Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2020 – 07:28 AM BST

PDB ID	:	3X09
Title	:	Crystal structure of PIP4KIIBETA F205L complex with AMP
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Deposited on	:	2014-10-09
Resolution	:	2.70 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	Percentile Ranks	Value
Rfree		0.255
Clashscore		24
Ramachandran outliers		0.3%
Sidechain outliers		6.4%
RSRZ outliers		4.7%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
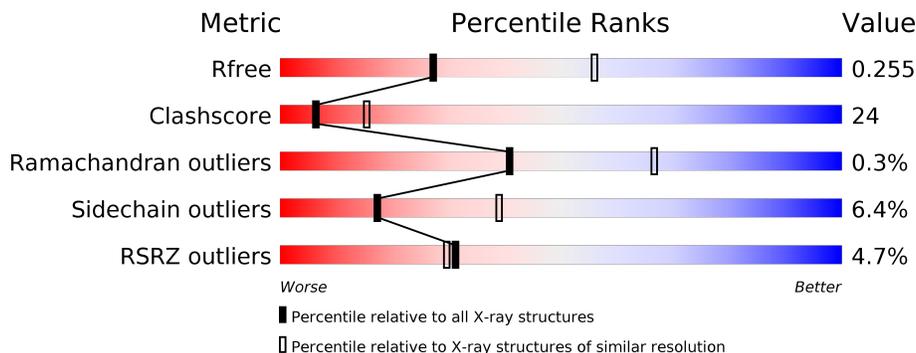
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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 <=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	393	% 52% 25% • 20%
1	B	393	6% 42% 33% • 22%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5274 atoms, of which 46 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 Phosphatidylinositol 5-phosphate 4-kinase type-2 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total 2592	C 1648	N 442	O 488	S 14	0	0	0
1	B	305	Total 2508	C 1603	N 431	O 461	S 13	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	EXPRESSION TAG	UNP P78356
A	25	PRO	-	EXPRESSION TAG	UNP P78356
A	26	ASN	-	EXPRESSION TAG	UNP P78356
A	27	CYS	-	EXPRESSION TAG	UNP P78356
A	28	ALA	-	EXPRESSION TAG	UNP P78356
A	29	PRO	-	EXPRESSION TAG	UNP P78356
A	30	GLY	-	EXPRESSION TAG	UNP P78356
A	205	LEU	PHE	ENGINEERED MUTATION	UNP P78356
B	24	GLY	-	EXPRESSION TAG	UNP P78356
B	25	PRO	-	EXPRESSION TAG	UNP P78356
B	26	ASN	-	EXPRESSION TAG	UNP P78356
B	27	CYS	-	EXPRESSION TAG	UNP P78356
B	28	ALA	-	EXPRESSION TAG	UNP P78356
B	29	PRO	-	EXPRESSION TAG	UNP P78356
B	30	GLY	-	EXPRESSION TAG	UNP P78356
B	205	LEU	PHE	ENGINEERED MUTATION	UNP P78356

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).
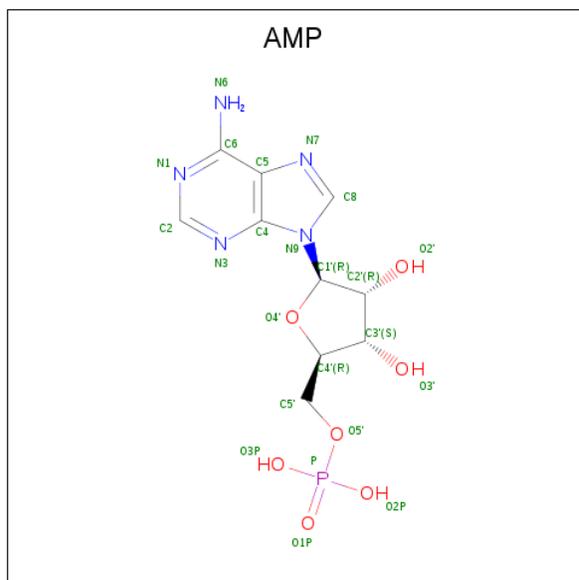
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			33	10	10	5	7	1		
2	A	1	Total	C	H	N	O	P	0	0
			35	10	12	5	7	1		
2	A	1	Total	C	H	N	O	P	0	0
			35	10	12	5	7	1		
2	B	1	Total	C	H	N	O	P	0	0
			35	10	12	5	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	O	0	0
			23	23		
3	B	13	Total	O	0	0
			13	13		

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: Phosphatidylinositol 5-phosphate 4-kinase type-2 beta

Chain A:

