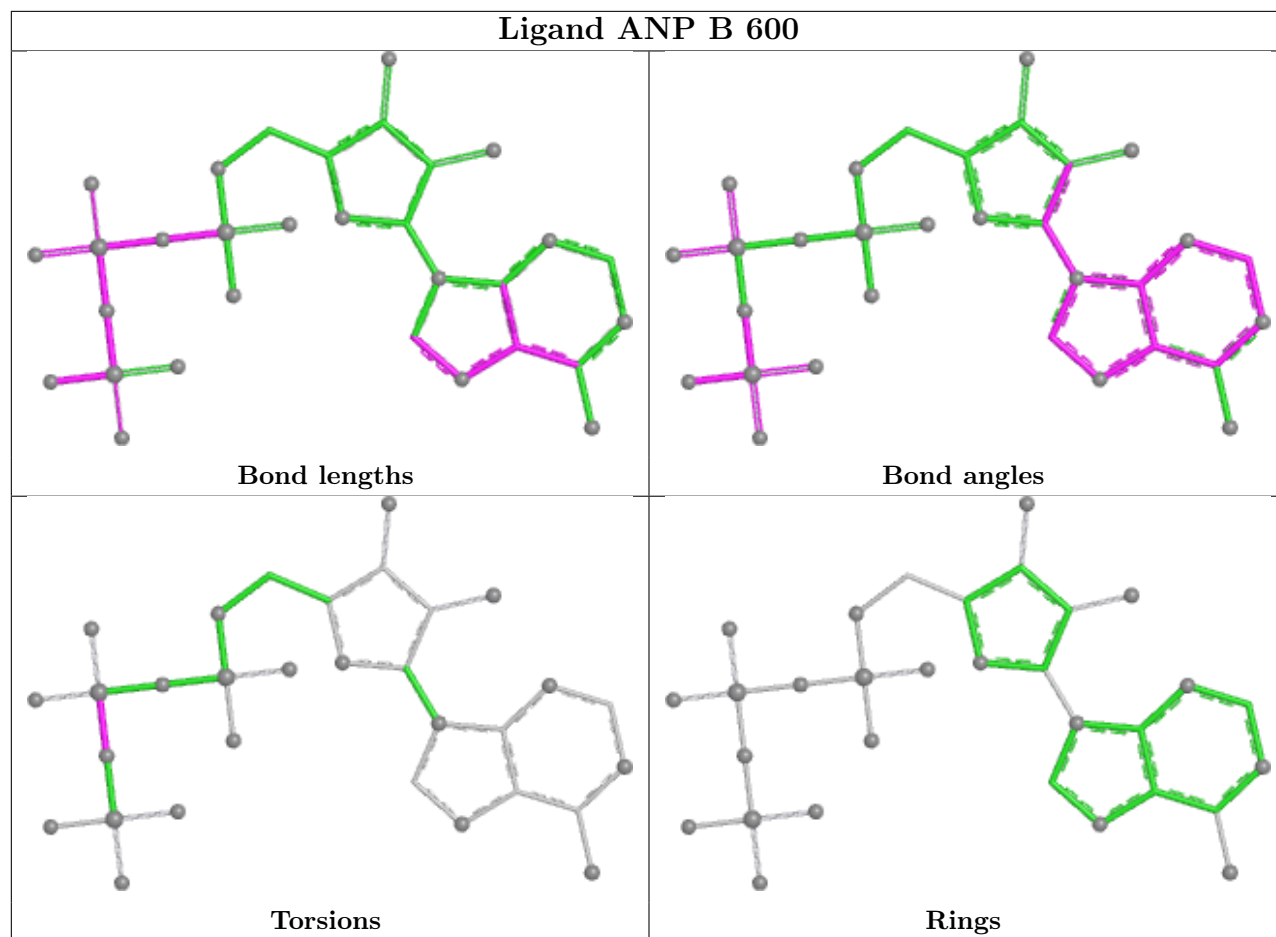
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	414/451 (91%)	0.18	14 (3%) 48 45	12, 20, 35, 51	0
1	B	417/451 (92%)	0.27	17 (4%) 41 38	11, 19, 35, 58	0
All	All	831/902 (92%)	0.23	31 (3%) 45 42	11, 20, 35, 58	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	343	LEU	6.0
1	B	436	ALA	5.0
1	A	342	GLU	4.8
1	B	57	VAL	4.8
1	B	336	GLY	4.7
1	B	155	GLY	4.2
1	B	344	SER	3.6
1	B	341	ALA	3.6
1	B	438	ASN	3.4
1	A	3	MET	3.2
1	A	155	GLY	3.1
1	A	158	SER	3.1
1	B	340	GLU	3.0
1	A	67	HIS	2.9
1	B	338	PRO	2.8
1	B	279	GLU	2.7
1	A	437	GLU	2.7
1	B	280	ASP	2.6
1	B	71	GLU	2.6
1	A	436	ALA	2.6
1	B	333	CYS	2.4
1	A	303	ARG	2.4
1	A	335	GLU	2.4
1	A	99	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	45	ARG	2.3
1	B	335	GLU	2.3
1	A	394	PRO	2.2
1	B	332	ILE	2.2
1	B	135	ASN	2.1
1	A	98	GLY	2.1
1	A	73	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

