Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 10:43 PM EDT

PDB ID	:	1CJA
Title	:	ACTIN-FRAGMIN KINASE, CATALYTIC DOMAIN FROM PHYSARUM POLYCEPHALUM
Authors	:	Steinbacher, S.; Hof, P.; Eichinger, L.; Schleicher, M.; Gettemans, J.; Vandekerckhove, J.; Huber, R.; Benz, J.
Deposited on	:	1999-04-08
Resolution	:	2.90 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 (i) 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 (1)) were used in the production of this report:

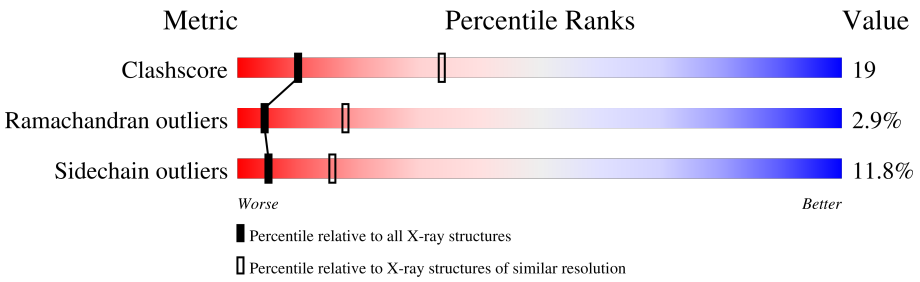
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.90 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	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	342	58% 31% 5% • •
1	B	342	56% 32% 6% • •

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	AMP	A	425	X	-	-	-
2	AMP	B	525	X	-	-	-

2 Entry composition (i)

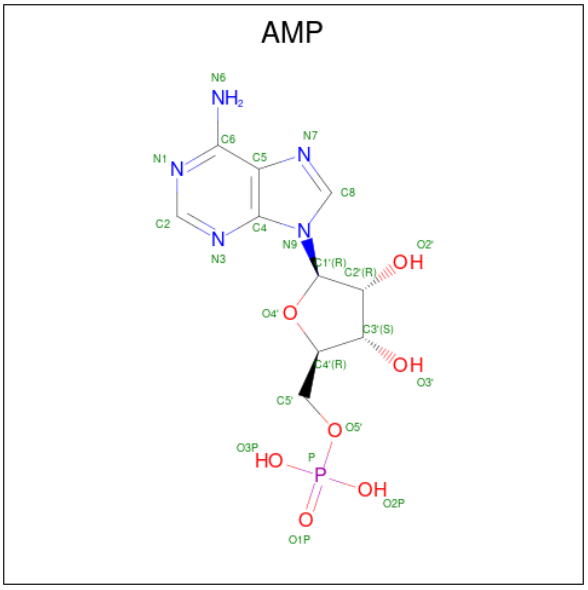
There are 2 unique types of molecules in this entry. The entry contains 6286 atoms, of which 1138 are hydrogens and 0 are deuteriums.

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 PROTEIN (ACTIN-FRAGMIN KINASE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	327	3120	1612	569	438	488	13	569	0	0
1	B	327	3120	1612	569	438	488	13	569	0	0

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	23	10	5	7	1	0	0
2	B	1	23	10	5	7	1	0	0

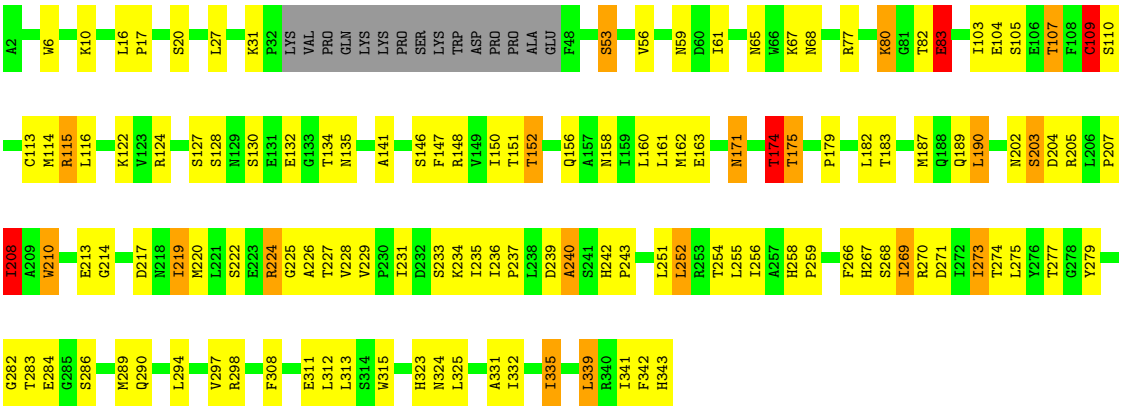
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