- Molecule 1: Phosphatidylinositol 5-phosphate 4-kinase type-2 beta

Chain B:
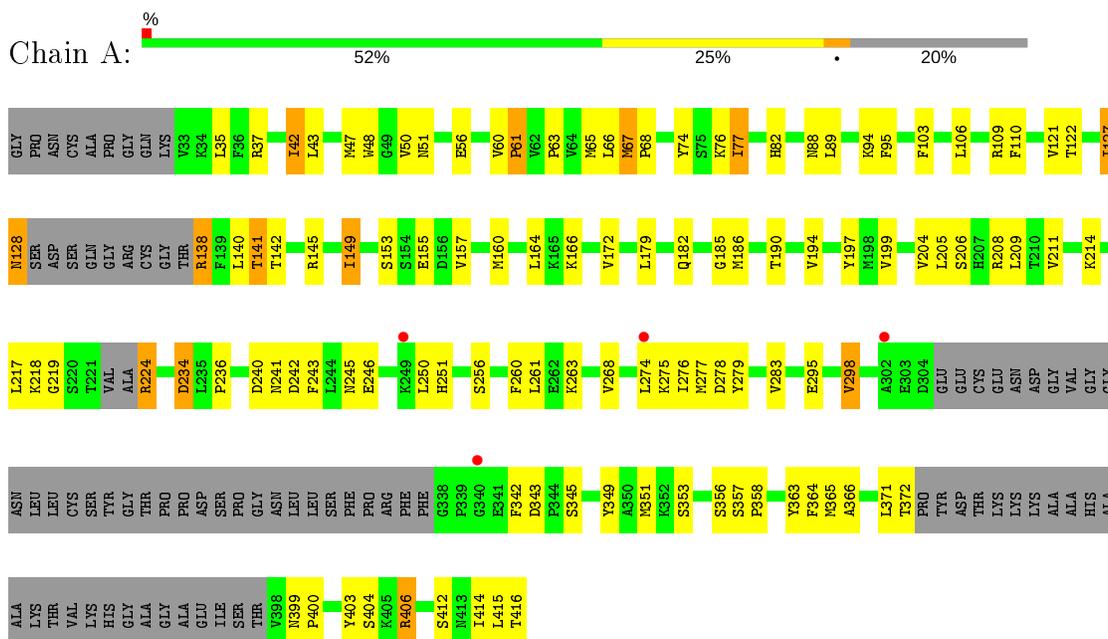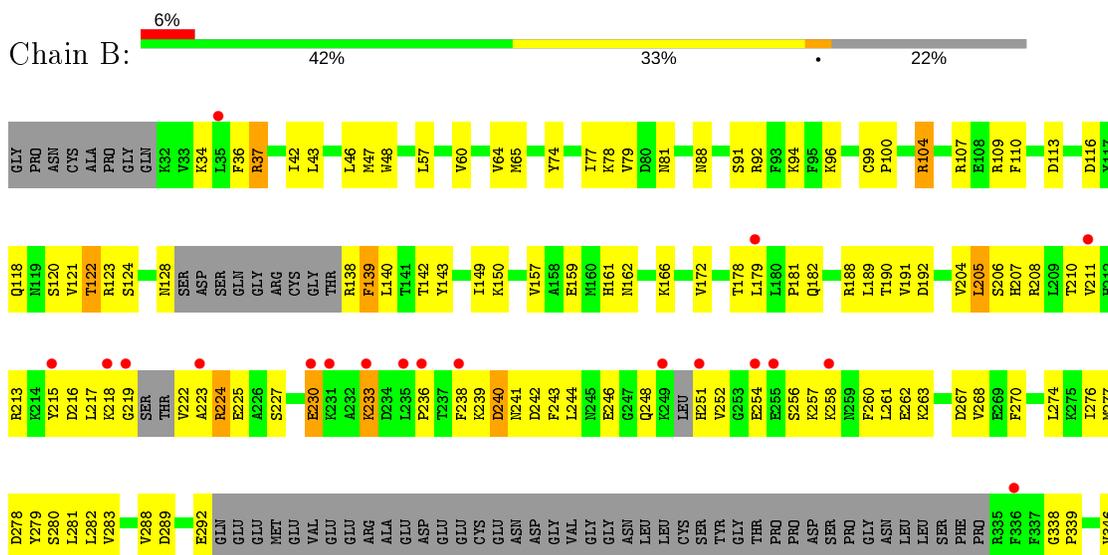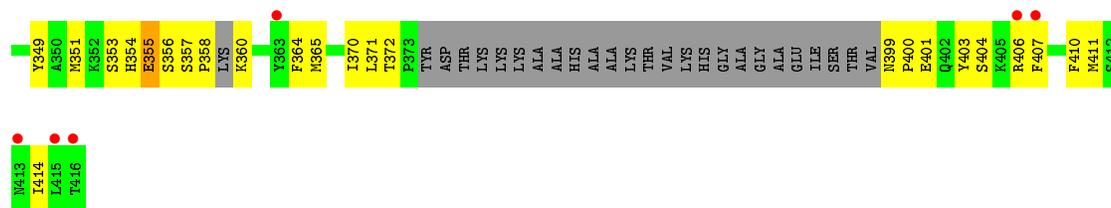
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	108.27Å 183.42Å 107.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.64 – 2.70 70.37 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (53.64-2.70) 99.5 (70.37-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.42 (at 2.69Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.3_928)	Depositor
R, R_{free}	0.203 , 0.260 0.198 , 0.255	Depositor DCC
R_{free} test set	1479 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	65.2	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 59.4	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.010 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.020 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5274	wwPDB-VP
Average B, all atoms (Å^2)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.45	0/2643	0.62	0/3554
1	B	0.44	0/2559	0.59	0/3439
All	All	0.45	0/5202	0.60	0/6993

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2592	0	2563	104	0
1	B	2508	0	2490	149	0
2	A	69	34	36	3	0
2	B	23	12	12	3	0
3	A	23	0	0	3	0
3	B	13	0	0	1	0
All	All	5228	46	5101	248	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 24.

