



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 15, 2023 – 02:13 PM JST

PDB ID : 6JBK
Title : Crystal structure of an actin monomer in complex with the nucleator Cordon-Bleu WH2-motif peptide mutant. T22V
Authors : Scipion, C.P.M.; Robinson, R.C.
Deposited on : 2019-01-25
Resolution : 2.45 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

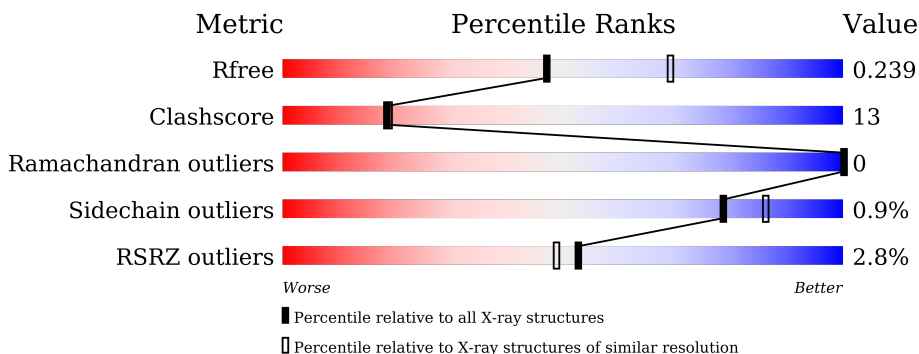
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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.



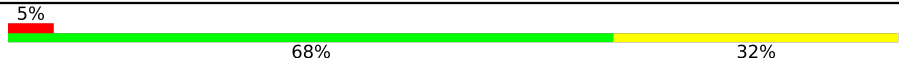

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	377	 1% 74% 20% 6%
1	C	377	 2% 74% 19% 6%
1	E	377	 3% 68% 25% 6%
1	G	377	 4% 73% 20% 6%
2	B	22	 9% 50% 45% 5%
2	D	22	 5% 55% 45% 5%

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Mol	Chain	Length	Quality of chain
2	F	22	 5% 68% 32%
2	H	22	 9% 68% 32%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12365 atoms, of which 88 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	353	2795	1750	38	459	530	18	0	0	0
1	C	353	2782	1750	25	459	530	18	0	0	0
1	E	353	2782	1750	25	459	530	18	0	0	0
1	G	353	2757	1750	459	530	18		0	0	0

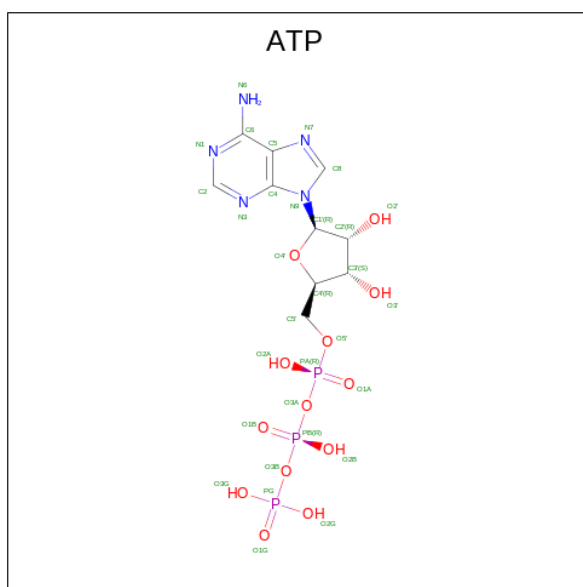
- Molecule 2 is a protein called Peptide from Protein cordon-bleu.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	22	168	102	34	31	1	0	0	0
2	D	22	168	102	34	31	1	0	0	0
2	F	22	168	102	34	31	1	0	0	0
2	H	22	168	102	34	31	1	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	87	VAL	THR	engineered mutation	UNP Q5NBX1
D	87	VAL	THR	engineered mutation	UNP Q5NBX1
F	87	VAL	THR	engineered mutation	UNP Q5NBX1
H	87	VAL	THR	engineered mutation	UNP Q5NBX1

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Ca 2	0	0
4	C	2	Total Ca 2	0	0
4	E	2	Total Ca 2	0	0
4	G	2	Total Ca 2	0	0

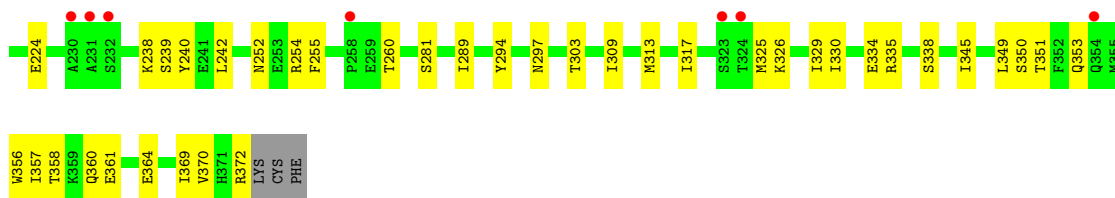
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	99	Total O 99	0	0

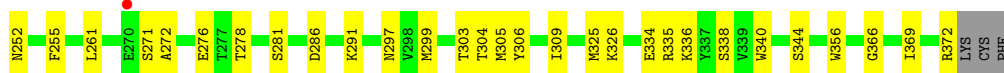
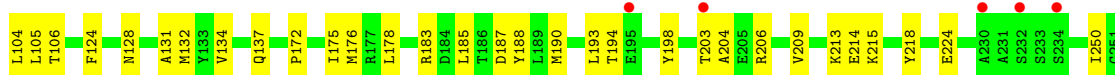
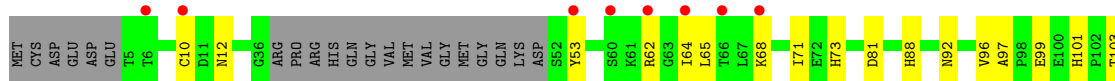
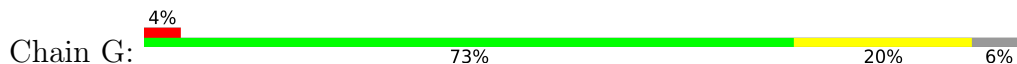
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	3	Total O 3 3	0	0
5	C	135	Total O 135 135	0	0
5	D	2	Total O 2 2	0	0
5	E	113	Total O 113 113	0	0
5	F	1	Total O 1 1	0	0
5	G	87	Total O 87 87	0	0
5	H	5	Total O 5 5	0	0



- Molecule 1: Actin, alpha skeletal muscle



- Molecule 2: Peptide from Protein cordon-bleu



- Molecule 2: Peptide from Protein cordon-bleu



- Molecule 2: Peptide from Protein cordon-bleu



- Molecule 2: Peptide from Protein cordon-bleu



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.22Å 81.19Å 89.87Å 90.62° 107.19° 109.63°	Depositor
Resolution (Å)	19.96 – 2.45 19.96 – 2.45	Depositor EDS
% Data completeness (in resolution range)	91.3 (19.96-2.45) 91.5 (19.96-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.44Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.187 , 0.239 0.187 , 0.239	Depositor DCC
R_{free} test set	2476 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtrriage
Anisotropy	0.049	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.000 for h,-h-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12365	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.09 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3509e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HIC, ATP, CA

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	0.33	0/2803	0.56	0/3800
1	C	0.33	0/2803	0.57	0/3800
1	E	0.32	0/2803	0.55	0/3800
1	G	0.32	0/2803	0.55	0/3800
2	B	0.32	0/169	0.51	0/221
2	D	0.30	0/169	0.53	0/221
2	F	0.31	0/169	0.51	0/221
2	H	0.30	0/169	0.47	0/221
All	All	0.32	0/11888	0.55	0/16084

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	2757	38	2726	64	0
1	C	2757	25	2726	77	0
1	E	2757	25	2726	78	0
1	G	2757	0	2726	63	0
2	B	168	0	175	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	168	0	175	24	0
2	F	168	0	175	15	0
2	H	168	0	175	5	0
3	A	31	0	12	2	0
3	C	31	0	12	2	0
3	E	31	0	12	0	0
3	G	31	0	12	1	0
4	A	2	0	0	0	0
4	C	2	0	0	0	0
4	E	2	0	0	0	0
4	G	2	0	0	0	0
5	A	99	0	0	10	0
5	B	3	0	0	1	0
5	C	135	0	0	10	0
5	D	2	0	0	1	0
5	E	113	0	0	5	0
5	F	1	0	0	0	0
5	G	87	0	0	8	0
5	H	5	0	0	0	0
All	All	12277	88	11652	310	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 13.

