



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:15 PM UTC

PDB ID : 4GY2 / pdb_00004gy2
Title : Crystal structure of apo-Ia-actin complex
Authors : Tsurumura, T.; Oda, M.; Nagahama, M.; Tsuge, H.
Deposited on : 2012-09-05
Resolution : 2.71 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

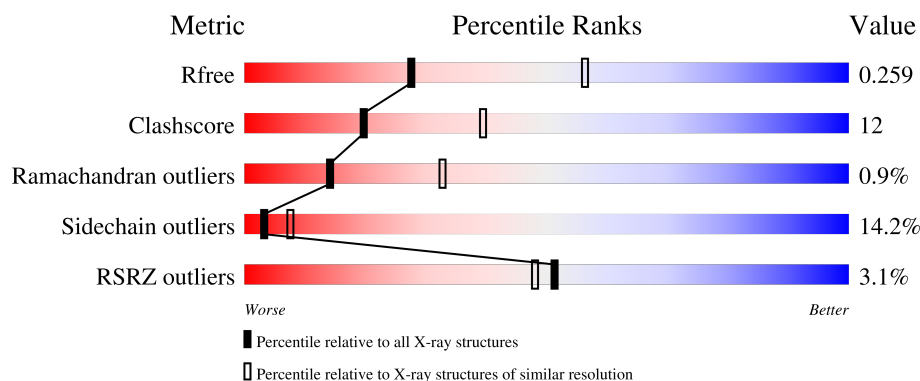
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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 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	418	 72% 19% 6% ..
2	B	375	 6% 63% 27% 5% ..

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6373 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Iota toxin component Ia.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	0	0
			3347	2134	551	659	3			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	ARG	-	expression tag	UNP Q46220
A	-3	GLY	-	expression tag	UNP Q46220
A	-2	SER	-	expression tag	UNP Q46220
A	-1	HIS	-	expression tag	UNP Q46220
A	0	MET	-	expression tag	UNP Q46220

- Molecule 2 is a protein called Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	360	Total	C	N	O	S	0	0	0
			2817	1785	474	539	19			

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

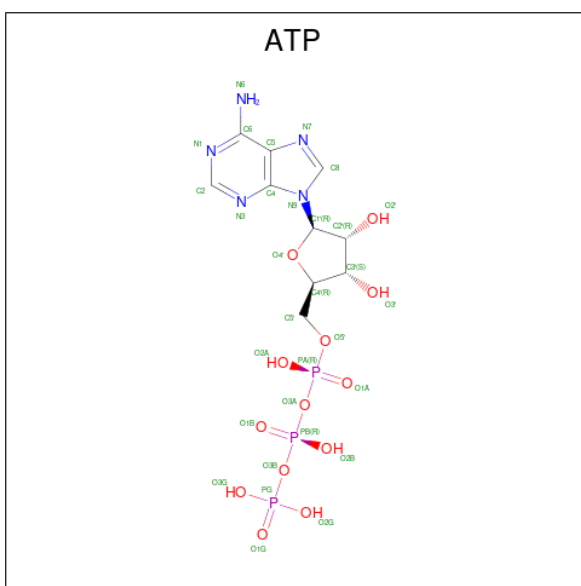


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

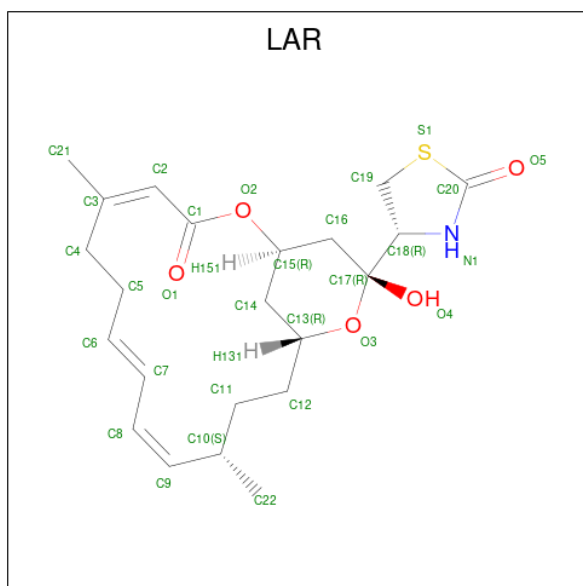
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 6 is LATRUNCULIN A (CCD ID: LAR) (formula: $C_{22}H_{31}NO_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			29	22	1	5	1		