All (248) 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:B:218:LYS:HE2	1:B:403:TYR:OH	1.43	1.18
1:B:225:GLU:HG2	1:B:241:ASN:HB2	1.25	1.14
1:A:77:ILE:HD11	1:B:77:ILE:HD11	1.31	1.11
1:A:42:ILE:H	1:A:42:ILE:HD12	1.22	1.01
1:B:222:VAL:HG12	1:B:223:ALA:H	1.28	0.97
1:A:77:ILE:HD11	1:B:77:ILE:CD1	1.95	0.97
1:B:94:LYS:HB2	1:B:190:THR:HB	1.45	0.96
1:B:222:VAL:HG12	1:B:223:ALA:N	1.80	0.96
1:A:138:ARG:HH11	1:A:138:ARG:HG2	1.30	0.93
1:B:110:PHE:CE2	1:B:182:GLN:HG2	2.04	0.92
1:A:155:GLU:N	1:A:155:GLU:OE2	2.05	0.90
1:B:179:LEU:HG	1:B:263:LYS:HG2	1.53	0.89
1:B:218:LYS:HZ3	1:B:278:ASP:HA	1.35	0.89
1:A:415:LEU:O	1:A:416:THR:HG23	1.75	0.87
1:A:77:ILE:CD1	1:B:77:ILE:HD11	2.04	0.87
1:B:222:VAL:CG1	1:B:223:ALA:H	1.88	0.86
1:B:218:LYS:CE	1:B:278:ASP:C	2.44	0.86
1:B:218:LYS:NZ	1:B:278:ASP:HA	1.91	0.84
1:B:139:PHE:O	1:B:139:PHE:CD2	2.29	0.84
1:B:258:LYS:O	1:B:262:GLU:HG2	1.77	0.83
1:A:204:VAL:HG23	2:A:501:AMP:C6	2.14	0.82
1:B:218:LYS:HE2	1:B:403:TYR:HH	1.38	0.82
1:B:139:PHE:O	1:B:139:PHE:HD2	1.61	0.82
1:A:166:LYS:HD2	1:A:274:LEU:HD21	1.61	0.81
1:B:215:TYR:HB3	1:B:217:LEU:HD21	1.61	0.80
1:B:225:GLU:CG	1:B:241:ASN:HB2	2.08	0.80
1:B:243:PHE:HE2	1:B:414:ILE:HG22	1.45	0.80
1:B:78:LYS:HD2	1:B:94:LYS:HE2	1.63	0.80
1:A:138:ARG:HH11	1:A:138:ARG:CG	1.94	0.80
1:B:268:VAL:HG12	1:B:404:SER:HB2	1.63	0.80
1:A:42:ILE:CD1	1:A:42:ILE:H	1.95	0.79
1:B:252:VAL:CG1	1:B:256:SER:HB2	2.10	0.79
1:B:118:GLN:O	1:B:122:THR:HB	1.82	0.79
1:B:218:LYS:HG2	1:B:403:TYR:OH	1.82	0.79
1:B:218:LYS:CE	1:B:403:TYR:OH	2.29	0.78
1:A:42:ILE:N	1:A:42:ILE:HD12	1.98	0.78
1:B:219:GLY:O	1:B:406:ARG:HD3	1.83	0.77
1:A:67:MET:HA	1:A:67:MET:HE2	1.67	0.77
1:B:222:VAL:CG1	1:B:223:ALA:N	2.47	0.77
1:B:218:LYS:HE3	1:B:278:ASP:O	1.83	0.77
1:B:236:PRO:HG2	1:B:238:PHE:CE1	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:SER:HB3	1:A:351:MET:CE	2.16	0.76
1:B:283:VAL:HG22	1:B:365:MET:HG2	1.66	0.76
1:B:218:LYS:NZ	1:B:278:ASP:CA	2.50	0.74
1:B:277:MET:O	1:B:278:ASP:HB2	1.87	0.73
1:B:252:VAL:HG13	1:B:256:SER:HB2	1.69	0.73
1:B:34:LYS:NZ	1:B:122:THR:HG21	2.04	0.72
1:B:236:PRO:HG2	1:B:238:PHE:HE1	1.52	0.72
1:B:288:VAL:CG1	1:B:339:PRO:HB2	2.18	0.72
1:A:295:GLU:O	1:A:298:VAL:HG12	1.90	0.71
1:B:218:LYS:HE3	1:B:278:ASP:C	2.10	0.71
1:A:260:PHE:CD2	1:A:415:LEU:HD11	2.26	0.70
1:B:139:PHE:C	1:B:139:PHE:CD2	2.64	0.70
1:A:141:THR:HG22	1:A:142:THR:O	1.91	0.70
1:A:204:VAL:HG13	1:A:366:ALA:HB3	1.74	0.70
1:B:243:PHE:HE2	1:B:414:ILE:CG2	2.04	0.70
1:A:204:VAL:HG23	2:A:501:AMP:N6	2.07	0.70
1:A:67:MET:HA	1:A:67:MET:CE	2.22	0.69
1:B:46:LEU:HD21	1:B:149:ILE:HD13	1.72	0.69
1:B:240:ASP:N	1:B:240:ASP:OD1	2.19	0.68
1:A:140:LEU:HB2	1:A:149:ILE:HB	1.76	0.67
1:B:109:ARG:CZ	1:B:172:VAL:HG22	2.25	0.67
1:A:208:ARG:HH22	1:A:342:PHE:HA	1.61	0.66
1:A:399:ASN:HB3	1:A:400:PRO:CD	2.24	0.66
1:A:141:THR:CG2	1:A:142:THR:O	2.44	0.66
1:A:94:LYS:HB2	1:A:190:THR:HB	1.78	0.65
1:B:407:PHE:O	1:B:411:MET:HG2	1.97	0.65
1:A:219:GLY:O	1:A:406:ARG:HD2	1.96	0.65
1:A:218:LYS:HD2	1:A:403:TYR:OH	1.97	0.65
1:B:78:LYS:HD2	1:B:94:LYS:CE	2.26	0.65
1:A:349:TYR:CD1	1:A:366:ALA:HB2	2.32	0.65
1:B:268:VAL:CG1	1:B:404:SER:HB2	2.27	0.65
1:B:246:GLU:HG3	1:B:246:GLU:O	1.97	0.64
1:B:191:VAL:O	1:B:192:ASP:HB2	1.97	0.64
1:B:218:LYS:CE	1:B:278:ASP:O	2.44	0.63
1:B:243:PHE:CE2	1:B:414:ILE:CG2	2.81	0.63
1:B:254:GLU:HG2	1:B:258:LYS:HE3	1.79	0.63
1:B:37:ARG:HG2	1:B:88:ASN:OD1	1.98	0.63
1:B:120:SER:O	1:B:142:THR:HB	1.98	0.63
1:B:224:ARG:C	1:B:225:GLU:HG3	2.19	0.62
1:A:399:ASN:HB3	1:A:400:PRO:HD2	1.82	0.62
1:A:399:ASN:CB	1:A:400:PRO:CD	2.77	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:LYS:HG2	1:A:279:TYR:O	2.00	0.61
1:B:240:ASP:HB3	1:B:410:PHE:CZ	2.36	0.61
1:A:261:LEU:HD21	1:A:412:SER:HA	1.83	0.61
1:B:205:LEU:HG	1:B:211:VAL:HG21	1.81	0.61
1:A:256:SER:HB3	1:A:351:MET:HE1	1.82	0.61
1:B:238:PHE:HB3	1:B:242:ASP:HB2	1.82	0.60
1:A:242:ASP:O	1:A:246:GLU:HG2	2.01	0.60
1:B:218:LYS:CE	1:B:278:ASP:HA	2.31	0.60
1:B:213:ARG:NH2	1:B:246:GLU:OE1	2.33	0.60
1:A:206:SER:HB2	1:A:364:PHE:CE2	2.37	0.60
1:A:66:LEU:O	1:A:67:MET:HE2	2.00	0.60
1:A:415:LEU:O	1:A:416:THR:CG2	2.47	0.59
1:B:244:LEU:HD11	1:B:410:PHE:HE1	1.67	0.59
1:B:230:GLU:O	1:B:233:LYS:HG2	2.02	0.59
1:B:206:SER:HB2	1:B:364:PHE:CE2	2.38	0.59
1:A:43:LEU:HD21	1:A:140:LEU:HD11	1.85	0.58
1:A:277:MET:O	1:A:278:ASP:HB2	2.03	0.58
1:B:166:LYS:HD2	1:B:274:LEU:HD21	1.85	0.58
1:A:138:ARG:NH1	1:A:138:ARG:CG	2.60	0.58
1:A:224:ARG:O	1:A:241:ASN:OD1	2.22	0.57
1:B:204:VAL:HG23	2:B:501:AMP:C6	2.39	0.57
1:B:218:LYS:CE	1:B:278:ASP:CA	2.83	0.57
1:B:243:PHE:CE2	1:B:414:ILE:HG22	2.34	0.56
1:A:51:ASN:HB2	1:A:122:THR:HG21	1.87	0.56
1:B:236:PRO:CG	1:B:238:PHE:CE1	2.88	0.56
1:B:224:ARG:CZ	1:B:239:LYS:HD3	2.37	0.55
1:B:204:VAL:HG23	2:B:501:AMP:N1	2.21	0.55
1:A:217:LEU:HD13	1:A:414:ILE:HD11	1.87	0.55
1:B:399:ASN:N	1:B:400:PRO:CD	2.69	0.54
1:A:127:ILE:O	1:A:127:ILE:HG12	2.08	0.54
1:B:218:LYS:HZ3	1:B:278:ASP:CA	2.12	0.54
1:B:34:LYS:HZ3	1:B:122:THR:HG21	1.70	0.54
1:B:34:LYS:HD3	1:B:122:THR:HG23	1.90	0.53
1:A:77:ILE:CG1	1:B:77:ILE:HD11	2.38	0.53
1:A:157:VAL:HG21	1:A:197:TYR:CD2	2.44	0.53
1:B:355:GLU:N	1:B:355:GLU:OE2	2.42	0.53
1:B:204:VAL:HA	1:B:349:TYR:CD2	2.43	0.53
1:A:241:ASN:O	1:A:245:ASN:HB2	2.08	0.53
1:B:60:VAL:O	1:B:104:ARG:NH2	2.37	0.52
1:A:128:ASN:HB3	1:A:140:LEU:HD23	1.90	0.52
1:B:34:LYS:CE	1:B:122:THR:HG21	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:TRP:HH2	1:B:77:ILE:HD13	1.74	0.52
1:B:140:LEU:HB2	1:B:149:ILE:HB	1.91	0.52
1:B:189:LEU:N	1:B:189:LEU:HD12	2.24	0.52
1:B:81:ASN:O	1:B:91:SER:HB3	2.10	0.52
1:A:268:VAL:CG1	1:A:404:SER:HA	2.40	0.51
1:B:227:SER:OG	1:B:230:GLU:HB2	2.10	0.51