All (310) 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:119:MET:SD	5:A:595:HOH:O	2.24	0.94
1:E:216:LEU:HD22	1:E:238:LYS:HG2	1.52	0.92
1:E:194:THR:HG22	1:E:199:SER:HA	1.53	0.90
1:A:24:ASP:OD1	2:B:85:ARG:NH1	2.05	0.90
1:G:187:ASP:OD1	1:G:206:ARG:NH2	2.04	0.89
1:E:194:THR:HA	1:E:198:TYR:O	1.72	0.89
1:C:341:ILE:HD13	2:D:81:ARG:HD2	1.55	0.87
1:C:148:THR:HB	2:D:72:MET:CE	2.04	0.87
1:G:278:THR:HG21	1:G:297:ASN:HD21	1.38	0.87
1:A:222:ASP:OD2	1:A:225:ASN:ND2	2.07	0.86
1:C:193:LEU:HD21	1:C:250:ILE:HG21	1.58	0.86
1:C:270:GLU:OE2	5:C:501:HOH:O	1.95	0.85
1:G:81:ASP:OD2	5:G:501:HOH:O	1.95	0.84
1:A:194:THR:HA	1:A:198:TYR:O	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:67:LEU:HD13	2:F:67:LEU:HD22	1.60	0.83
1:E:239:SER:O	5:E:501:HOH:O	1.97	0.82
2:H:81:ARG:HA	2:H:84:LEU:HD12	1.61	0.82
1:C:276:GLU:OE2	5:C:502:HOH:O	1.95	0.82
1:C:118:LYS:NZ	5:C:506:HOH:O	2.13	0.81
1:C:190:MET:HE1	1:C:206:ARG:HG3	1.60	0.81
1:G:68:LYS:HB2	5:G:501:HOH:O	1.81	0.81
1:E:187:ASP:OD1	1:E:206:ARG:NH1	2.13	0.80
1:E:335:ARG:HA	1:E:338:SER:OG	1.80	0.79
1:G:183:ARG:HG3	1:G:206:ARG:HH11	1.48	0.79
1:A:341:ILE:HD13	2:B:81:ARG:HD2	1.62	0.79
1:E:325:MET:HA	1:E:325:MET:HE3	1.65	0.79
1:G:188:TYR:OH	5:G:502:HOH:O	2.00	0.79
1:A:288:ASP:OD1	5:A:501:HOH:O	2.01	0.78
1:C:148:THR:HB	2:D:72:MET:HE3	1.66	0.78
2:B:80:GLY:O	5:B:101:HOH:O	2.04	0.74
1:E:183:ARG:HG3	1:E:206:ARG:HH22	1.51	0.74
2:D:74:ALA:O	2:D:78:SER:HB3	1.87	0.74
1:C:295:ALA:HB2	1:C:326:LYS:HE3	1.70	0.74
1:C:372:ARG:HD2	1:C:372:ARG:O	1.87	0.74
1:G:62:ARG:NH2	1:G:204:ALA:HB2	2.04	0.72
1:C:65:LEU:O	5:C:504:HOH:O	2.07	0.71
1:C:148:THR:HB	2:D:72:MET:HE1	1.71	0.71
1:C:372:ARG:NH1	5:C:503:HOH:O	2.02	0.71
1:C:190:MET:CE	1:C:206:ARG:HG3	2.20	0.71
1:C:352:PHE:HA	1:C:355:MET:CE	2.22	0.70
1:G:299:MET:HE3	1:G:304:THR:HB	1.76	0.68
1:G:185:LEU:HD11	1:G:261:LEU:HD21	1.76	0.68
1:C:57:GLU:OE1	5:C:505:HOH:O	2.11	0.67
1:C:335:ARG:HA	1:C:338:SER:OG	1.95	0.67
1:C:352:PHE:HA	1:C:355:MET:HE3	1.75	0.67
1:G:99:GLU:HG3	5:G:506:HOH:O	1.94	0.67
1:A:187:ASP:OD1	1:A:206:ARG:NH1	2.26	0.67
1:G:132:MET:HE1	1:G:134:VAL:HG23	1.75	0.67
1:E:121:GLN:OE1	5:E:502:HOH:O	2.12	0.66
1:E:369:ILE:HD11	1:E:372:ARG:HD2	1.76	0.66
1:E:216:LEU:CD2	1:E:238:LYS:HG2	2.25	0.66
2:D:67:LEU:CD2	2:F:67:LEU:HD13	2.26	0.66
1:E:62:ARG:HD2	1:E:62:ARG:O	1.95	0.66
1:G:299:MET:HE1	1:G:309:ILE:HG23	1.77	0.65
1:C:194:THR:HA	1:C:198:TYR:O	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:252:ASN:HA	1:E:255:PHE:CE2	2.31	0.65
1:C:106:THR:HB	1:C:137:GLN:HG3	1.79	0.65
1:E:62:ARG:NH1	1:E:65:LEU:O	2.31	0.64
1:C:196:ARG:HD2	1:C:253:GLU:OE2	1.96	0.64
2:D:81:ARG:HA	2:D:84:LEU:HD12	1.78	0.64
1:E:132:MET:CE	1:E:134:VAL:HG23	2.28	0.64
1:G:194:THR:HA	1:G:198:TYR:O	1.97	0.63
1:E:132:MET:HE3	1:E:134:VAL:HG23	1.80	0.63
1:A:105:LEU:HB3	1:A:119:MET:HE1	1.78	0.63
1:G:183:ARG:HG3	1:G:206:ARG:NH1	2.13	0.63
1:G:335:ARG:HA	1:G:338:SER:OG	1.99	0.63
1:A:335:ARG:HA	1:A:338:SER:OG	1.98	0.63
1:C:372:ARG:O	5:C:507:HOH:O	2.16	0.63
1:E:216:LEU:O	1:E:254:ARG:HD2	1.99	0.63
1:A:132:MET:HE1	1:A:134:VAL:HG23	1.79	0.63
1:C:366:GLY:O	1:C:369:ILE:HG22	1.98	0.63
1:C:124:PHE:CE2	1:C:132:MET:HG2	2.33	0.62
1:G:88:HIS:HA	1:G:92:ASN:OD1	2.01	0.61
2:F:81:ARG:HA	2:F:84:LEU:HD12	1.81	0.61
1:E:5:THR:HG22	1:E:5:THR:O	2.00	0.61
1:A:5:THR:O	1:A:5:THR:HG22	2.01	0.60
1:E:5:THR:HG23	1:E:100:GLU:O	2.01	0.60
1:A:124:PHE:CE2	1:A:132:MET:HG2	2.37	0.60
1:E:196:ARG:O	1:E:196:ARG:HG2	2.01	0.60
1:E:208:ILE:HG21	1:E:242:LEU:HD22	1.84	0.60
1:E:196:ARG:HD3	5:E:547:HOH:O	2.02	0.59
1:E:219:VAL:HG21	1:E:309:ILE:CD1	2.31	0.59
1:C:62:ARG:CD	1:C:203:THR:HG21	2.32	0.58
1:C:180:LEU:HD13	1:C:267:ILE:HD11	1.86	0.58
1:E:358:THR:OG1	1:E:361:GLU:HG3	2.03	0.58
1:A:252:ASN:HA	1:A:255:PHE:CE2	2.38	0.58
1:G:124:PHE:CE2	1:G:132:MET:HG2	2.38	0.58
1:G:299:MET:HE1	1:G:309:ILE:CG2	2.33	0.58
1:A:242:LEU:O	5:A:502:HOH:O	2.17	0.58
1:C:167:GLU:CA	2:D:72:MET:HE2	2.34	0.58
1:G:366:GLY:O	1:G:369:ILE:HG22	2.04	0.58
1:A:272:ALA:HB1	1:A:276:GLU:OE2	2.04	0.57
1:E:183:ARG:HG3	1:E:206:ARG:NH2	2.16	0.57
1:A:106:THR:HB	1:A:137:GLN:HG3	1.87	0.57
2:D:67:LEU:HD23	2:D:67:LEU:N	2.20	0.57
1:E:369:ILE:CD1	1:E:372:ARG:HD2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:GLU:O	1:A:209:VAL:HG23	2.05	0.56
1:G:224:GLU:HB3	5:G:522:HOH:O	2.04	0.56
1:A:291:LYS:HD2	1:A:325:MET:SD	2.46	0.56
2:B:78:SER:O	2:B:83:LYS:HG3	2.06	0.56
1:A:180:LEU:HD11	1:A:260:THR:HG22	1.88	0.55
2:D:67:LEU:HD22	2:F:67:LEU:HD13	1.88	0.55
1:G:278:THR:CG2	1:G:297:ASN:HD21	2.15	0.55
2:H:81:ARG:HA	2:H:84:LEU:CD1	2.32	0.55
1:C:204:ALA:O	1:C:208:ILE:HG12	2.07	0.55
1:C:303:THR:HG22	1:C:303:THR:O	2.06	0.55
1:G:190:MET:HG2	1:G:209:VAL:HG21	1.87	0.55
1:G:305:MET:SD	1:G:336:LYS:HG3	2.47	0.55
1:A:299:MET:CE	1:A:309:ILE:HG23	2.37	0.54