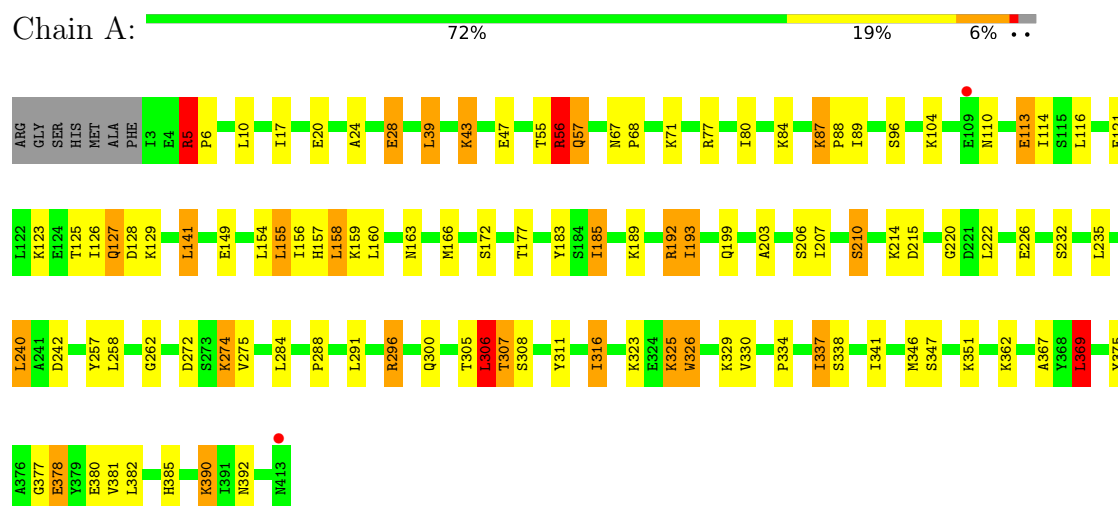
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	89	Total	O	0	0
			89	89		
7	B	54	Total	O	0	0
			54	54		

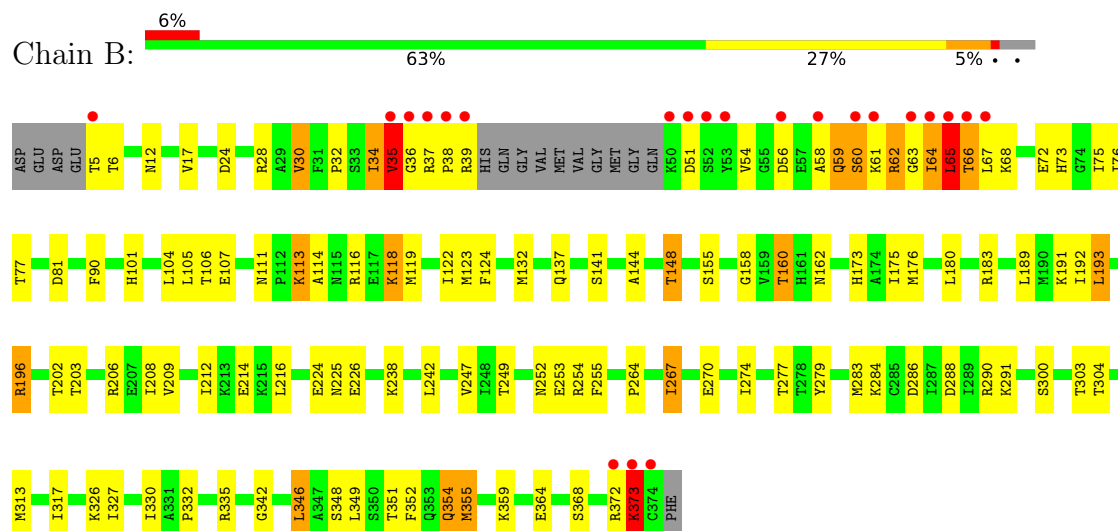
3 Residue-property plots [i](#)