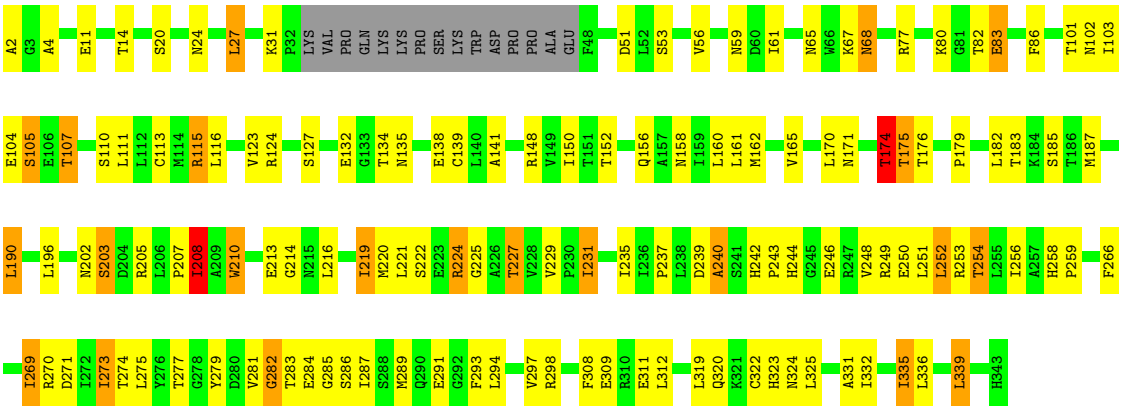
• Molecule 1: PROTEIN (ACTIN-FRAGMIN KINASE)

Chain A: 58% 31% 5% • •



• Molecule 1: PROTEIN (ACTIN-FRAGMIN KINASE)

Chain B: 56% 32% 6% • •



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	178.90Å 178.90Å 59.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 2.90	Depositor
% Data completeness (in resolution range)	90.8 (15.00-2.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.198 , 0.272	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6286	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

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	0.61	2/2596 (0.1%)	0.76	0/3516
1	B	0.50	0/2596	0.70	0/3516
All	All	0.56	2/5192 (0.0%)	0.73	0/7032

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	109	CYS	CB-SG	-5.41	1.73	1.81
1	A	113	CYS	CB-SG	-5.16	1.73	1.81

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	2551	569	2569	94	0
1	B	2551	569	2569	102	0
2	A	23	0	11	3	0
2	B	23	0	11	3	0
All	All	5148	1138	5160	196	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 19.