1:C:314:GLN:OE1	5:C:508:HOH:O	2.18	0.54
2:D:67:LEU:HD21	2:F:67:LEU:HD13	1.90	0.54
2:D:67:LEU:CD1	2:F:67:LEU:HD22	2.34	0.54
1:G:132:MET:HE1	1:G:134:VAL:CG2	2.37	0.54
1:E:211:ASP:O	1:E:215:LYS:HG2	2.07	0.54
1:E:219:VAL:HG21	1:E:309:ILE:HD12	1.90	0.54
1:A:187:ASP:OD1	1:A:206:ARG:NH2	2.39	0.54
1:A:132:MET:CE	1:A:134:VAL:HG23	2.38	0.54
2:B:81:ARG:HA	2:B:84:LEU:HD12	1.90	0.54
1:E:351:THR:HG23	2:F:71:LEU:CD1	2.38	0.53
2:F:67:LEU:HD23	2:F:68:HIS:H	1.73	0.53
1:C:190:MET:HE1	1:C:206:ARG:CG	2.36	0.53
1:E:190:MET:HG2	1:E:209:VAL:HG21	1.91	0.53
1:A:366:GLY:O	1:A:369:ILE:HG22	2.09	0.53
1:G:291:LYS:HB2	5:G:538:HOH:O	2.09	0.53
1:G:104:LEU:HD23	1:G:104:LEU:C	2.29	0.52
1:A:53:TYR:CD2	1:A:65:LEU:HD11	2.44	0.52
1:A:128:ASN:OD1	1:A:359:LYS:NZ	2.29	0.52
1:G:193:LEU:HD21	1:G:250:ILE:HG21	1.92	0.52
1:E:88:HIS:HA	1:E:92:ASN:ND2	2.26	0.51
1:A:213:LYS:HD2	1:A:306:TYR:OH	2.10	0.51
1:C:340:TRP:CZ3	1:C:344:SER:HB2	2.45	0.51
1:E:132:MET:HG2	1:E:133:TYR:N	2.25	0.51
1:C:352:PHE:HA	1:C:355:MET:HE2	1.92	0.51
2:F:67:LEU:HG	2:F:68:HIS:N	2.25	0.51
2:B:74:ALA:O	2:B:78:SER:HB3	2.11	0.51
1:G:303:THR:HG22	1:G:303:THR:O	2.10	0.51
1:C:148:THR:CB	2:D:72:MET:HE3	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:82:GLU:HG3	1:C:267:ILE:HB	1.92	0.51
1:C:299:MET:HE1	1:C:309:ILE:HG23	1.92	0.51
2:F:67:LEU:HD23	2:F:67:LEU:N	2.26	0.51
1:E:123:MET:O	1:E:129:VAL:HG22	2.11	0.51
1:G:99:GLU:OE2	1:G:128:ASN:ND2	2.44	0.51
1:G:99:GLU:HG2	1:G:99:GLU:O	2.10	0.51
1:G:176:MET:HE2	1:G:176:MET:HA	1.92	0.51
1:C:132:MET:HE1	1:C:134:VAL:HG23	1.92	0.50
1:C:252:ASN:HA	1:C:255:PHE:CE2	2.47	0.50
1:E:193:LEU:HD13	1:E:200:PHE:CE2	2.46	0.50
1:E:351:THR:HG21	2:F:71:LEU:HA	1.93	0.50
1:G:132:MET:CE	1:G:134:VAL:HG23	2.39	0.50
1:A:24:ASP:OD2	1:A:28:ARG:NH1	2.45	0.50
1:A:372:ARG:NH1	1:G:372:ARG:HE	2.09	0.50
1:C:291:LYS:NZ	1:C:326:LYS:H	2.10	0.50
1:A:161:HIS:HD2	5:A:596:HOH:O	1.94	0.50
1:C:193:LEU:HD21	1:C:250:ILE:CG2	2.37	0.50
1:E:334:GLU:OE1	1:E:334:GLU:N	2.42	0.50
1:E:205:GLU:O	1:E:209:VAL:HG23	2.11	0.49
1:C:272:ALA:HB1	1:C:276:GLU:OE2	2.12	0.49
1:A:303:THR:O	1:A:303:THR:HG22	2.12	0.49
1:E:349:LEU:O	1:E:353:GLN:NE2	2.34	0.49
1:G:291:LYS:HE2	1:G:325:MET:SD	2.53	0.49
1:A:291:LYS:NZ	1:A:326:LYS:H	2.11	0.49
1:C:291:LYS:HD2	1:C:325:MET:SD	2.52	0.49
1:C:167:GLU:HA	2:D:72:MET:CE	2.43	0.48
1:A:52:SER:N	5:A:514:HOH:O	2.46	0.48
1:C:124:PHE:CZ	1:C:132:MET:HG2	2.47	0.48
2:D:78:SER:O	2:D:83:LYS:HG3	2.13	0.48
1:E:57:GLU:HG2	1:E:61:LYS:HE2	1.95	0.48
1:E:147:ARG:NH2	1:E:330:ILE:HG12	2.28	0.48
1:E:208:ILE:HG21	1:E:242:LEU:CD2	2.43	0.48
1:E:219:VAL:HG21	1:E:309:ILE:HD13	1.96	0.48
1:A:213:LYS:O	1:A:217:CYS:HB2	2.14	0.48
1:A:305:MET:SD	1:A:336:LYS:HG3	2.53	0.48
1:E:297:ASN:HB2	1:E:329:ILE:HD13	1.94	0.48
1:C:62:ARG:HD2	1:C:203:THR:HG21	1.95	0.48
1:E:360:GLN:O	1:E:364:GLU:HG3	2.14	0.48
1:C:193:LEU:CD2	1:C:250:ILE:HG21	2.38	0.48
2:D:67:LEU:HD23	2:D:67:LEU:H	1.77	0.48
1:G:291:LYS:NZ	1:G:326:LYS:H	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:LEU:HB3	1:A:119:MET:CE	2.44	0.48
1:E:16:LEU:HD23	1:E:32:PRO:HA	1.96	0.48
1:C:162:ASN:HB2	1:C:176:MET:HB2	1.96	0.47
1:A:214:GLU:HG2	3:A:401:ATP:C4	2.50	0.47
1:C:214:GLU:HG2	3:C:401:ATP:C5	2.49	0.47
1:A:214:GLU:HG2	3:A:401:ATP:C5	2.50	0.47
1:E:294:TYR:CD2	1:E:325:MET:HG2	2.50	0.47
1:E:357:ILE:CD1	1:E:370:VAL:HG23	2.44	0.47
1:G:106:THR:HB	1:G:137:GLN:HG3	1.96	0.47
1:A:237:GLU:O	1:A:238:LYS:HD2	2.14	0.47
2:B:83:LYS:HE2	1:C:179:ASP:O	2.14	0.47
1:A:193:LEU:HD21	1:A:250:ILE:HG21	1.97	0.47
1:C:299:MET:CE	1:C:309:ILE:HG23	2.43	0.47
1:E:88:HIS:HA	1:E:92:ASN:HD22	1.80	0.47
1:G:12:ASN:HB2	5:G:513:HOH:O	2.15	0.47
1:A:105:LEU:HG	1:A:119:MET:HE2	1.97	0.46
1:E:103:THR:O	1:E:132:MET:HA	2.16	0.46
1:A:53:TYR:HD2	1:A:65:LEU:HD11	1.80	0.46
1:A:161:HIS:HE1	5:A:522:HOH:O	1.98	0.46
1:A:183:ARG:HG3	1:A:206:ARG:HH21	1.79	0.46
1:E:62:ARG:HD3	1:E:67:LEU:CD1	2.46	0.46
1:A:70:PRO:CG	1:A:85:ILE:HD12	2.46	0.46
1:A:88:HIS:HA	1:A:92:ASN:OD1	2.15	0.46
1:A:313:MET:CE	1:A:317:ILE:HD11	2.45	0.46
1:C:132:MET:CE	1:C:134:VAL:HG23	2.46	0.46
1:C:295:ALA:CB	1:C:326:LYS:HE3	2.43	0.46
1:C:210:ARG:HD3	5:C:572:HOH:O	2.14	0.46
1:C:167:GLU:C	2:D:72:MET:HE2	2.36	0.46
2:D:67:LEU:HG	2:D:68:HIS:N	2.31	0.46
1:E:172:PRO:HA	1:E:175:ILE:HD12	1.98	0.46
1:E:303:THR:HG22	1:E:303:THR:O	2.16	0.46
1:A:316:GLU:OE2	1:A:316:GLU:HA	2.16	0.45
1:E:18:LYS:HG3	1:E:30:VAL:HG22	1.98	0.45
1:E:289:ILE:HG12	1:E:289:ILE:O	2.15	0.45
1:E:325:MET:CE	1:E:326:LYS:H	2.28	0.45
1:G:10:CYS:HB3	1:G:105:LEU:HD23	1.97	0.45
1:G:103:THR:O	1:G:132:MET:HA	2.16	0.45
1:C:242:LEU:HB3	1:C:243:PRO:HD2	1.99	0.45
1:E:351:THR:HG23	2:F:71:LEU:HD12	1.98	0.45
1:G:131:ALA:HB1	1:G:356:TRP:HB3	1.98	0.45
1:G:176:MET:HG3	1:G:281:SER:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:MET:HE2	1:C:176:MET:HA	1.99	0.45