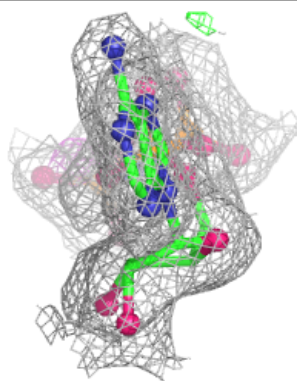
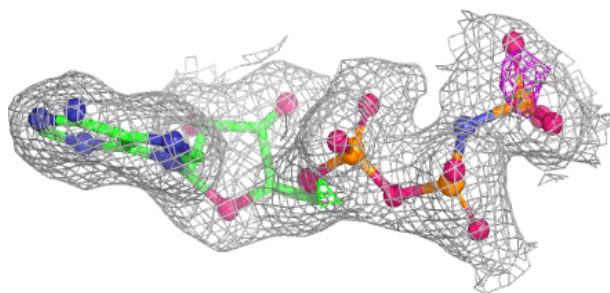
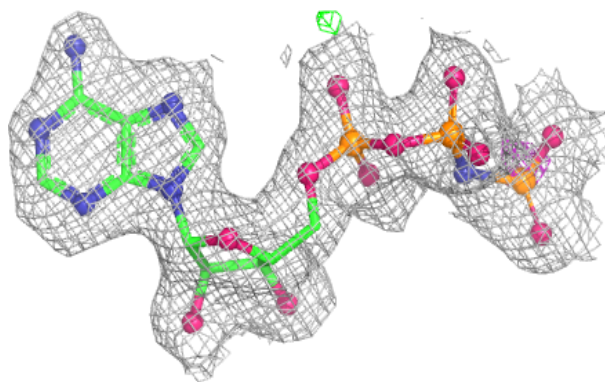
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	ZN	B	700	1/1	0.83	0.10	43,43,43,43	0
5	MG	A	1438	1/1	0.85	0.10	31,31,31,31	0
5	MG	B	1439	1/1	0.93	0.14	41,41,41,41	0
3	ANP	B	600	31/31	0.96	0.06	14,18,25,26	0
3	ANP	A	600	31/31	0.96	0.06	16,18,25,26	0
2	5MY	B	500	32/32	0.98	0.05	13,16,22,23	0
2	5MY	A	500	32/32	0.98	0.05	13,18,23,24	0
4	ZN	A	700	1/1	0.99	0.02	22,22,22,22	0

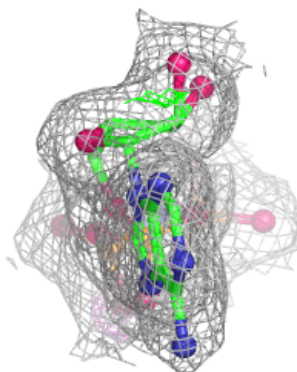
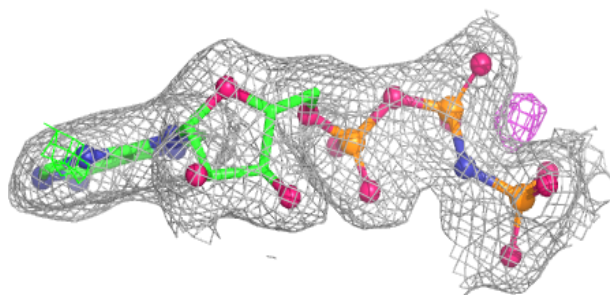
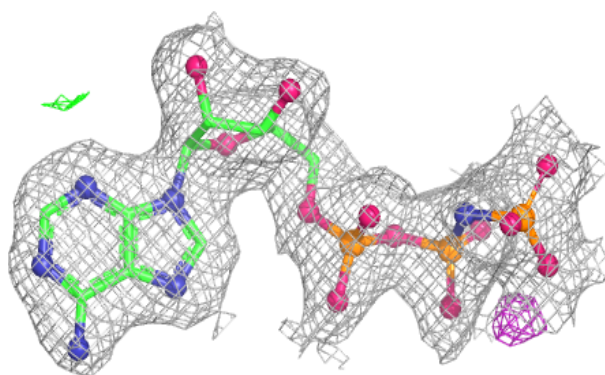
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP B 600:

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

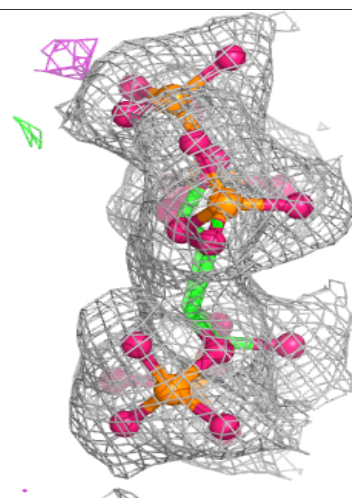
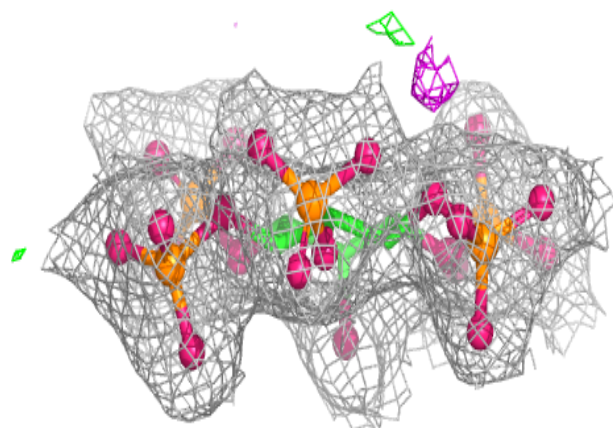
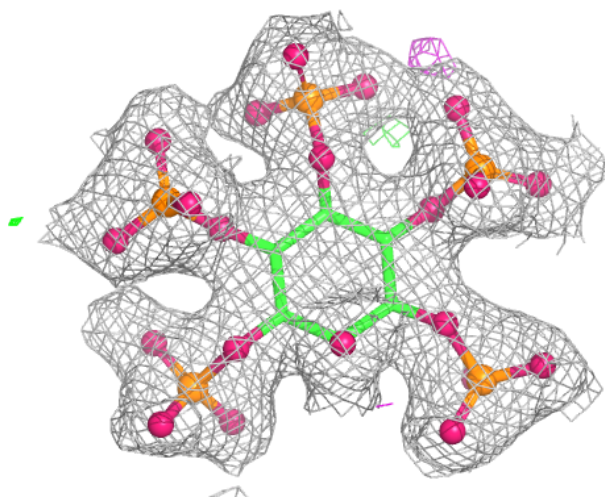
**Electron density around ANP A 600:**

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



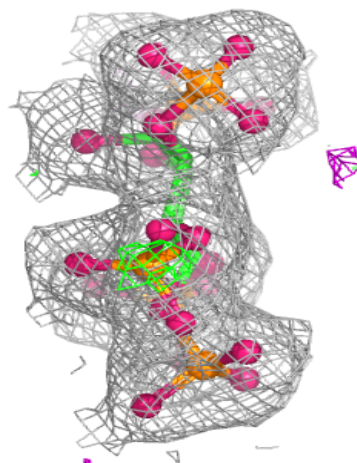
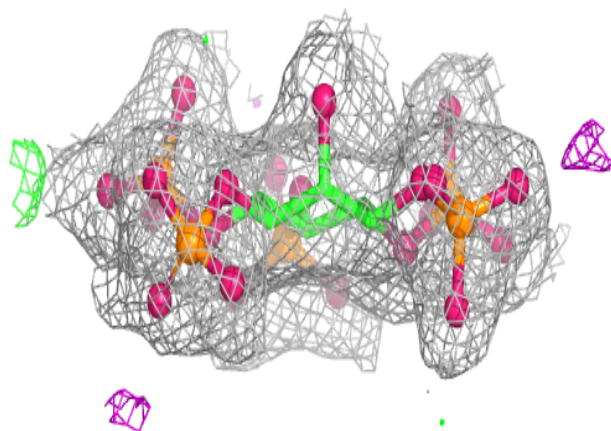
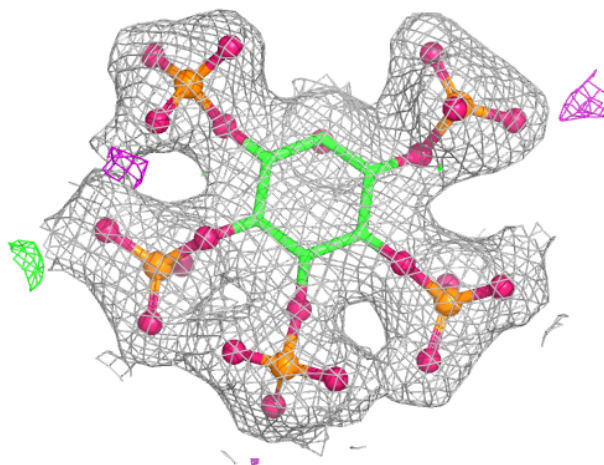
Electron density around 5MY B 500:

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



Electron density around 5MY A 500:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.