All (196) 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:273:ILE:O	1:B:277:THR:HG22	1.70	0.92
1:A:273:ILE:O	1:A:277:THR:HG22	1.70	0.92
1:B:115:ARG:HD2	1:B:308:PHE:HE1	1.37	0.89
1:A:207:PRO:HA	1:A:210:TRP:CD1	2.07	0.89
1:B:148:ARG:O	1:B:152:THR:HG22	1.72	0.89
1:A:148:ARG:O	1:A:152:THR:HG22	1.76	0.85
1:B:224:ARG:O	1:B:227:THR:HG22	1.77	0.85
1:B:82:THR:O	1:B:83:GLU:HB3	1.80	0.82
1:A:224:ARG:O	1:A:227:THR:HG22	1.80	0.81
1:B:312:LEU:HD23	1:B:332:ILE:HG23	1.63	0.81
1:A:82:THR:O	1:A:83:GLU:HB3	1.81	0.81
1:A:104:GLU:HG3	1:A:325:LEU:HG	1.64	0.80
1:B:104:GLU:HG3	1:B:325:LEU:HG	1.65	0.79
1:B:103:ILE:O	1:B:107:THR:HG23	1.87	0.75
1:A:103:ILE:O	1:A:107:THR:HG23	1.86	0.74
1:A:312:LEU:HB3	1:A:332:ILE:HD13	1.68	0.74
1:B:102:ASN:OD1	1:B:105:SER:HB2	1.88	0.73
1:A:82:THR:HG22	2:A:425:AMP:O3P	1.89	0.73
1:A:312:LEU:HD23	1:A:332:ILE:HG23	1.72	0.71
1:B:86:PHE:HZ	1:B:152:THR:HG21	1.56	0.71
1:B:207:PRO:HA	1:B:210:TRP:CD1	2.27	0.70
1:B:277:THR:HG23	1:B:279:TYR:H	1.56	0.69
1:B:335:ILE:HG13	1:B:336:LEU:N	2.08	0.69
1:A:286:SER:O	1:A:290:GLN:HG3	1.92	0.68
1:B:208:ILE:HD11	1:B:251:LEU:HD22	1.75	0.68
1:B:252:LEU:O	1:B:256:ILE:HG13	1.95	0.67
1:A:207:PRO:HA	1:A:210:TRP:HD1	1.56	0.66
1:A:266:PHE:HA	1:A:269:ILE:HG22	1.77	0.66
1:B:207:PRO:HA	1:B:210:TRP:HD1	1.61	0.66
1:A:297:VAL:HG22	1:A:342:PHE:CE2	2.31	0.66
1:B:127:SER:HA	1:B:158:ASN:ND2	2.10	0.66
1:B:270:ARG:NE	1:B:282:GLY:HA2	2.11	0.66
1:B:179:PRO:HG3	1:B:279:TYR:CE2	2.30	0.65
1:A:204:ASP:HB2	1:A:234:LYS:HE2	1.78	0.65
1:A:190:LEU:HD11	1:A:219:ILE:HD11	1.77	0.65
1:B:266:PHE:HA	1:B:269:ILE:HG22	1.79	0.64
1:B:242:HIS:HB3	1:B:243:PRO:HD2	1.79	0.64
1:B:269:ILE:HD12	1:B:289:MET:CE	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:PHE:O	1:B:297:VAL:HG23	1.98	0.64
1:A:127:SER:HA	1:A:158:ASN:ND2	2.15	0.62
1:A:162:MET:CE	2:A:425:AMP:HN61	2.12	0.62
1:B:67:LYS:HE3	1:B:135:ASN:HD21	1.65	0.62
1:B:115:ARG:HD2	1:B:308:PHE:CE1	2.26	0.61
1:B:116:LEU:HD12	1:B:196:LEU:HD13	1.81	0.61
1:A:297:VAL:HG13	1:A:342:PHE:CD2	2.35	0.61
1:B:220:MET:HB2	1:B:229:VAL:HG13	1.83	0.60
1:A:20:SER:HB2	1:A:225:GLY:HA3	1.83	0.60
1:A:269:ILE:C	1:A:269:ILE:HD13	2.21	0.59
1:B:182:LEU:HD22	1:B:187:MET:CE	2.31	0.59
1:A:127:SER:HA	1:A:158:ASN:HD22	1.67	0.59
1:B:244:HIS:O	1:B:248:VAL:HG12	2.01	0.59
1:B:269:ILE:HD12	1:B:289:MET:HE3	1.85	0.58
1:A:110:SER:O	1:A:114:MET:HG3	2.02	0.58
1:A:77:ARG:HH21	1:A:83:GLU:HG2	1.68	0.58
1:A:82:THR:HG23	1:A:83:GLU:H	1.70	0.57
1:B:141:ALA:HB2	1:B:150:ILE:HD11	1.87	0.57
1:B:319:LEU:HG	1:B:325:LEU:HB3	1.87	0.57
1:B:174:THR:HG23	1:B:175:THR:H	1.70	0.57
1:A:271:ASP:O	1:A:274:THR:HB	2.04	0.56
1:B:77:ARG:HH21	1:B:83:GLU:HG2	1.69	0.56
1:B:107:THR:HG22	1:B:160:LEU:HD11	1.86	0.56
1:A:277:THR:HG23	1:A:279:TYR:H	1.68	0.56
1:A:130:SER:O	1:A:134:THR:HG22	2.06	0.56
1:B:51:ASP:OD1	1:B:53:SER:HB3	2.06	0.56
1:A:208:ILE:HD11	1:A:251:LEU:HD22	1.88	0.55
1:A:220:MET:HG3	1:A:231:ILE:HD12	1.87	0.55