1:B:43:LEU:HD21	1:B:140:LEU:HD11	1.91	0.51
1:A:234:ASP:O	1:A:236:PRO:HD3	2.11	0.51
1:A:371:LEU:O	1:A:372:THR:CB	2.58	0.51
1:B:218:LYS:HE2	1:B:278:ASP:C	2.30	0.51
1:A:343:ASP:OD2	1:A:345:SER:OG	2.26	0.50
1:B:166:LYS:HD2	1:B:274:LEU:CD2	2.41	0.50
1:B:218:LYS:CG	1:B:403:TYR:OH	2.56	0.50
1:B:256:SER:HB3	1:B:351:MET:CE	2.42	0.50
1:B:224:ARG:O	1:B:225:GLU:HG3	2.12	0.50
1:A:204:VAL:HG23	2:A:501:AMP:N1	2.27	0.49
1:B:215:TYR:CB	1:B:217:LEU:HD21	2.36	0.49
1:A:204:VAL:CG1	1:A:366:ALA:HB3	2.40	0.49
1:B:281:LEU:HD12	1:B:282:LEU:N	2.27	0.49
1:B:34:LYS:CE	1:B:122:THR:CG2	2.90	0.49
1:A:274:LEU:O	1:A:275:LYS:HB2	2.12	0.49
1:A:141:THR:CG2	1:A:142:THR:N	2.76	0.49
1:A:256:SER:HB3	1:A:351:MET:HE2	1.94	0.49
1:B:189:LEU:N	1:B:189:LEU:CD1	2.76	0.48
1:A:109:ARG:NH1	1:A:172:VAL:HG22	2.29	0.48
1:A:185:GLY:HA2	3:A:603:HOH:O	2.13	0.48
1:A:128:ASN:C	1:A:128:ASN:HD22	2.17	0.48
1:B:218:LYS:NZ	1:B:278:ASP:C	2.66	0.48
1:A:77:ILE:HG22	1:A:95:PHE:HB3	1.95	0.48
1:B:99:CYS:N	1:B:100:PRO:CD	2.77	0.48
1:A:250:LEU:HD22	1:A:363:TYR:CE2	2.49	0.47
1:B:354:HIS:ND1	1:B:356:SER:HB2	2.29	0.47
1:B:254:GLU:CG	1:B:258:LYS:HE3	2.42	0.47
1:B:43:LEU:HD21	1:B:140:LEU:CD1	2.44	0.47
1:A:357:SER:OG	1:A:358:PRO:HD2	2.14	0.47
1:A:141:THR:HG23	1:A:145:ARG:HA	1.97	0.47
1:A:204:VAL:HG13	1:A:366:ALA:CB	2.43	0.47
1:A:217:LEU:CD1	1:A:414:ILE:HD11	2.44	0.47
1:B:218:LYS:HE2	1:B:278:ASP:HA	1.94	0.47
1:B:225:GLU:HA	1:B:239:LYS:HB2	1.97	0.47
1:B:289:ASP:O	1:B:292:GLU:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:ARG:NH2	1:B:239:LYS:HD3	2.31	0.46
1:B:181:PRO:HG2	1:B:370:ILE:HG12	1.96	0.46
1:B:411:MET:O	1:B:414:ILE:HG12	2.15	0.46
1:B:113:ASP:HB3	1:B:116:ASP:OD1	2.16	0.46
1:B:256:SER:O	1:B:260:PHE:HB3	2.16	0.46
1:A:219:GLY:O	1:A:406:ARG:CD	2.62	0.46
1:B:230:GLU:HA	1:B:233:LYS:HD3	1.98	0.46
1:B:79:VAL:O	1:B:92:ARG:HA	2.15	0.46
1:B:243:PHE:CE1	1:B:248:GLN:HB3	2.51	0.45
1:B:233:LYS:CB	1:B:233:LYS:NZ	2.79	0.45
1:A:56:GLU:HG2	3:A:621:HOH:O	2.16	0.45
1:B:57:LEU:O	1:B:104:ARG:NH2	2.50	0.45
1:B:256:SER:HB3	1:B:351:MET:HE2	1.98	0.45
1:B:110:PHE:CZ	1:B:182:GLN:HG2	2.47	0.45
1:A:166:LYS:CD	1:A:274:LEU:HD21	2.40	0.44
1:B:215:TYR:HB3	1:B:217:LEU:CD2	2.41	0.44
1:A:160:MET:O	1:A:164:LEU:HB2	2.16	0.44
1:B:37:ARG:HD3	1:B:88:ASN:OD1	2.17	0.44
1:A:67:MET:HE1	1:A:68:PRO:HD3	1.99	0.44
1:B:96:LYS:HB3	1:B:188:ARG:HB3	1.98	0.44
1:A:106:LEU:HA	1:A:106:LEU:HD23	1.84	0.44
1:A:43:LEU:O	1:A:47:MET:HG3	2.17	0.44
1:B:104:ARG:HA	1:B:107:ARG:NH1	2.33	0.44
1:A:138:ARG:CB	1:A:138:ARG:NH1	2.81	0.44
1:A:35:LEU:HB3	1:A:88:ASN:ND2	2.33	0.44
1:B:218:LYS:NZ	1:B:278:ASP:O	2.49	0.44
1:A:160:MET:CE	1:A:164:LEU:HD13	2.47	0.44
1:B:218:LYS:HG3	1:B:279:TYR:O	2.17	0.44
1:A:218:LYS:HE2	1:A:224:ARG:CZ	2.48	0.43
1:B:159:GLU:O	1:B:162:ASN:HB3	2.18	0.43
1:A:103:PHE:HA	1:A:106:LEU:HB2	2.00	0.43
1:A:251:HIS:O	1:A:353:SER:HA	2.17	0.43
1:A:74:TYR:C	1:A:74:TYR:CD1	2.92	0.43
1:B:216:ASP:C	1:B:217:LEU:HD23	2.38	0.43
1:B:251:HIS:HB2	1:B:357:SER:HB2	1.99	0.43
1:A:190:THR:HA	1:A:194:VAL:O	2.19	0.43
1:B:219:GLY:N	1:B:240:ASP:OD2	2.52	0.43
1:B:371:LEU:O	1:B:372:THR:HG23	2.18	0.43
1:A:186:MET:HG3	1:A:199:VAL:HG22	2.00	0.43
1:A:63:PRO:HB2	1:A:65:MET:O	2.19	0.43
1:B:225:GLU:HB3	1:B:242:ASP:OD1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:LEU:HG	1:A:263:LYS:HB3	2.00	0.43
1:A:77:ILE:HD12	1:B:79:VAL:HG22	2.01	0.43
1:B:157:VAL:O	1:B:161:HIS:HD2	2.01	0.43
1:B:204:VAL:HA	1:B:349:TYR:HD2	1.83	0.43
1:A:218:LYS:HB3	1:A:403:TYR:OH	2.19	0.43
1:B:207:HIS:CE1	1:B:346:VAL:HG11	2.53	0.42
1:B:233:LYS:NZ	1:B:233:LYS:HB3	2.34	0.42
1:B:36:PHE:HD1	1:B:47:MET:HB3	1.84	0.42
1:B:34:LYS:HE2	1:B:122:THR:CG2	2.48	0.42
1:B:64:VAL:HG23	1:B:65:MET:HG2	2.01	0.42
1:A:43:LEU:CD2	1:A:140:LEU:HD11	2.50	0.42
1:A:268:VAL:HG13	1:A:279:TYR:OH	2.20	0.42
1:A:48:TRP:HB2	1:A:89:LEU:HD21	2.01	0.42
2:B:501:AMP:N6	3:B:611:HOH:O	2.52	0.42
1:A:276:ILE:HG22	1:A:277:MET:N	2.35	0.42
1:B:224:ARG:O	1:B:225:GLU:CG	2.67	0.42
1:A:206:SER:HB2	1:A:364:PHE:CZ	2.55	0.42
1:B:218:LYS:HE2	1:B:278:ASP:CA	2.50	0.42
1:A:243:PHE:HZ	1:A:414:ILE:HG23	1.85	0.41
1:A:141:THR:HG23	1:A:142:THR:N	2.34	0.41
1:B:233:LYS:HG2	1:B:233:LYS:H	1.53	0.41
1:B:37:ARG:CG	1:B:88:ASN:OD1	2.66	0.41
1:B:121:VAL:O	1:B:121:VAL:HG12	2.19	0.41
1:A:110:PHE:CE1	1:A:182:GLN:HB3	2.55	0.41
1:A:153:SER:O	1:A:157:VAL:HG23	2.20	0.41
1:B:213:ARG:CZ	1:B:246:GLU:OE1	2.68	0.41
1:B:244:LEU:HD11	1:B:410:PHE:CE1	2.52	0.41
1:B:267:ASP:O	1:B:270:PHE:HB3	2.21	0.41
1:A:283:VAL:HG22	1:A:365:MET:HG2	2.02	0.41
1:B:288:VAL:HG12	1:B:339:PRO:HB2	1.98	0.41
1:A:109:ARG:HG2	3:A:610:HOH:O	2.21	0.41
1:A:109:ARG:CZ	1:A:172:VAL:HG22	2.51	0.41
1:A:209:LEU:HD23	1:A:209:LEU:N	2.36	0.41
1:A:60:VAL:HA	1:A:61:PRO:HD2	1.88	0.41
1:A:82:HIS:HB2	1:B:74:TYR:CZ	2.56	0.40
1:B:257:LYS:O	1:B:261:LEU:HG	2.20	0.40
1:A:219:GLY:O	1:A:406:ARG:NE	2.54	0.40
1:B:150:LYS:HB2	1:B:150:LYS:HE3	1.88	0.40
1:B:358:PRO:O	1:B:360:LYS:N	2.54	0.40
1:A:50:VAL:HG21	1:A:121:VAL:HG11	2.03	0.40
1:B:124:SER:HB3	1:B:143:TYR:CD2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:LEU:HD22	1:A:211:VAL:HG21	2.04	0.40
1:B:276:ILE:HG22	1:B:277:MET:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	305/393 (78%)	285 (93%)	19 (6%)	1 (0%)	41	66
1	B	291/393 (74%)	274 (94%)	16 (6%)	1 (0%)	41	66
All	All	596/786 (76%)	559 (94%)	35 (6%)	2 (0%)	41	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	338	GLY
1	A	61	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	293/352 (83%)	276 (94%)	17 (6%)	20	43
1	B	282/352 (80%)	262 (93%)	20 (7%)	14	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	575/704 (82%)	538 (94%)	37 (6%)	17 39