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: Iota toxin component Ia



- Molecule 2: Actin, alpha skeletal muscle



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.44Å 135.87Å 153.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.19 – 2.71 37.19 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.5 (37.19-2.71) 99.6 (37.19-2.71)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.29 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.199 , 0.257 0.199 , 0.259	Depositor DCC
R_{free} test set	1605 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 23.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6373	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LAR, CA, PO4, ATP

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	0.89	1/3415 (0.0%)	1.15	10/4614 (0.2%)
2	B	1.03	3/2877 (0.1%)	1.19	14/3899 (0.4%)
All	All	0.96	4/6292 (0.1%)	1.17	24/8513 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	66	THR	N-CA	6.77	1.54	1.45
1	A	87	LYS	N-CA	5.47	1.50	1.45
2	B	173	HIS	CG-CD2	5.26	1.41	1.35
2	B	175	ILE	C-O	-5.13	1.19	1.24

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	66	THR	N-CA-C	10.28	125.00	110.50
1	A	56	ARG	N-CA-C	8.15	122.18	111.75
1	A	5	ARG	CA-C-N	-6.76	113.83	120.52
1	A	5	ARG	C-N-CA	-6.76	113.83	120.52
1	A	326	TRP	N-CA-C	6.74	122.04	113.55
2	B	148	THR	N-CA-C	-6.41	106.67	114.75
2	B	304	THR	N-CA-C	-5.98	105.84	113.02
1	A	17	ILE	CB-CA-C	-5.96	104.23	112.04
1	A	308	SER	CA-C-N	-5.87	113.64	119.56
1	A	308	SER	C-N-CA	-5.87	113.64	119.56
2	B	144	ALA	CA-C-N	-5.83	114.49	123.17
2	B	144	ALA	C-N-CA	-5.83	114.49	123.17
2	B	348	SER	N-CA-C	-5.77	106.58	113.97
2	B	342	GLY	N-CA-C	-5.73	105.44	112.77
2	B	38	PRO	N-CA-C	5.67	120.39	111.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	148	THR	CB-CA-C	5.46	116.20	109.16
2	B	65	LEU	CA-C-N	5.23	129.16	120.94
2	B	65	LEU	C-N-CA	5.23	129.16	120.94
2	B	51	ASP	N-CA-C	5.18	118.07	111.69
2	B	124	PHE	N-CA-C	5.13	116.96	111.36
2	B	290	ARG	N-CA-C	5.12	116.55	111.07
1	A	377	GLY	CA-C-N	-5.08	116.24	122.84
1	A	377	GLY	C-N-CA	-5.08	116.24	122.84
1	A	337	ILE	CB-CA-C	-5.00	104.13	110.98

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3347	0	3329	70	0
2	B	2817	0	2793	75	0
3	A	5	0	0	1	0
4	B	1	0	0	0	0
5	B	31	0	12	2	0
6	B	29	0	31	2	0
7	A	89	0	0	11	0
7	B	54	0	0	6	0
All	All	6373	0	6165	143	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 12.