1:B:246:GLU:HA	1:B:249:ARG:HH11	1.72	0.55
1:A:269:ILE:HD13	1:A:269:ILE:O	2.07	0.55
1:B:256:ILE:O	1:B:259:PRO:HD3	2.07	0.55
1:B:24:ASN:HB3	1:B:27:LEU:HD22	1.89	0.55
1:B:162:MET:HE3	2:B:525:AMP:HN61	1.72	0.54
1:A:242:HIS:HB3	1:A:243:PRO:HD2	1.89	0.54
1:B:282:GLY:O	1:B:284:GLU:N	2.41	0.54
1:A:127:SER:OG	1:A:323:HIS:HD2	1.90	0.54
1:B:253:ARG:HA	1:B:256:ILE:HD12	1.89	0.54
1:B:323:HIS:O	1:B:325:LEU:N	2.41	0.53
1:A:67:LYS:HE3	1:A:135:ASN:HD21	1.72	0.53
1:B:103:ILE:HG13	1:B:160:LEU:HD13	1.90	0.53
1:A:27:LEU:HD23	1:A:222:SER:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:LEU:HD22	1:A:187:MET:CE	2.39	0.52
1:A:162:MET:HE3	2:A:425:AMP:HN61	1.73	0.52
1:B:134:THR:O	1:B:138:GLU:HG3	2.10	0.52
1:B:246:GLU:HA	1:B:249:ARG:NH1	2.24	0.52
1:A:252:LEU:O	1:A:256:ILE:HG13	2.09	0.52
1:B:269:ILE:C	1:B:269:ILE:HD13	2.30	0.52
1:A:141:ALA:HB2	1:A:150:ILE:HD11	1.90	0.51
1:A:146:SER:O	1:A:147:PHE:HB2	2.10	0.51
1:B:124:ARG:NH2	1:B:132:GLU:OE1	2.43	0.51
1:A:274:THR:HA	1:A:279:TYR:O	2.10	0.51
1:B:4:ALA:HB3	1:B:322:CYS:SG	2.50	0.51
1:A:335:ILE:HD12	1:A:339:LEU:HD22	1.93	0.51
1:B:222:SER:HB3	1:B:227:THR:HG23	1.93	0.51
1:A:174:THR:HG23	1:A:175:THR:H	1.76	0.51
1:A:266:PHE:HA	1:A:269:ILE:CG2	2.40	0.51
1:A:105:SER:O	1:A:109:CYS:HB2	2.11	0.50
1:A:323:HIS:O	1:A:325:LEU:N	2.45	0.50
1:B:82:THR:HG23	1:B:83:GLU:N	2.26	0.50
1:A:207:PRO:HD3	1:A:214:GLY:HA3	1.94	0.50
1:B:281:VAL:HG22	1:B:281:VAL:O	2.12	0.50
1:B:294:LEU:HB3	1:B:298:ARG:NH1	2.26	0.50
1:B:179:PRO:HG3	1:B:279:TYR:HE2	1.74	0.50
1:B:287:ILE:O	1:B:291:GLU:HG3	2.12	0.50
1:A:207:PRO:HD3	1:A:214:GLY:CA	2.42	0.49
1:A:82:THR:HG23	1:A:83:GLU:N	2.27	0.49
1:A:269:ILE:HD12	1:A:289:MET:HE3	1.92	0.49
1:A:171:ASN:HD21	1:A:217:ASP:HA	1.76	0.49
1:B:203:SER:HB3	1:B:210:TRP:CD2	2.48	0.49
1:A:124:ARG:NH2	1:A:132:GLU:OE1	2.45	0.49
1:B:309:GLU:HB2	1:B:336:LEU:HD21	1.94	0.49
1:B:335:ILE:HD12	1:B:339:LEU:CD2	2.43	0.49
1:B:82:THR:HG23	1:B:83:GLU:H	1.78	0.48
1:B:170:LEU:HD13	1:B:221:LEU:HD11	1.95	0.48
1:A:77:ARG:NH1	1:A:148:ARG:HD3	2.29	0.48
1:A:256:ILE:O	1:A:259:PRO:HD3	2.14	0.48
1:B:82:THR:HG22	2:B:525:AMP:O3P	2.14	0.47
1:A:282:GLY:O	1:A:284:GLU:N	2.47	0.47
1:A:312:LEU:HB3	1:A:332:ILE:CD1	2.42	0.47
1:B:207:PRO:HD3	1:B:214:GLY:HA3	1.96	0.47
1:B:2:ALA:N	1:B:323:HIS:CE1	2.83	0.47
1:B:289:MET:HB3	1:B:289:MET:HE2	1.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:CYS:SG	1:B:196:LEU:HD21	2.55	0.47
1:B:123:VAL:HG23	1:B:160:LEU:HG	1.97	0.47
1:B:250:GLU:O	1:B:254:THR:HG22	2.14	0.47
1:A:207:PRO:HA	1:A:210:TRP:NE1	2.30	0.47
1:B:190:LEU:HD11	1:B:219:ILE:HD11	1.97	0.47
1:A:189:GLN:NE2	1:A:228:VAL:H	2.12	0.47
1:A:252:LEU:HD12	1:A:252:LEU:HA	1.72	0.47
1:A:65:ASN:OD1	1:A:68:ASN:HB2	2.15	0.46
1:B:269:ILE:HD12	1:B:289:MET:HE1	1.97	0.46
1:A:67:LYS:HE3	1:A:135:ASN:ND2	2.31	0.46
1:A:31:LYS:HA	1:A:53:SER:HB2	1.98	0.46
1:A:103:ILE:HG13	1:A:160:LEU:HD13	1.97	0.45
1:A:203:SER:HB3	1:A:210:TRP:CD2	2.52	0.45