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	42	ILE
1	A	67	MET
1	A	76	LYS
1	A	77	ILE
1	A	127	ILE
1	A	128	ASN
1	A	138	ARG
1	A	141	THR
1	A	149	ILE
1	A	214	LYS
1	A	224	ARG
1	A	234	ASP
1	A	240	ASP
1	A	298	VAL
1	A	356	SER
1	A	406	ARG
1	B	37	ARG
1	B	42	ILE
1	B	104	ARG
1	B	122	THR
1	B	123	ARG
1	B	128	ASN
1	B	138	ARG
1	B	139	PHE
1	B	178	THR
1	B	205	LEU
1	B	208	ARG
1	B	210	THR
1	B	224	ARG
1	B	230	GLU
1	B	233	LYS
1	B	240	ASP
1	B	280	SER
1	B	353	SER
1	B	355	GLU
1	B	401	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	408	ASN
1	B	115	GLN
1	B	128	ASN
1	B	161	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	AMP	A	501	-	22,25,25	0.95	1 (4%)	25,38,38	1.56	5 (20%)
2	AMP	A	502	-	22,25,25	0.99	1 (4%)	25,38,38	1.31	3 (12%)
2	AMP	A	503	-	22,25,25	0.95	1 (4%)	25,38,38	1.19	3 (12%)
2	AMP	B	501	-	22,25,25	0.88	1 (4%)	25,38,38	1.39	4 (16%)