1:E:132:MET:HG2	1:E:133:TYR:H	1.82	0.45
1:G:183:ARG:NH2	5:G:519:HOH:O	2.50	0.45
1:G:213:LYS:HD2	1:G:306:TYR:OH	2.16	0.45
1:E:70:PRO:HG3	1:E:85:ILE:HD12	1.99	0.45
2:F:72:MET:O	2:F:76:HIS:HD2	1.99	0.45
1:G:272:ALA:HB1	1:G:276:GLU:HB2	1.98	0.44
1:G:278:THR:HG21	1:G:297:ASN:ND2	2.18	0.44
1:G:299:MET:CE	1:G:304:THR:HB	2.44	0.44
1:C:104:LEU:C	1:C:104:LEU:HD23	2.37	0.44
1:E:351:THR:CG2	2:F:71:LEU:HD12	2.47	0.44
5:A:519:HOH:O	2:B:86:LYS:HG3	2.16	0.44
1:E:132:MET:HE1	1:E:134:VAL:HG23	1.99	0.44
1:C:207:GLU:OE1	1:C:210:ARG:NH2	2.40	0.44
1:C:303:THR:O	1:C:303:THR:CG2	2.66	0.44
1:G:99:GLU:O	1:G:99:GLU:CG	2.66	0.44
1:C:83:GLU:OE2	1:C:126:THR:HG21	2.17	0.44
1:A:176:MET:HB3	5:A:574:HOH:O	2.18	0.43
1:E:70:PRO:CG	1:E:85:ILE:HD12	2.48	0.43
1:C:137:GLN:HG2	1:C:339:VAL:HG11	2.00	0.43
1:E:164:PRO:HG2	1:E:174:ALA:HB3	1.99	0.43
1:E:351:THR:HG23	2:F:71:LEU:HD13	1.99	0.43
1:A:187:ASP:CG	1:A:206:ARG:HH22	2.22	0.43
1:A:272:ALA:HB1	1:A:276:GLU:CD	2.39	0.43
1:A:363:ASP:HA	5:A:555:HOH:O	2.18	0.43
1:E:28:ARG:HG3	5:E:560:HOH:O	2.16	0.43
1:E:210:ARG:O	1:E:214:GLU:HG3	2.18	0.43
1:C:355:MET:CE	2:D:71:LEU:HD22	2.47	0.43
1:E:345:ILE:O	1:E:349:LEU:HG	2.19	0.43
1:G:218:TYR:O	1:G:255:PHE:HA	2.18	0.43
1:C:167:GLU:HA	2:D:72:MET:HE2	1.99	0.43
1:E:131:ALA:HB1	1:E:356:TRP:HB3	2.01	0.43
1:A:179:ASP:HB2	5:A:533:HOH:O	2.18	0.43
1:C:189:LEU:HD23	1:C:213:LYS:HB2	2.00	0.43
1:G:214:GLU:HG2	3:G:401:ATP:C5	2.54	0.43
1:E:176:MET:HG3	1:E:281:SER:HB2	2.00	0.43
2:H:73:GLU:OE1	2:H:73:GLU:HA	2.19	0.43
1:G:252:ASN:HA	1:G:255:PHE:CE2	2.54	0.42
1:A:132:MET:HE1	1:A:134:VAL:CG2	2.48	0.42
1:C:372:ARG:HD2	5:C:507:HOH:O	2.18	0.42
1:E:357:ILE:HD11	1:E:370:VAL:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:LEU:C	1:A:104:LEU:HD23	2.40	0.42
1:A:369:ILE:HG13	1:A:369:ILE:O	2.19	0.42
1:E:212:ILE:HG12	1:E:240:TYR:CG	2.54	0.42
1:E:180:LEU:HD11	1:E:260:THR:HG22	2.00	0.42
1:G:12:ASN:HB3	1:G:71:ILE:CD1	2.50	0.42
1:C:355:MET:HE1	2:D:71:LEU:HD22	2.00	0.42
1:G:334:GLU:OE1	1:G:334:GLU:N	2.49	0.42
2:B:67:LEU:HD22	2:H:67:LEU:HB2	2.00	0.42
1:A:180:LEU:CD2	1:A:261:LEU:HD23	2.50	0.42
1:G:172:PRO:HA	1:G:175:ILE:HD12	2.02	0.42
1:E:162:ASN:HB2	1:E:176:MET:HB2	2.02	0.42
1:A:291:LYS:HZ1	1:A:326:LYS:H	1.66	0.42
1:C:8:LEU:HG	1:C:101:HIS:HB3	2.02	0.42
1:C:369:ILE:O	1:C:369:ILE:HG13	2.19	0.41
1:G:96:VAL:CG2	1:G:101:HIS:CD2	3.02	0.41
2:H:66:SER:HB3	2:H:69:SER:HB2	2.02	0.41
1:C:12:ASN:HB3	1:C:71:ILE:CD1	2.50	0.41
1:G:178:LEU:HD13	1:G:271:SER:OG	2.21	0.41
1:A:218:TYR:O	1:A:255:PHE:HA	2.20	0.41
1:A:364:GLU:O	1:G:286:ASP:HB3	2.20	0.41
1:C:193:LEU:CD2	1:C:250:ILE:CG2	2.98	0.41
1:G:96:VAL:HG22	1:G:97:ALA:N	2.35	0.41
1:C:178:LEU:HG	1:C:180:LEU:HB3	2.01	0.41
1:G:64:ILE:O	1:G:64:ILE:CG1	2.68	0.41
1:G:185:LEU:HD11	1:G:261:LEU:CD2	2.48	0.41
1:A:187:ASP:OD1	1:A:206:ARG:CZ	2.69	0.41
1:E:224:GLU:HB2	5:E:536:HOH:O	2.20	0.41
1:A:128:ASN:CG	1:A:359:LYS:HZ1	2.16	0.41
1:C:183:ARG:HG3	1:C:206:ARG:HH22	1.86	0.41
1:C:286:ASP:O	1:C:289:ILE:HG22	2.20	0.41
2:D:86:LYS:NZ	5:D:101:HOH:O	2.08	0.41
1:G:53:TYR:CD2	1:G:65:LEU:HD11	2.56	0.41
1:A:180:LEU:HD23	1:A:180:LEU:C	2.41	0.41
2:B:67:LEU:O	2:B:71:LEU:N	2.49	0.41
1:C:36:GLY:O	1:C:65:LEU:HD22	2.20	0.41
1:C:36:GLY:HA2	1:C:67:LEU:HD23	2.03	0.41
1:E:36:GLY:HA2	1:E:66:THR:O	2.20	0.41
1:G:96:VAL:HG21	1:G:101:HIS:CD2	2.56	0.41
1:C:306:TYR:CZ	3:C:401:ATP:H2	2.39	0.41
2:D:67:LEU:CD2	2:D:67:LEU:H	2.34	0.41
1:G:340:TRP:CZ3	1:G:344:SER:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ASN:HB2	1:A:176:MET:HB2	2.03	0.40
2:B:86:LYS:N	2:B:86:LYS:HD2	2.36	0.40
1:E:68:LYS:HD2	1:E:81:ASP:OD2	2.20	0.40
1:E:313:MET:CE	1:E:317:ILE:HD11	2.51	0.40
1:A:345:ILE:O	1:A:349:LEU:HG	2.21	0.40
1:E:132:MET:HE2	1:E:357:ILE:HD12	2.03	0.40
1:C:291:LYS:HZ1	1:C:326:LYS:H	1.69	0.40
1:G:303:THR:O	1:G:303:THR:CG2	2.70	0.40
1:E:216:LEU:HD22	1:E:238:LYS:CG	2.35	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	348/377 (92%)	342 (98%)	6 (2%)	0	100	100
1	C	348/377 (92%)	344 (99%)	4 (1%)	0	100	100
1	E	348/377 (92%)	338 (97%)	10 (3%)	0	100	100
1	G	348/377 (92%)	343 (99%)	5 (1%)	0	100	100
2	B	20/22 (91%)	20 (100%)	0	0	100	100
2	D	20/22 (91%)	20 (100%)	0	0	100	100
2	F	20/22 (91%)	20 (100%)	0	0	100	100
2	H	20/22 (91%)	20 (100%)	0	0	100	100
All	All	1472/1596 (92%)	1447 (98%)	25 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	298/319 (93%)	297 (100%)	1 (0%)	92	95
1	C	298/319 (93%)	296 (99%)	2 (1%)	84	90
1	E	298/319 (93%)	294 (99%)	4 (1%)	69	79
1	G	298/319 (93%)	296 (99%)	2 (1%)	84	90
2	B	18/18 (100%)	17 (94%)	1 (6%)	21	27
2	D	18/18 (100%)	18 (100%)	0	100	100
2	F	18/18 (100%)	18 (100%)	0	100	100
2	H	18/18 (100%)	17 (94%)	1 (6%)	21	27
All	All	1264/1348 (94%)	1253 (99%)	11 (1%)	78	86