1:B:65:ASN:OD1	1:B:68:ASN:HB2	2.17	0.45
1:B:67:LYS:HE3	1:B:135:ASN:ND2	2.30	0.45
1:A:268:SER:O	1:A:271:ASP:HB2	2.17	0.45
1:B:150:ILE:HD13	1:B:150:ILE:HA	1.82	0.45
1:A:341:ILE:C	1:A:343:HIS:H	2.20	0.45
1:B:239:ASP:O	1:B:240:ALA:HB3	2.16	0.45
1:B:127:SER:OG	1:B:323:HIS:HD2	1.99	0.45
1:A:115:ARG:NH1	1:A:311:GLU:OE1	2.49	0.45
1:B:170:LEU:CD1	1:B:221:LEU:HD11	2.47	0.45
1:B:170:LEU:HD23	1:B:216:LEU:HD23	1.98	0.45
1:B:161:LEU:HA	1:B:161:LEU:HD23	1.60	0.45
1:A:308:PHE:HE2	1:A:335:ILE:HD11	1.82	0.44
1:B:124:ARG:HH22	1:B:132:GLU:CD	2.21	0.44
1:A:148:ARG:O	1:A:152:THR:CG2	2.58	0.44
1:A:124:ARG:HH22	1:A:132:GLU:CD	2.21	0.44
1:B:116:LEU:HD23	1:B:116:LEU:HA	1.80	0.44
1:B:269:ILE:O	1:B:273:ILE:HG22	2.18	0.44
1:B:256:ILE:HG13	1:B:256:ILE:H	1.64	0.44
1:B:312:LEU:HD21	1:B:335:ILE:CD1	2.48	0.44
1:A:109:CYS:HB3	1:A:233:SER:HB2	2.00	0.44
1:A:122:LYS:HE3	1:A:122:LYS:HB2	1.82	0.44
1:A:315:TRP:CD1	1:A:315:TRP:N	2.84	0.43
1:B:235:ILE:HG22	1:B:237:PRO:HD3	2.00	0.43
1:A:190:LEU:HD13	1:A:228:VAL:HG21	2.00	0.43
1:B:271:ASP:O	1:B:274:THR:HB	2.18	0.43
1:B:207:PRO:HD3	1:B:214:GLY:CA	2.48	0.43
1:B:281:VAL:HG22	1:B:285:GLY:HA3	2.00	0.43
1:A:331:ALA:O	1:A:335:ILE:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:PRO:HG3	1:A:279:TYR:CE2	2.54	0.43
1:B:110:SER:O	1:B:113:CYS:HB2	2.19	0.43
1:A:6:TRP:NE1	1:A:10:LYS:HE3	2.33	0.43
1:B:162:MET:CE	2:B:525:AMP:HN61	2.31	0.43
1:B:11:GLU:O	1:B:14:THR:HB	2.18	0.43
1:B:269:ILE:HD13	1:B:269:ILE:O	2.19	0.43
1:A:161:LEU:HD23	1:A:161:LEU:HA	1.79	0.43
1:B:31:LYS:HG3	1:B:51:ASP:OD1	2.19	0.42
1:B:20:SER:HB2	1:B:225:GLY:HA3	2.01	0.42
1:B:61:ILE:O	1:B:124:ARG:NH1	2.52	0.42
1:A:269:ILE:HD12	1:A:289:MET:CE	2.48	0.42
1:A:236:ILE:HA	1:A:237:PRO:HD2	1.88	0.42
1:A:267:HIS:O	1:A:270:ARG:HB3	2.20	0.42
1:A:80:LYS:N	1:A:80:LYS:HD2	2.35	0.42
1:A:289:MET:HE2	1:A:289:MET:HB3	1.53	0.42
1:B:220:MET:SD	1:B:231:ILE:HD12	2.60	0.42
1:B:165:VAL:HG11	1:B:229:VAL:HG11	2.02	0.41
1:B:113:CYS:SG	1:B:196:LEU:CD2	3.08	0.41
1:A:16:LEU:HA	1:A:17:PRO:HD3	1.78	0.41
1:A:313:LEU:HD23	1:A:313:LEU:HA	1.94	0.41
1:A:275:LEU:C	1:A:275:LEU:HD13	2.41	0.41
1:A:294:LEU:HD13	1:A:298:ARG:HH12	1.86	0.41
1:B:339:LEU:HD13	1:B:339:LEU:HA	1.81	0.41
1:A:27:LEU:CD2	1:A:226:ALA:HA	2.51	0.41
1:A:109:CYS:SG	1:A:235:ILE:CG1	3.09	0.41
1:A:222:SER:HB3	1:A:227:THR:HG23	2.02	0.41
1:B:107:THR:O	1:B:111:LEU:HG	2.20	0.41
1:A:239:ASP:O	1:A:240:ALA:HB3	2.21	0.41
1:A:61:ILE:O	1:A:124:ARG:NH1	2.53	0.40
1:A:116:LEU:HD23	1:A:116:LEU:HA	1.73	0.40
1:B:175:THR:HG23	1:B:176:THR:N	2.36	0.40
1:B:175:THR:O	1:B:179:PRO:HD3	2.21	0.40
1:A:77:ARG:HH12	1:A:148:ARG:HD3	1.85	0.40
1:B:127:SER:HA	1:B:158:ASN:HD22	1.84	0.40
1:B:242:HIS:CB	1:B:243:PRO:HD2	2.45	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	323/342 (94%)	294 (91%)	21 (6%)	8 (2%)	5 21
1	B	323/342 (94%)	286 (88%)	26 (8%)	11 (3%)	3 15
All	All	646/684 (94%)	580 (90%)	47 (7%)	19 (3%)	4 18