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	AMP	A	501	-	-	6/6/26/26	0/3/3/3
2	AMP	A	502	-	-	1/6/26/26	0/3/3/3
2	AMP	A	503	-	-	3/6/26/26	0/3/3/3
2	AMP	B	501	-	-	2/6/26/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	AMP	C5-C4	2.85	1.48	1.40
2	A	502	AMP	C5-C4	2.71	1.48	1.40
2	B	501	AMP	C5-C4	2.42	1.47	1.40
2	A	503	AMP	C5-C4	2.30	1.47	1.40

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	502	AMP	C4-C5-N7	-3.46	105.79	109.40
2	B	501	AMP	N3-C2-N1	-3.22	123.64	128.68
2	A	503	AMP	C4-C5-N7	-3.06	106.21	109.40
2	A	501	AMP	N3-C2-N1	-2.96	124.04	128.68
2	A	501	AMP	C4-C5-N7	-2.89	106.39	109.40
2	A	501	AMP	C3'-C2'-C1'	2.78	105.16	100.98
2	B	501	AMP	O3P-P-O5'	-2.76	99.40	106.73
2	B	501	AMP	C4-C5-N7	-2.75	106.53	109.40
2	A	501	AMP	O3P-P-O5'	-2.63	99.73	106.73
2	A	503	AMP	N3-C2-N1	-2.61	124.60	128.68
2	A	501	AMP	C2-N1-C6	2.29	122.67	118.75
2	A	502	AMP	N3-C2-N1	-2.29	125.11	128.68
2	A	502	AMP	O3P-P-O5'	-2.16	101.00	106.73
2	B	501	AMP	C2-N1-C6	2.09	122.33	118.75
2	A	503	AMP	O2P-P-O1P	2.03	118.62	110.68

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	AMP	C5'-O5'-P-O2P
2	A	501	AMP	C5'-O5'-P-O3P
2	A	501	AMP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	A	501	AMP	C3'-C4'-C5'-O5'
2	A	503	AMP	C5'-O5'-P-O1P
2	A	503	AMP	C5'-O5'-P-O2P
2	A	503	AMP	C5'-O5'-P-O3P
2	B	501	AMP	O4'-C4'-C5'-O5'
2	B	501	AMP	C3'-C4'-C5'-O5'
2	A	501	AMP	C5'-O5'-P-O1P
2	A	502	AMP	C5'-O5'-P-O1P
2	A	501	AMP	C4'-C5'-O5'-P

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	AMP	3	0
2	B	501	AMP	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 then 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 A 501