All (143) 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:156:ILE:HA	7:A:789:HOH:O	1.42	1.17
2:B:283:MET:HE1	7:B:530:HOH:O	1.63	0.99
1:A:57:GLN:HE21	1:A:57:GLN:H	0.99	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:ILE:HD13	1:A:316:ILE:H	1.27	0.95
1:A:89:ILE:HG21	1:A:166:MET:HE1	1.51	0.93
2:B:196:ARG:HH22	2:B:249:THR:HG22	1.36	0.89
2:B:183:ARG:HD2	7:B:528:HOH:O	1.78	0.82
1:A:89:ILE:HG21	1:A:166:MET:CE	2.09	0.82
1:A:369:LEU:HD22	1:A:382:LEU:HB2	1.60	0.81
1:A:57:GLN:H	1:A:57:GLN:NE2	1.77	0.81
2:B:111:ASN:HD21	2:B:119:MET:HE1	1.51	0.75
2:B:160:THR:CG2	2:B:180:LEU:O	2.36	0.73
2:B:332:PRO:O	2:B:335:ARG:HB2	1.88	0.73
1:A:57:GLN:HG2	1:A:214:LYS:HB3	1.71	0.72
1:A:316:ILE:H	1:A:316:ILE:CD1	2.03	0.72
2:B:160:THR:HG23	2:B:180:LEU:O	1.90	0.71
2:B:352:PHE:O	2:B:355:MET:HB2	1.90	0.71
1:A:20:GLU:OE1	1:A:177:THR:OG1	2.08	0.71
1:A:296:ARG:HD2	7:A:764:HOH:O	1.92	0.69
2:B:162:ASN:ND2	2:B:277:THR:OG1	2.25	0.69
2:B:35:VAL:HG22	2:B:36:GLY:N	2.08	0.68
1:A:316:ILE:HD13	1:A:316:ILE:N	2.07	0.67
2:B:346:LEU:HD22	2:B:352:PHE:CD1	2.31	0.66
2:B:32:PRO:HB3	6:B:403:LAR:H121	1.78	0.66
1:A:20:GLU:CD	1:A:141:LEU:HD22	2.20	0.66
1:A:311:TYR:OH	7:A:752:HOH:O	2.10	0.66
2:B:313:MET:HG3	2:B:317:ILE:HD12	1.78	0.66
1:A:84:LYS:HD3	1:A:163:ASN:O	1.96	0.65
2:B:35:VAL:HG13	2:B:81:ASP:OD2	1.96	0.65
2:B:35:VAL:CG1	2:B:81:ASP:OD2	2.45	0.65
2:B:354:GLN:HE21	2:B:354:GLN:H	1.44	0.65
1:A:323:LYS:HE2	7:A:717:HOH:O	1.96	0.64
1:A:192:ARG:O	1:A:193:ILE:HD12	1.98	0.64
1:A:288:PRO:O	1:A:362:LYS:HE2	1.97	0.64
1:A:390:LYS:HG2	1:A:392:ASN:ND2	2.15	0.62
1:A:5:ARG:NH1	1:A:88:PRO:O	2.34	0.61
1:A:114:ILE:O	1:A:192:ARG:NH2	2.34	0.61
1:A:57:GLN:HE21	1:A:57:GLN:N	1.84	0.60
2:B:104:LEU:C	2:B:104:LEU:HD23	2.26	0.60
2:B:90:PHE:HZ	2:B:123:MET:CE	2.14	0.60
1:A:67:ASN:OD1	1:A:68:PRO:HD2	2.02	0.60
1:A:337:ILE:HD12	1:A:337:ILE:N	2.17	0.60
2:B:61:LYS:HD3	2:B:65:LEU:HG	1.84	0.60
2:B:176:MET:HE3	2:B:176:MET:HA	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:MET:HE1	1:A:378:GLU:HB3	1.85	0.59
2:B:216:LEU:O	2:B:254:ARG:HG3	2.03	0.59
1:A:28:GLU:HB2	7:A:739:HOH:O	2.03	0.58
2:B:12:ASN:ND2	7:B:507:HOH:O	2.36	0.58
1:A:203:ALA:O	7:A:789:HOH:O	2.17	0.58
2:B:279:TYR:CE1	2:B:283:MET:HE3	2.39	0.58
2:B:72:GLU:HB2	7:B:529:HOH:O	2.04	0.57
2:B:72:GLU:HB3	7:B:526:HOH:O	2.04	0.57
1:A:306:LEU:HB2	7:A:753:HOH:O	2.04	0.57
2:B:105:LEU:HD12	2:B:132:MET:HE2	1.86	0.57
2:B:106:THR:HB	2:B:137:GLN:HG3	1.87	0.57
2:B:59:GLN:HE21	2:B:59:GLN:HA	1.70	0.56
2:B:300:SER:HA	2:B:335:ARG:HG2	1.88	0.56
1:A:155:LEU:O	7:A:789:HOH:O	2.18	0.55
2:B:317:ILE:HG22	2:B:327:ILE:HD13	1.88	0.55
2:B:73:HIS:HD2	2:B:158:GLY:O	1.90	0.55
2:B:155:SER:HA	2:B:160:THR:HB	1.89	0.55
2:B:118:LYS:O	2:B:122:ILE:HG13	2.07	0.55
2:B:196:ARG:NH2	2:B:249:THR:HG22	2.14	0.55
1:A:378:GLU:HG3	7:A:771:HOH:O	2.05	0.54
1:A:192:ARG:O	1:A:193:ILE:CD1	2.55	0.54
2:B:17:VAL:O	2:B:30:VAL:HA	2.08	0.54
1:A:5:ARG:NH2	3:A:600:PO4:O4	2.40	0.54
1:A:242:ASP:OD1	1:A:274:LYS:HD2	2.08	0.53
1:A:220:GLY:HA3	1:A:341:ILE:HD13	1.89	0.53
2:B:62:ARG:O	2:B:66:THR:HA	2.09	0.53
2:B:62:ARG:O	2:B:66:THR:HG22	2.09	0.53
2:B:90:PHE:HZ	2:B:123:MET:HE1	1.74	0.53
1:A:183:TYR:CD2	1:A:207:ILE:HD12	2.44	0.52