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	175	THR
1	A	283	THR
1	B	175	THR
1	B	282	GLY
1	B	283	THR
1	A	83	GLU
1	A	205	ARG
1	A	208	ILE
1	A	224	ARG
1	A	240	ALA
1	B	83	GLU
1	B	174	THR
1	B	205	ARG
1	B	224	ARG
1	B	240	ALA
1	B	331	ALA
1	A	174	THR
1	B	185	SER
1	B	208	ILE

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	288/302 (95%)	255 (88%)	33 (12%)	5 17
1	B	288/302 (95%)	253 (88%)	35 (12%)	5 15
All	All	576/604 (95%)	508 (88%)	68 (12%)	5 16

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	SER
1	A	56	VAL
1	A	59	ASN
1	A	80	LYS
1	A	83	GLU
1	A	107	THR
1	A	109	CYS
1	A	115	ARG
1	A	128	SER
1	A	151	THR
1	A	152	THR
1	A	156	GLN
1	A	163	GLU
1	A	171	ASN
1	A	174	THR
1	A	183	THR
1	A	190	LEU
1	A	202	ASN
1	A	203	SER
1	A	208	ILE
1	A	210	TRP
1	A	213	GLU
1	A	219	ILE
1	A	229	VAL
1	A	252	LEU
1	A	254	THR
1	A	255	LEU
1	A	258	HIS
1	A	269	ILE
1	A	273	ILE
1	A	324	ASN
1	A	335	ILE
1	A	339	LEU

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Mol	Chain	Res	Type
1	B	27	LEU
1	B	56	VAL
1	B	59	ASN
1	B	68	ASN
1	B	80	LYS
1	B	101	THR
1	B	105	SER
1	B	107	THR
1	B	115	ARG
1	B	139	CYS
1	B	156	GLN
1	B	171	ASN
1	B	174	THR
1	B	183	THR
1	B	190	LEU
1	B	202	ASN
1	B	203	SER
1	B	208	ILE
1	B	210	TRP
1	B	213	GLU
1	B	219	ILE
1	B	227	THR
1	B	231	ILE
1	B	252	LEU
1	B	254	THR
1	B	258	HIS
1	B	269	ILE
1	B	273	ILE
1	B	275	LEU
1	B	286	SER
1	B	311	GLU
1	B	320	GLN
1	B	324	ASN
1	B	335	ILE
1	B	339	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	70	GLN
1	A	129	ASN