Bond lengths

Bond angles

Torsions

Rings

Ligand AMP A 502

Bond lengths

Bond angles

Torsions

Rings

Ligand AMP A 503

Bond lengths

Bond angles

Torsions

Rings

Ligand AMP B 501

Bond lengths

Bond angles

Torsions

Rings
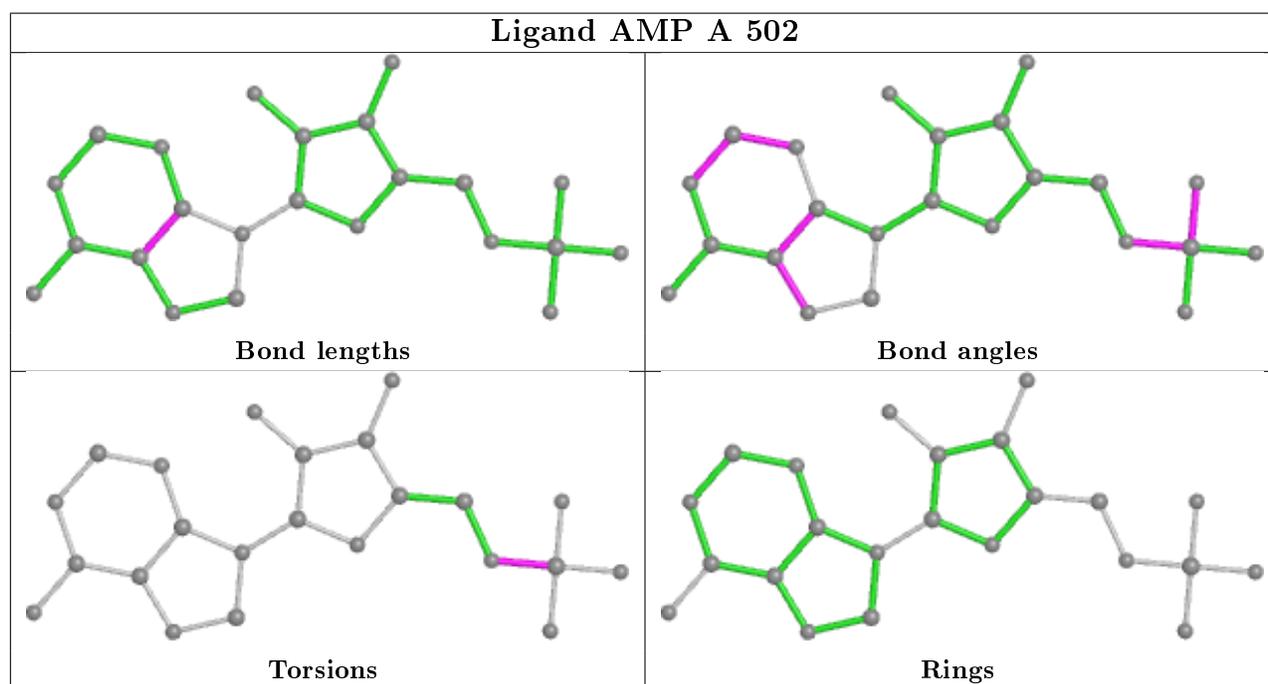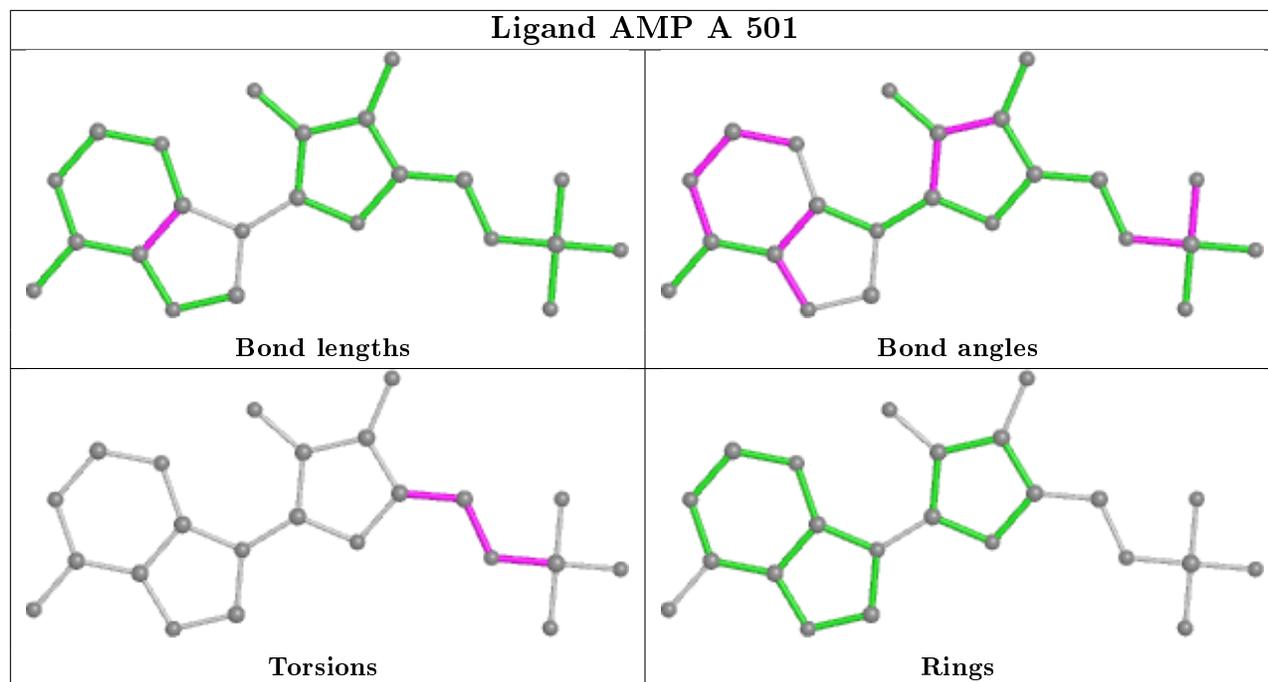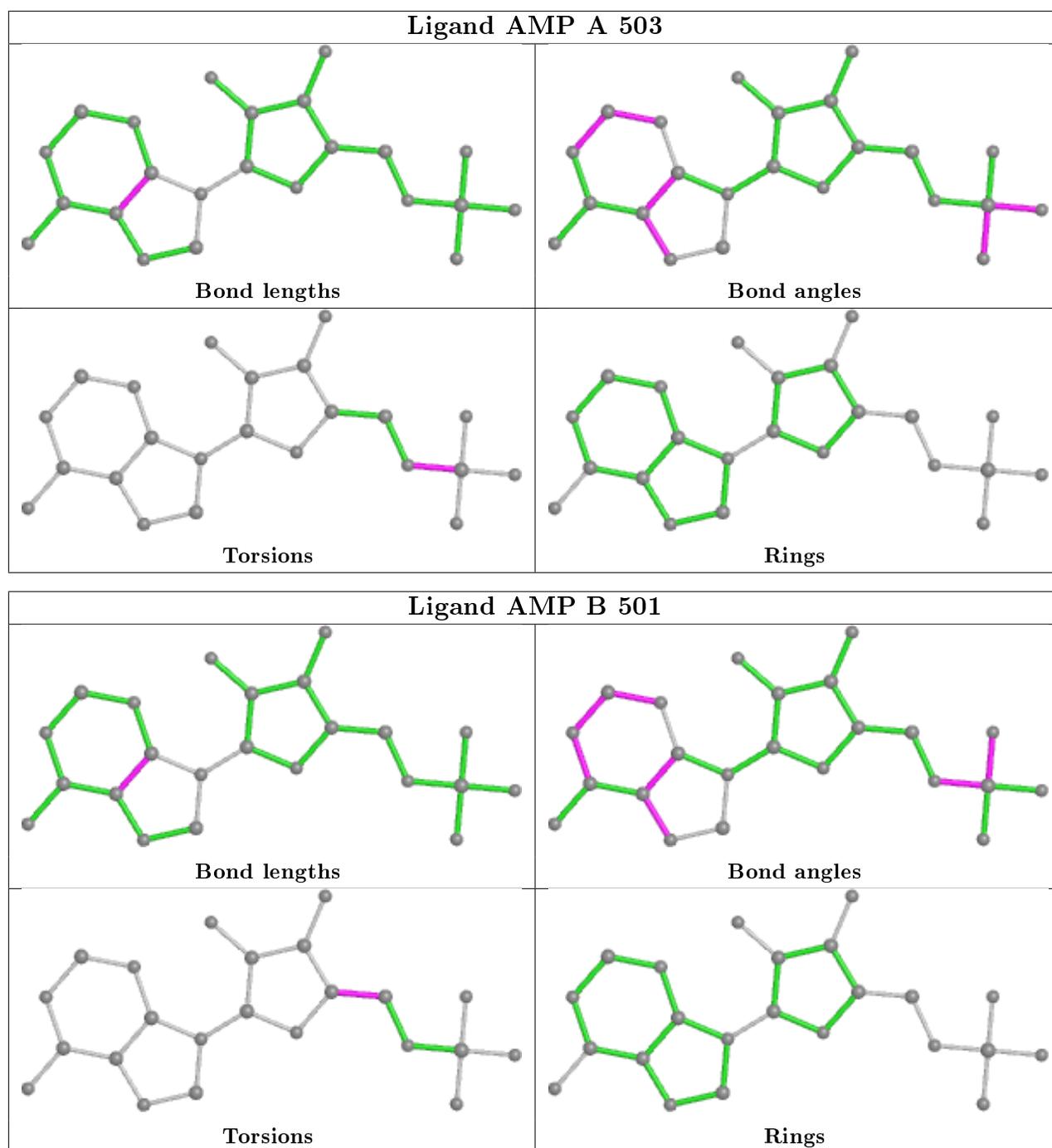
5.7 Other polymers (i)