2:B:107:GLU:OE2	2:B:116:ARG:HD3	2.09	0.52
2:B:65:LEU:N	2:B:65:LEU:CD2	2.73	0.52
2:B:65:LEU:N	2:B:65:LEU:HD22	2.24	0.52
1:A:351:LYS:HB2	2:B:270:GLU:O	2.10	0.51
1:A:369:LEU:CD2	1:A:382:LEU:HB2	2.35	0.51
1:A:5:ARG:HG2	1:A:6:PRO:O	2.11	0.51
1:A:305:THR:C	1:A:307:THR:H	2.19	0.51
2:B:6:THR:O	2:B:101:HIS:HD2	1.94	0.51
2:B:58:ALA:C	2:B:60:SER:H	2.18	0.50
1:A:158:LEU:HD13	1:A:160:LEU:HD23	1.93	0.50
1:A:347:SER:OG	2:B:176:MET:HE2	2.11	0.50
1:A:257:TYR:OH	1:A:272:ASP:OD1	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:372:ARG:O	2:B:373:LYS:CB	2.59	0.50
2:B:77:THR:OG1	7:B:529:HOH:O	2.16	0.49
2:B:90:PHE:CZ	2:B:123:MET:HE1	2.47	0.49
1:A:104:LYS:HE3	1:A:121:GLU:OE1	2.13	0.49
2:B:214:GLU:HG2	5:B:402:ATP:C5	2.48	0.49
1:A:334:PRO:O	1:A:385:HIS:HB2	2.13	0.48
2:B:35:VAL:HG11	2:B:81:ASP:OD2	2.14	0.48
2:B:24:ASP:OD2	2:B:28:ARG:NH2	2.36	0.47
2:B:274:ILE:HG13	2:B:313:MET:HE1	1.96	0.47
1:A:325:LYS:HB3	1:A:326:TRP:CD1	2.50	0.47
1:A:39:LEU:O	1:A:43:LYS:HG2	2.14	0.47
2:B:208:ILE:O	2:B:212:ILE:HG13	2.14	0.47
2:B:226:GLU:HB3	2:B:255:PHE:CE1	2.49	0.47
2:B:64:ILE:C	2:B:65:LEU:HD22	2.40	0.46
2:B:264:PRO:O	2:B:267:ILE:HG22	2.15	0.46
2:B:113:LYS:O	2:B:114:ALA:C	2.58	0.46
2:B:189:LEU:HG	2:B:193:LEU:HD22	1.98	0.46
1:A:57:GLN:HG2	1:A:214:LYS:HD3	1.98	0.46
1:A:337:ILE:HD12	1:A:337:ILE:H	1.77	0.46
1:A:24:ALA:O	1:A:28:GLU:HB2	2.16	0.46
1:A:89:ILE:HG21	1:A:166:MET:HE3	1.95	0.45
2:B:35:VAL:CG2	2:B:36:GLY:N	2.79	0.45
2:B:76:ILE:HD12	2:B:119:MET:HE2	1.98	0.45
1:A:157:HIS:N	7:A:789:HOH:O	2.48	0.45
1:A:367:ALA:O	1:A:381:VAL:HA	2.16	0.45
2:B:63:GLY:HA2	2:B:66:THR:HG23	1.98	0.45
2:B:214:GLU:HG2	5:B:402:ATP:C4	2.52	0.45
1:A:338:SER:HB2	1:A:380:GLU:OE1	2.17	0.45
1:A:113:GLU:HA	1:A:199:GLN:HE21	1.81	0.45
2:B:32:PRO:HB2	2:B:34:ILE:HG13	1.99	0.45
2:B:39:ARG:H	2:B:65:LEU:HD13	1.82	0.45
6:B:403:LAR:H61	6:B:403:LAR:H91	1.49	0.45
1:A:235:LEU:HD13	1:A:240:LEU:HA	1.99	0.44
2:B:330:ILE:HG22	2:B:332:PRO:HD3	1.98	0.44
1:A:5:ARG:NH1	1:A:89:ILE:HB	2.32	0.44
2:B:192:ILE:HD12	2:B:253:GLU:HG3	1.99	0.43
1:A:125:THR:O	1:A:129:LYS:HE3	2.18	0.43
1:A:390:LYS:HG2	1:A:392:ASN:HD21	1.82	0.43
1:A:257:TYR:CE2	1:A:262:GLY:HA3	2.53	0.43
2:B:216:LEU:O	2:B:254:ARG:CG	2.66	0.43
1:A:326:TRP:O	1:A:329:LYS:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:59:GLN:HG3	2:B:59:GLN:O	2.18	0.43
1:A:306:LEU:HD12	1:A:306:LEU:HA	1.76	0.43
1:A:375:TYR:OH	1:A:380:GLU:OE1	2.34	0.42
2:B:267:ILE:HG21	2:B:267:ILE:HD12	1.76	0.42
1:A:305:THR:C	1:A:307:THR:N	2.75	0.42
2:B:58:ALA:C	2:B:60:SER:N	2.77	0.42
1:A:123:LYS:O	1:A:127:GLN:HB2	2.19	0.42
1:A:185:ILE:HG21	1:A:185:ILE:HD13	1.62	0.41
2:B:372:ARG:O	2:B:373:LYS:HB3	2.21	0.41
1:A:183:TYR:CE2	1:A:207:ILE:HD12	2.55	0.41
1:A:338:SER:HB2	1:A:380:GLU:CD	2.46	0.41
1:A:56:ARG:NH2	1:A:215:ASP:OD2	2.54	0.41
2:B:111:ASN:ND2	2:B:119:MET:HE1	2.27	0.41
2:B:62:ARG:C	2:B:66:THR:HA	2.46	0.40
1:A:210:SER:HB2	7:A:759:HOH:O	2.20	0.40
1:A:347:SER:CB	2:B:176:MET:HE2	2.51	0.40
2:B:303:THR:O	2:B:303:THR:CG2	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	409/418 (98%)	390 (95%)	16 (4%)	3 (1%)	18	39
2	B	356/375 (95%)	335 (94%)	17 (5%)	4 (1%)	11	27
All	All	765/793 (96%)	725 (95%)	33 (4%)	7 (1%)	14	33