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	203	THR
2	B	85	ARG
1	C	203	THR
1	C	242	LEU
1	E	65	LEU
1	E	132	MET
1	E	202	THR
1	E	350	SER
1	G	203	THR
1	G	215	LYS
2	H	85	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	92	ASN
1	G	297	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](#)

4 non-standard protein/DNA/RNA residues 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
1	HIC	C	73	1	8,11,12	1.69	2 (25%)	6,14,16	0.86	0
1	HIC	A	73	1	8,11,12	1.65	1 (12%)	6,14,16	0.53	0
1	HIC	E	73	1	8,11,12	1.66	1 (12%)	6,14,16	0.87	0
1	HIC	G	73	1	8,11,12	1.71	2 (25%)	6,14,16	1.07	0

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
1	HIC	C	73	1	-	0/5/6/8	0/1/1/1
1	HIC	A	73	1	-	0/5/6/8	0/1/1/1
1	HIC	E	73	1	-	0/5/6/8	0/1/1/1
1	HIC	G	73	1	-	0/5/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	73	HIC	CD2-CG	3.77	1.41	1.36
1	E	73	HIC	CD2-CG	3.62	1.41	1.36
1	C	73	HIC	CD2-CG	3.57	1.41	1.36
1	A	73	HIC	CD2-CG	3.52	1.41	1.36
1	G	73	HIC	CZ-NE2	-2.03	1.42	1.48
1	C	73	HIC	CZ-NE2	-2.00	1.42	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 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
3	ATP	C	401	4	26,33,33	0.87	1 (3%)	31,52,52	1.37	4 (12%)
3	ATP	G	401	4	26,33,33	0.83	1 (3%)	31,52,52	1.35	4 (12%)
3	ATP	E	401	4	26,33,33	0.94	1 (3%)	31,52,52	1.32	3 (9%)
3	ATP	A	401	4	26,33,33	0.88	1 (3%)	31,52,52	1.40	5 (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
3	ATP	C	401	4	-	2/18/38/38	0/3/3/3
3	ATP	G	401	4	-	2/18/38/38	0/3/3/3
3	ATP	E	401	4	-	2/18/38/38	0/3/3/3
3	ATP	A	401	4	-	2/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	401	ATP	C5-C4	2.47	1.47	1.40
3	A	401	ATP	C5-C4	2.37	1.47	1.40
3	C	401	ATP	C5-C4	2.37	1.47	1.40
3	G	401	ATP	C5-C4	2.20	1.46	1.40

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	ATP	N3-C2-N1	-3.96	122.49	128.68
3	G	401	ATP	N3-C2-N1	-3.82	122.71	128.68
3	A	401	ATP	N3-C2-N1	-3.61	123.04	128.68
3	E	401	ATP	N3-C2-N1	-3.37	123.41	128.68
3	E	401	ATP	PA-O3A-PB	-2.88	122.94	132.83
3	A	401	ATP	C2-N1-C6	2.45	122.94	118.75
3	G	401	ATP	PA-O3A-PB	-2.42	124.52	132.83
3	A	401	ATP	C1'-N9-C4	-2.41	122.42	126.64
3	A	401	ATP	C4-C5-N7	-2.35	106.95	109.40
3	C	401	ATP	C4-C5-N7	-2.29	107.01	109.40
3	A	401	ATP	PA-O3A-PB	-2.26	125.06	132.83
3	G	401	ATP	C4-C5-N7	-2.23	107.08	109.40
3	C	401	ATP	C2-N1-C6	2.22	122.55	118.75
3	C	401	ATP	C1'-N9-C4	-2.08	122.98	126.64
3	G	401	ATP	C2-N1-C6	2.08	122.31	118.75
3	E	401	ATP	PB-O3B-PG	-2.07	125.72	132.83

There are no chirality outliers.

All (8) torsion outliers are listed below:

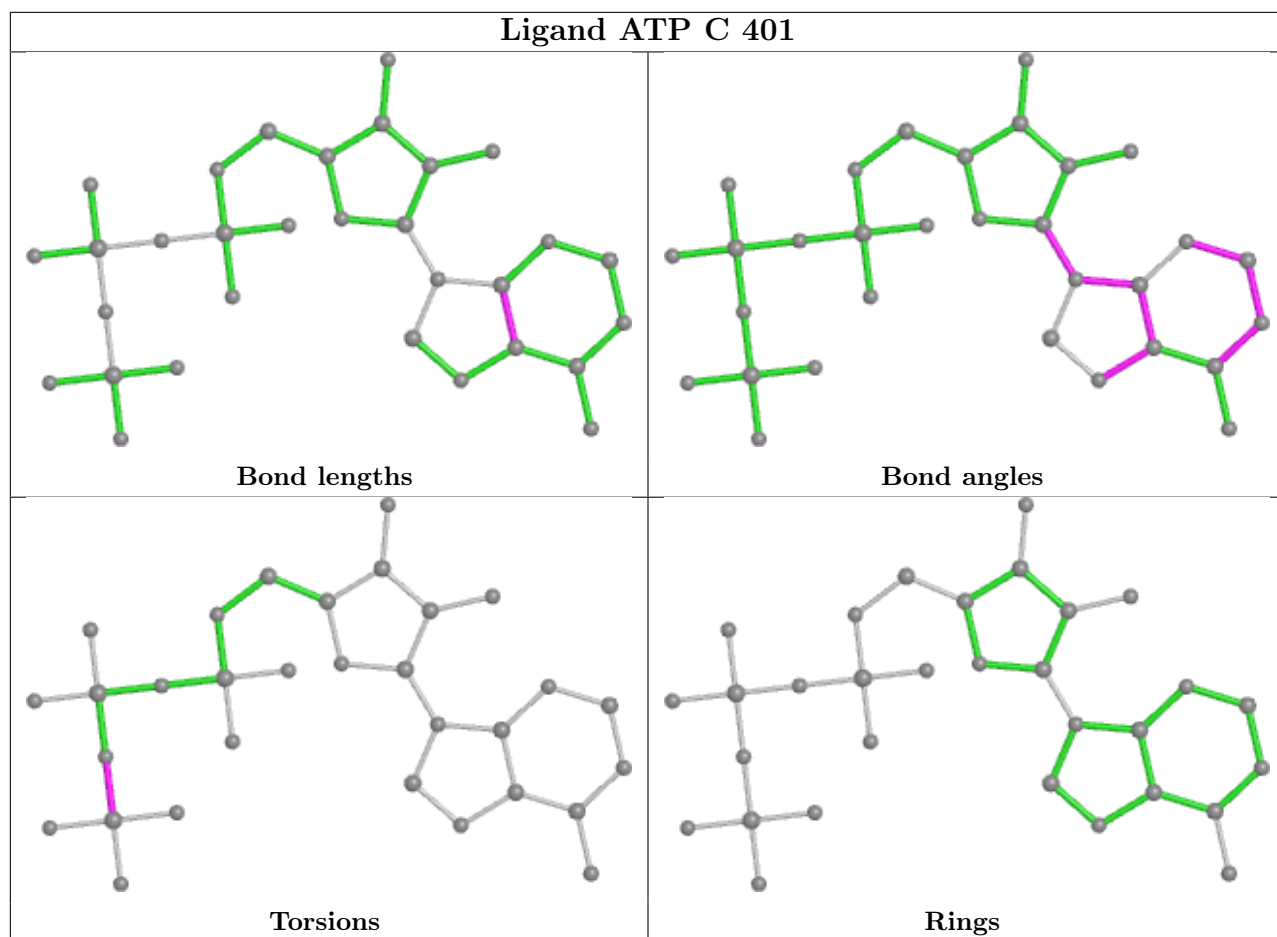
Mol	Chain	Res	Type	Atoms
3	A	401	ATP	PB-O3B-PG-O2G
3	E	401	ATP	PB-O3B-PG-O1G
3	A	401	ATP	PB-O3B-PG-O1G
3	C	401	ATP	PB-O3B-PG-O1G
3	G	401	ATP	PB-O3B-PG-O1G
3	C	401	ATP	PB-O3B-PG-O2G
3	E	401	ATP	PB-O3B-PG-O2G
3	G	401	ATP	PB-O3B-PG-O2G

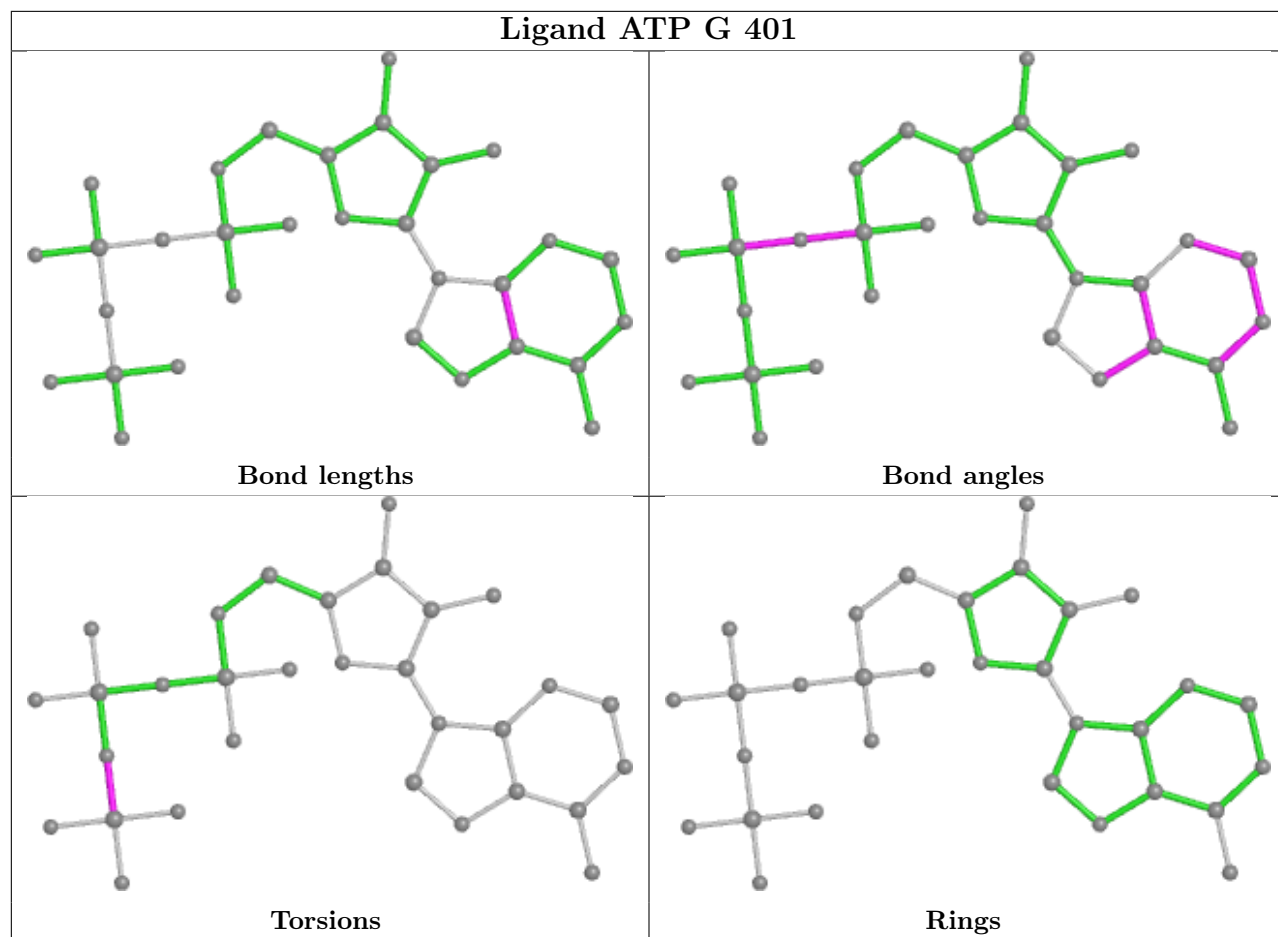
There are no ring outliers.

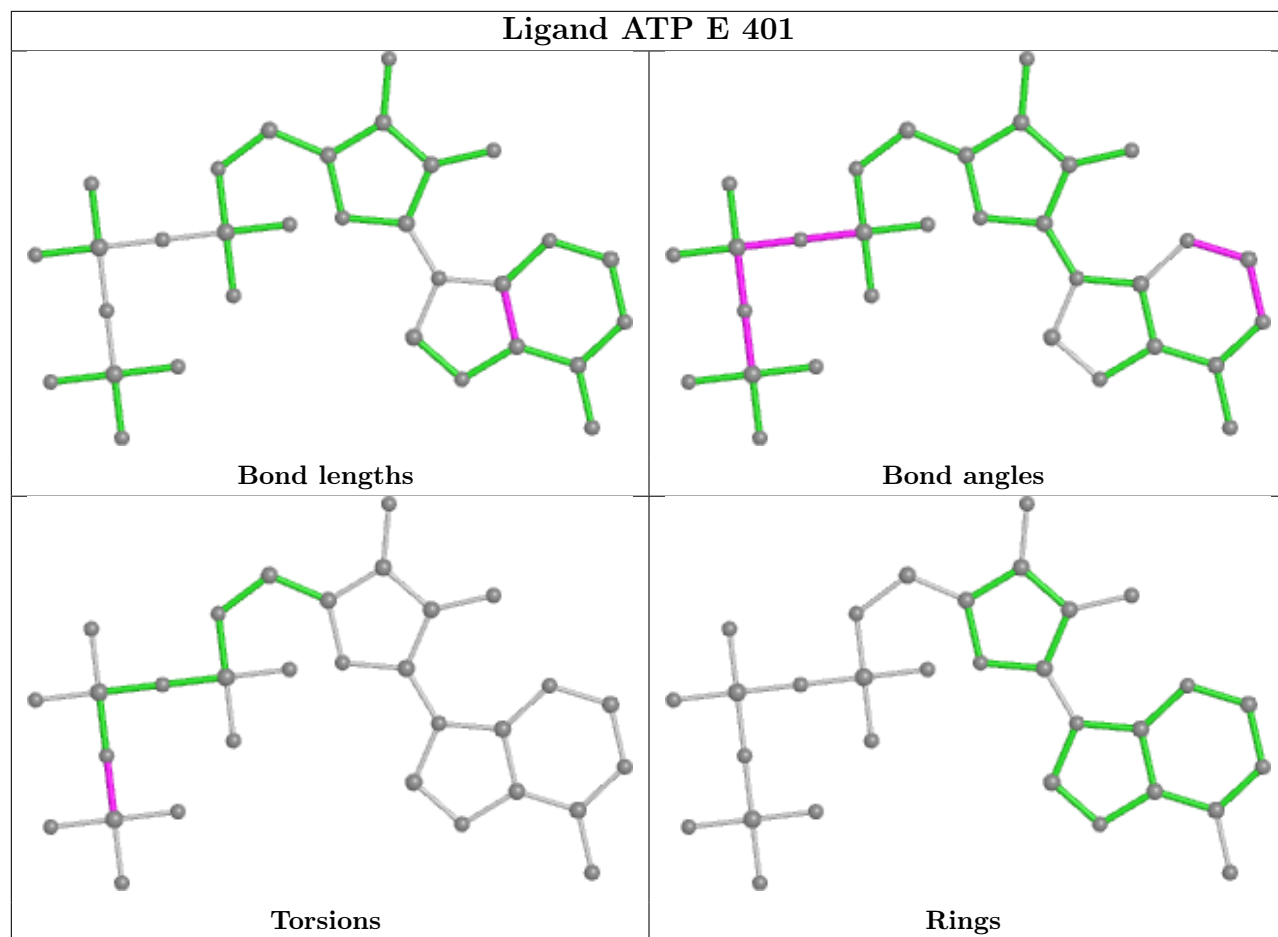
3 monomers are involved in 5 short contacts:

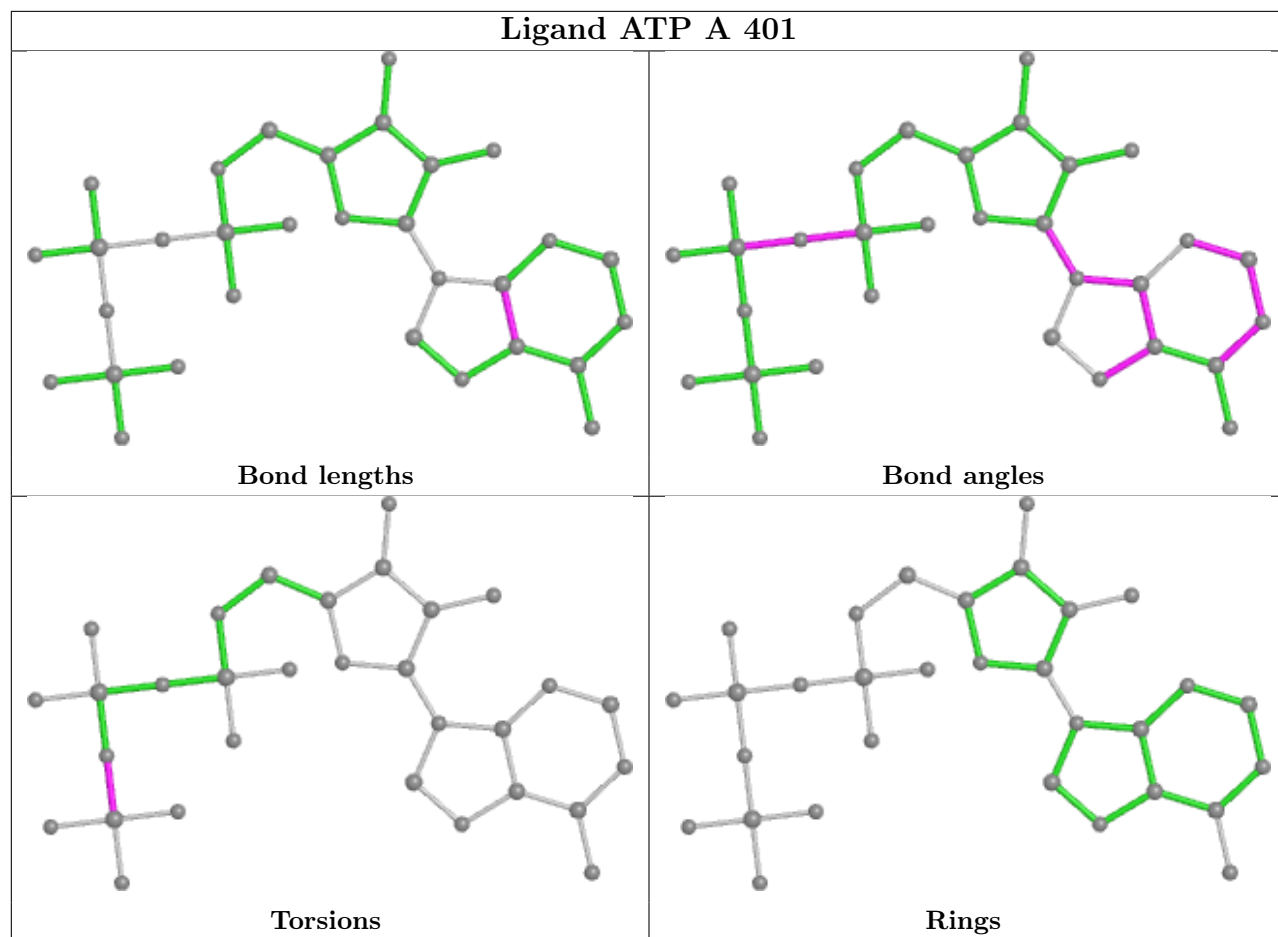
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	ATP	2	0
3	G	401	ATP	1	0
3	A	401	ATP	2	0

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	352/377 (93%)	-0.30	4 (1%) 80 80	17, 32, 69, 100	0
1	C	352/377 (93%)	-0.36	6 (1%) 70 67	18, 31, 59, 100	0
1	E	352/377 (93%)	-0.18	12 (3%) 45 41	21, 34, 67, 92	0
1	G	352/377 (93%)	-0.07	14 (3%) 38 35	22, 38, 74, 118	0
2	B	22/22 (100%)	-0.08	2 (9%) 9 6	39, 50, 78, 81	0
2	D	22/22 (100%)	0.06	1 (4%) 33 30	32, 48, 70, 85	0
2	F	22/22 (100%)	0.12	1 (4%) 33 30	43, 51, 82, 89	0
2	H	22/22 (100%)	0.26	2 (9%) 9 6	33, 46, 78, 101	0
All	All	1496/1596 (93%)	-0.21	42 (2%) 53 49	17, 34, 72, 118	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	64	ILE	8.4
1	G	64	ILE	5.3
1	G	232	SER	4.9
1	A	64	ILE	4.8
1	E	231	ALA	4.3
1	C	64	ILE	4.1
1	E	232	SER	4.1
1	G	203	THR	3.5
1	A	203	THR	3.4
1	G	66	THR	3.4
1	E	230	ALA	3.3
1	G	68	LYS	3.2
2	H	67	LEU	3.1
1	G	270	GLU	3.0
1	G	53	TYR	3.0
2	F	66	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	323	SER	2.9
1	C	53	TYR	2.9
1	G	195	GLU	2.9
1	E	203	THR	2.9
1	C	63	GLY	2.8
1	G	230	ALA	2.7
1	E	61	LYS	2.7
2	H	66	SER	2.6
2	D	66	SER	2.6
1	E	324	THR	2.5
1	G	62	ARG	2.4
1	E	66	THR	2.3
1	C	60	SER	2.3
1	E	63	GLY	2.2
2	B	67	LEU	2.2
2	B	66	SER	2.2
1	G	234	SER	2.1
1	G	60	SER	2.1
1	A	6	THR	2.1
1	E	258	PRO	2.0
1	G	6	THR	2.0
1	A	53	TYR	2.0
1	C	52	SER	2.0
1	C	10	CYS	2.0
1	G	10	CYS	2.0
1	E	354	GLN	2.0

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

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
1	HIC	E	73	11/12	0.95	0.12	23,26,31,33	0
1	HIC	G	73	11/12	0.96	0.15	37,45,55,57	0
1	HIC	A	73	11/12	0.97	0.11	22,24,29,32	0
1	HIC	C	73	11/12	0.97	0.11	31,35,40,41	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