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Mol	Chain	Res	Type
1	A	135	ASN
1	A	155	ASN
1	A	156	GLN
1	A	158	ASN
1	A	189	GLN
1	A	201	ASN
1	A	202	ASN
1	A	218	ASN
1	A	242	HIS
1	A	320	GLN
1	A	323	HIS
1	A	324	ASN
1	B	59	ASN
1	B	68	ASN
1	B	70	GLN
1	B	129	ASN
1	B	135	ASN
1	B	155	ASN
1	B	158	ASN
1	B	201	ASN
1	B	202	ASN
1	B	218	ASN
1	B	242	HIS
1	B	316	GLN
1	B	320	GLN
1	B	323	HIS
1	B	324	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	425	-	21,25,25	1.49	6 (28%)	23,38,38	3.41	5 (21%)
2	AMP	B	525	-	21,25,25	1.56	6 (28%)	23,38,38	3.52	6 (26%)

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	425	-	1/1/5/5	0/6/26/26	0/3/3/3
2	AMP	B	525	-	1/1/5/5	0/6/26/26	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	525	AMP	C1'-N9	-3.33	1.41	1.49
2	A	425	AMP	C1'-N9	-2.90	1.42	1.49
2	B	525	AMP	C8-N7	-2.59	1.30	1.34
2	A	425	AMP	P-O5'	-2.57	1.52	1.60
2	B	525	AMP	C3'-C4'	2.54	1.59	1.53
2	B	525	AMP	O5'-C5'	2.45	1.53	1.44
2	B	525	AMP	C2'-C3'	-2.45	1.46	1.53
2	A	425	AMP	O5'-C5'	2.33	1.53	1.44
2	B	525	AMP	P-O5'	-2.32	1.53	1.60
2	A	425	AMP	C2'-C3'	-2.23	1.47	1.53
2	A	425	AMP	C8-N7	-2.23	1.30	1.34
2	A	425	AMP	P-O2P	-2.04	1.47	1.54

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	525	AMP	O4'-C1'-N9	12.28	125.03	108.75
2	A	425	AMP	O4'-C1'-N9	12.13	124.83	108.75
2	B	525	AMP	C4'-O4'-C1'	-9.49	101.23	109.92
2	A	425	AMP	C4'-O4'-C1'	-9.05	101.64	109.92
2	B	525	AMP	O3P-P-O2P	-2.46	98.58	107.80
2	A	425	AMP	O3P-P-O2P	-2.45	98.60	107.80
2	B	525	AMP	O3'-C3'-C4'	2.29	117.66	111.08
2	B	525	AMP	O3P-P-O1P	2.19	119.36	110.83
2	B	525	AMP	C1'-N9-C4	-2.18	122.81	126.64
2	A	425	AMP	O3P-P-O1P	2.14	119.16	110.83
2	A	425	AMP	O3'-C3'-C4'	2.08	117.06	111.08

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	425	AMP	C1'
2	B	525	AMP	C1'

There are no torsion outliers.