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	373	LYS

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Mol	Chain	Res	Type
1	A	172	SER
1	A	306	LEU
2	B	35	VAL
1	A	369	LEU
2	B	60	SER
2	B	64	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	375/380 (99%)	324 (86%)	51 (14%)	3	8
2	B	306/318 (96%)	260 (85%)	46 (15%)	3	7
All	All	681/698 (98%)	584 (86%)	97 (14%)	3	7

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ARG
1	A	10	LEU
1	A	28	GLU
1	A	39	LEU
1	A	43	LYS
1	A	47	GLU
1	A	55	THR
1	A	56	ARG
1	A	57	GLN
1	A	71	LYS
1	A	77	ARG
1	A	80	ILE
1	A	87	LYS
1	A	96	SER
1	A	110	ASN
1	A	113	GLU
1	A	116	LEU

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Mol	Chain	Res	Type
1	A	126	ILE
1	A	127	GLN
1	A	128	ASP
1	A	141	LEU
1	A	149	GLU
1	A	154	LEU
1	A	155	LEU
1	A	158	LEU
1	A	159	LYS
1	A	185	ILE
1	A	189	LYS
1	A	192	ARG
1	A	193	ILE
1	A	206	SER
1	A	210	SER
1	A	222	LEU
1	A	226	GLU
1	A	232	SER
1	A	240	LEU
1	A	258	LEU
1	A	274	LYS
1	A	275	VAL
1	A	284	LEU
1	A	291	LEU
1	A	296	ARG
1	A	300	GLN
1	A	306	LEU
1	A	307	THR
1	A	316	ILE
1	A	325	LYS
1	A	330	VAL
1	A	369	LEU
1	A	378	GLU
1	A	390	LYS
2	B	5	THR
2	B	30	VAL
2	B	34	ILE
2	B	35	VAL
2	B	37	ARG
2	B	54	VAL
2	B	56	ASP
2	B	59	GLN