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	315/393 (80%)	0.51	4 (1%)	77 78	37, 69, 122, 144	0
1	B	305/393 (77%)	0.78	25 (8%)	11 9	39, 74, 137, 161	0
All	All	620/786 (78%)	0.64	29 (4%)	31 30	37, 71, 134, 161	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	215	TYR	4.5
1	B	238	PHE	4.3
1	B	415	LEU	4.2
1	B	336	PHE	4.0
1	B	254	GLU	3.7
1	B	211	VAL	3.6
1	B	363	TYR	3.6
1	B	251	HIS	3.5
1	B	219	GLY	3.3
1	B	236	PRO	3.3
1	B	233	LYS	3.2
1	B	218	LYS	3.1
1	B	223	ALA	3.1
1	B	249	LYS	3.1
1	B	258	LYS	2.9
1	B	407	PHE	2.7
1	A	302	ALA	2.6
1	A	340	GLY	2.4
1	B	255	GLU	2.4
1	A	274	LEU	2.3
1	B	35	LEU	2.3
1	B	416	THR	2.3
1	B	179	LEU	2.2
1	B	413	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	230	GLU	2.2
1	B	406	ARG	2.2
1	A	249	LYS	2.1
1	B	231	LYS	2.1
1	B	235	LEU	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 monosaccharides 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
2	AMP	B	501	23/23	0.83	0.43	118,147,189,194	0
2	AMP	A	501	23/23	0.89	0.35	64,140,183,194	0
2	AMP	A	503	23/23	0.95	0.18	52,71,87,89	0
2	AMP	A	502	23/23	0.95	0.19	53,69,83,91	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 AMP B 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
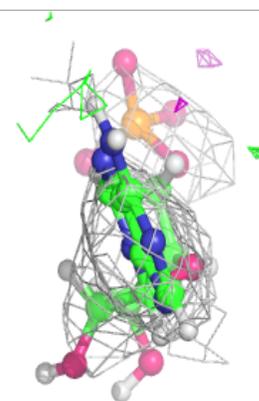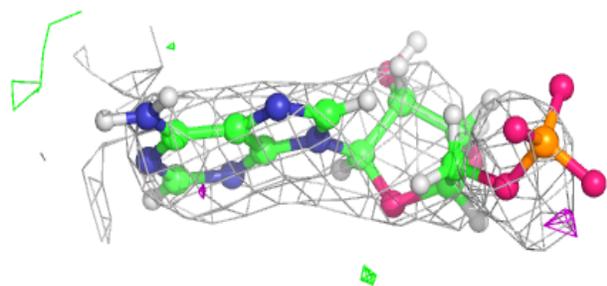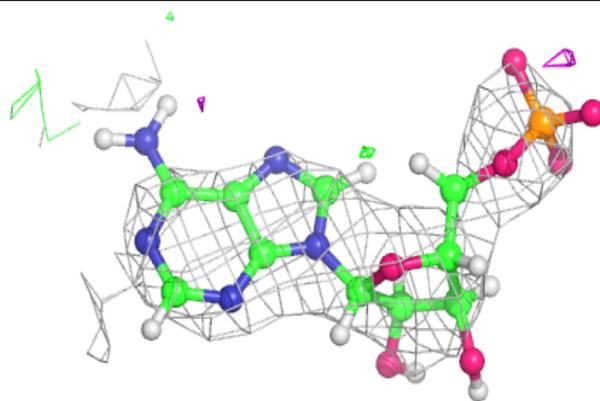
Electron density around AMP A 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
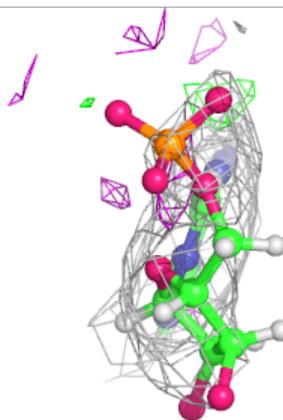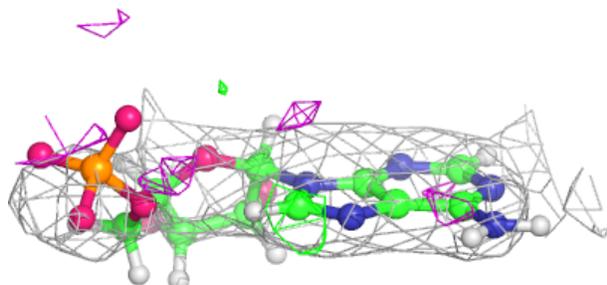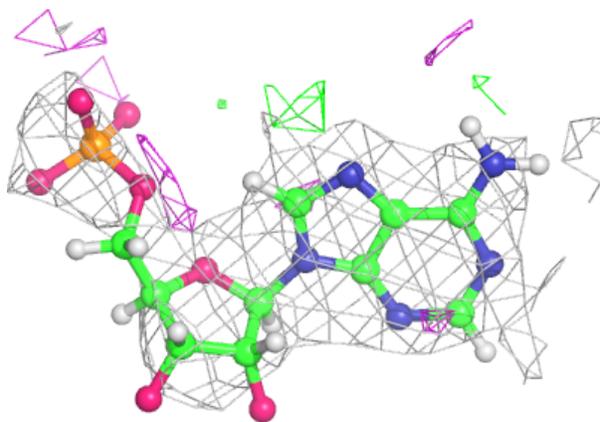
Electron density around AMP A 503:

$2mF_o$-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 502:

$2mF_o$-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.