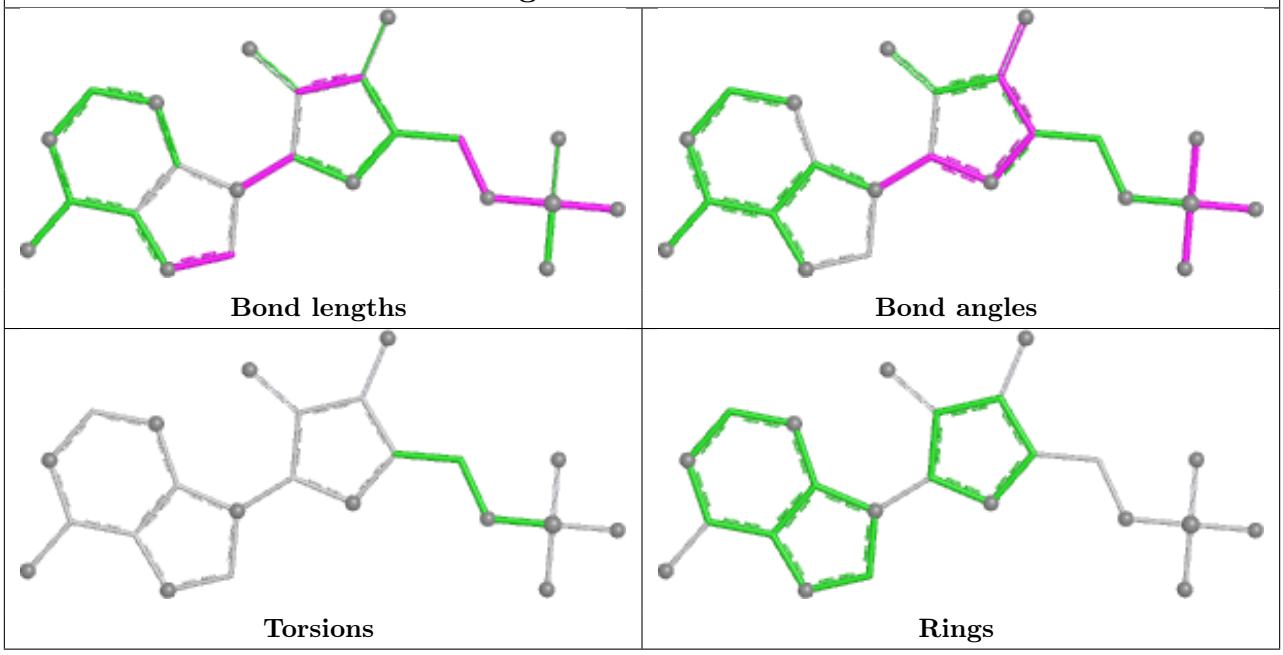
There are no ring outliers.

2 monomers are involved in 6 short contacts:

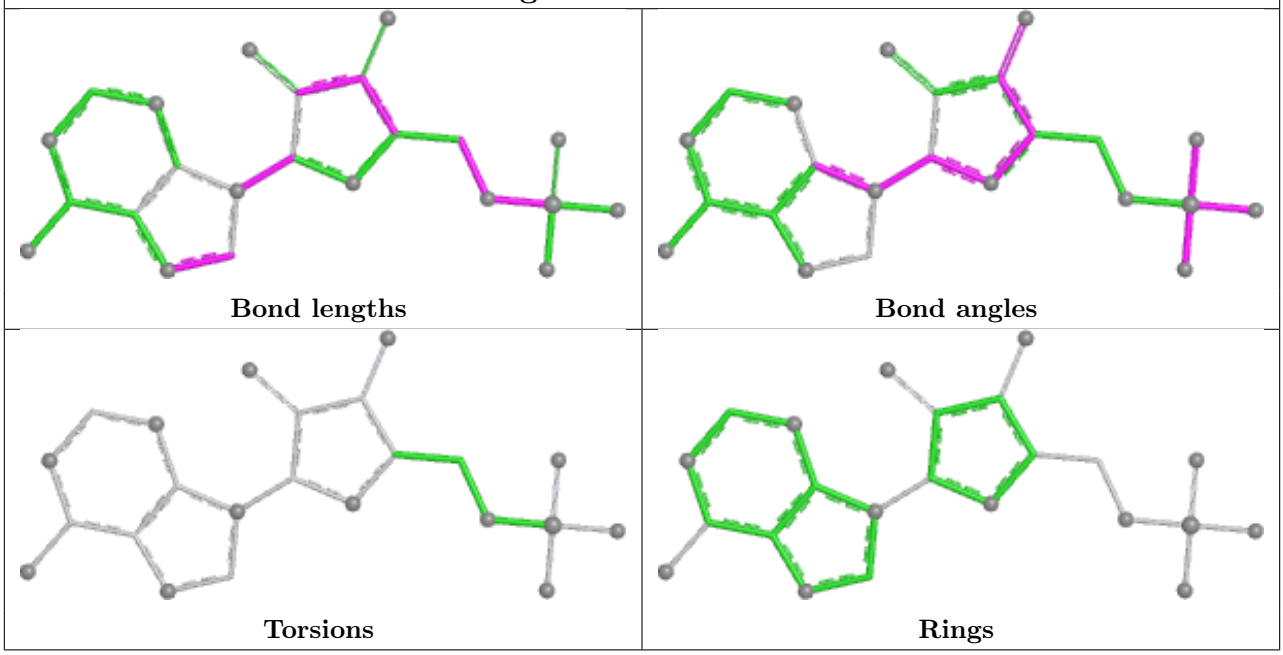
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	425	AMP	3	0
2	B	525	AMP	3	0

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 425



Ligand AMP B 525



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.