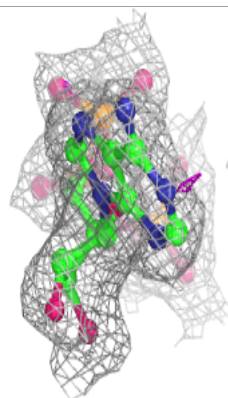
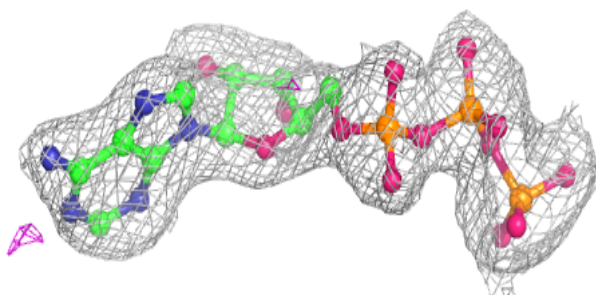
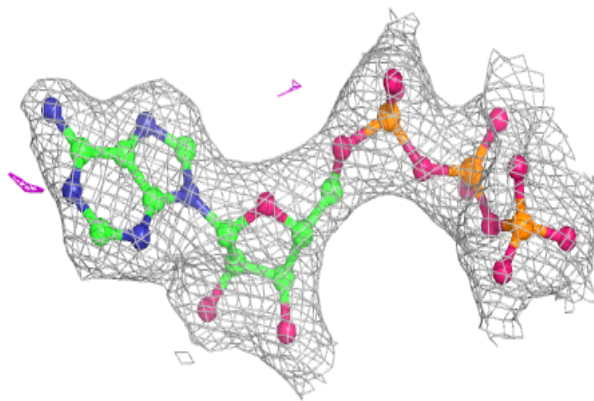
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CA	C	403	1/1	0.96	0.06	41,41,41,41	0
4	CA	G	403	1/1	0.96	0.09	48,48,48,48	0
4	CA	E	403	1/1	0.97	0.04	37,37,37,37	0
4	CA	A	403	1/1	0.97	0.04	51,51,51,51	0
3	ATP	A	401	31/31	0.98	0.08	15,24,29,30	0
3	ATP	C	401	31/31	0.98	0.09	19,26,30,31	0
4	CA	E	402	1/1	0.98	0.08	23,23,23,23	0
3	ATP	E	401	31/31	0.98	0.08	20,27,29,30	0
4	CA	G	402	1/1	0.98	0.10	26,26,26,26	0
3	ATP	G	401	31/31	0.98	0.09	23,26,30,32	0
4	CA	C	402	1/1	0.99	0.09	18,18,18,18	0
4	CA	A	402	1/1	0.99	0.10	20,20,20,20	0

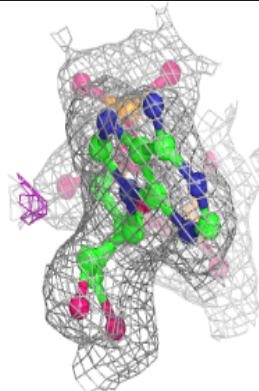
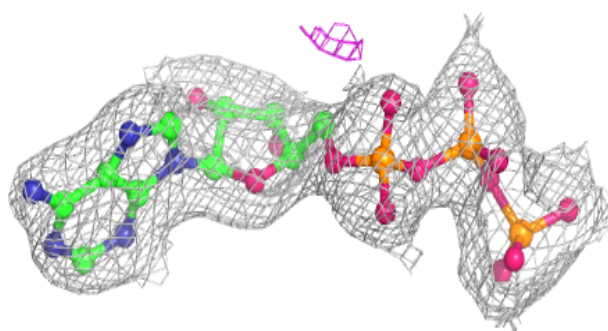
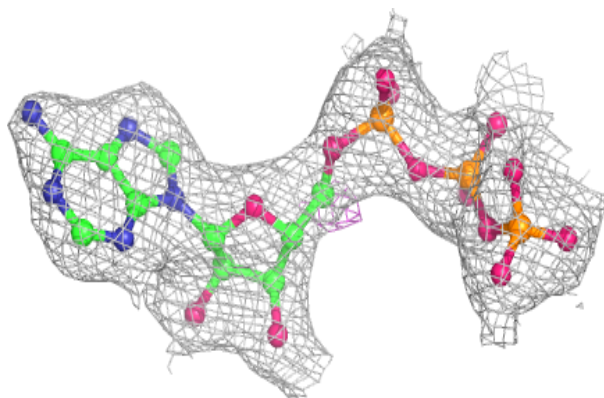
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP A 401:

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

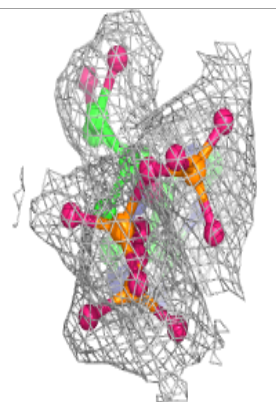
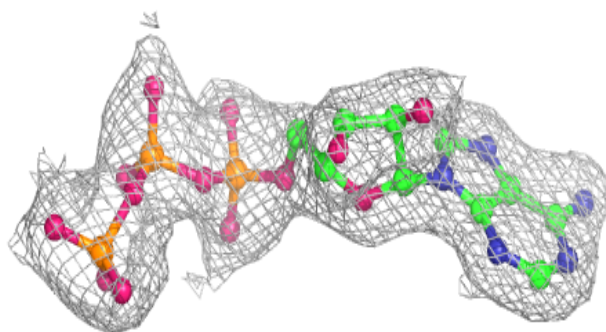
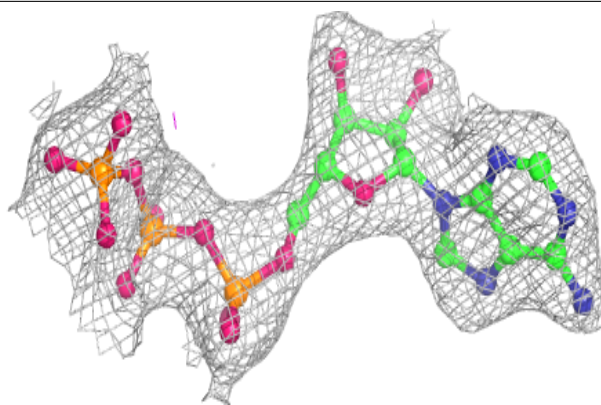
**Electron density around ATP C 401:**

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

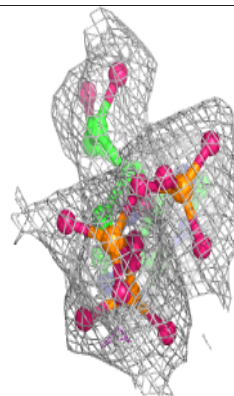
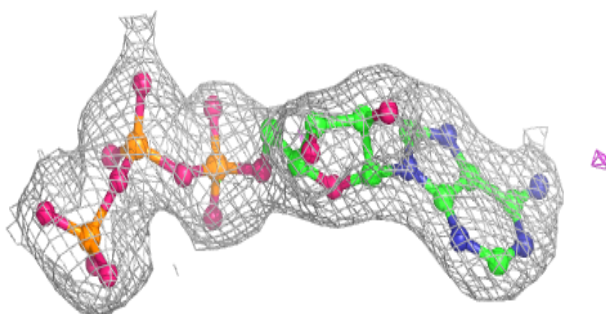
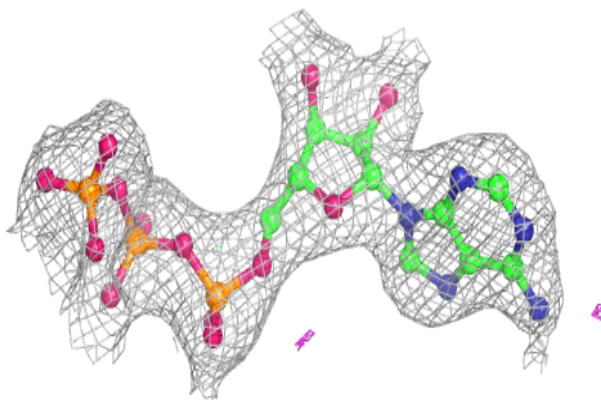


Electron density around ATP E 401:

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

**Electron density around ATP G 401:**

$2mF_o-DF_c$ (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.