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Mol	Chain	Res	Type
2	B	62	ARG
2	B	65	LEU
2	B	67	LEU
2	B	68	LYS
2	B	75	ILE
2	B	113	LYS
2	B	118	LYS
2	B	141	SER
2	B	148	THR
2	B	160	THR
2	B	191	LYS
2	B	193	LEU
2	B	196	ARG
2	B	202	THR
2	B	203	THR
2	B	206	ARG
2	B	209	VAL
2	B	224	GLU
2	B	225	ASN
2	B	238	LYS
2	B	242	LEU
2	B	247	VAL
2	B	252	ASN
2	B	267	ILE
2	B	284	LYS
2	B	286	ASP
2	B	288	ASP
2	B	291	LYS
2	B	326	LYS
2	B	346	LEU
2	B	349	LEU
2	B	351	THR
2	B	354	GLN
2	B	355	MET
2	B	359	LYS
2	B	364	GLU
2	B	368	SER
2	B	373	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	30	ASN
1	A	51	ASN
1	A	57	GLN
1	A	78	ASN
1	A	103	ASN
1	A	111	GLN
1	A	127	GLN
1	A	146	ASN
1	A	181	GLN
1	A	199	GLN
1	A	227	ASN
1	A	244	ASN
1	A	261	ASN
1	A	266	ASN
1	A	280	ASN
1	A	318	ASN
1	A	384	ASN
1	A	392	ASN
2	B	12	ASN
2	B	59	GLN
2	B	73	HIS
2	B	88	HIS
2	B	92	ASN
2	B	101	HIS
2	B	111	ASN
2	B	121	GLN
2	B	162	ASN
2	B	246	GLN
2	B	252	ASN
2	B	354	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	PO4	A	600	-	4,4,4	1.10	0	6,6,6	1.17	0
5	ATP	B	402	-	32,33,33	1.44	4 (12%)	48,52,52	1.60	11 (22%)
6	LAR	B	403	-	30,31,31	1.58	3 (10%)	32,43,43	1.97	9 (28%)

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
5	ATP	B	402	-	-	2/22/38/38	0/3/3/3
6	LAR	B	403	-	-	11/23/51/51	0/2/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	403	LAR	O2-C1	5.73	1.46	1.34
5	B	402	ATP	C5-C4	4.71	1.47	1.39
6	B	403	LAR	C20-S1	-4.23	1.68	1.77
5	B	402	ATP	C4-N9	-3.26	1.30	1.37
5	B	402	ATP	C8-N7	2.98	1.37	1.31
5	B	402	ATP	C5-N7	-2.96	1.33	1.39
6	B	403	LAR	O4-C17	2.02	1.44	1.40

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	403	LAR	O3-C17-C18	4.60	110.15	104.25
6	B	403	LAR	O2-C1-C2	4.53	121.70	111.20
5	B	402	ATP	C5-C4-N3	-4.01	121.20	126.72
6	B	403	LAR	O2-C15-C14	3.76	116.61	107.77
5	B	402	ATP	N3-C2-N1	-3.62	123.11	128.58
6	B	403	LAR	O1-C1-C2	-3.21	118.24	126.23
5	B	402	ATP	C2-N3-C4	2.97	119.08	111.83
5	B	402	ATP	O4'-C1'-C2'	-2.89	100.43	106.62
6	B	403	LAR	C14-C15-C16	2.83	116.59	111.02
6	B	403	LAR	C4-C5-C6	-2.75	106.59	112.57
5	B	402	ATP	C4-C5-N7	-2.74	107.45	110.58
5	B	402	ATP	O2G-PG-O3B	2.74	113.83	104.64
5	B	402	ATP	C2-N1-C6	2.66	123.11	118.73
6	B	403	LAR	C21-C3-C4	2.53	119.61	115.23
5	B	402	ATP	N3-C4-N9	2.50	131.41	127.17
5	B	402	ATP	O3'-C3'-C2'	-2.20	104.76	111.82
6	B	403	LAR	C19-S1-C20	2.18	93.30	92.04
6	B	403	LAR	O2-C1-O1	-2.05	120.05	123.34
5	B	402	ATP	C6-C5-N7	2.04	136.03	132.09
5	B	402	ATP	O3A-PA-O1A	-2.01	104.66	110.70

There are no chirality outliers.

All (13) torsion outliers are listed below:

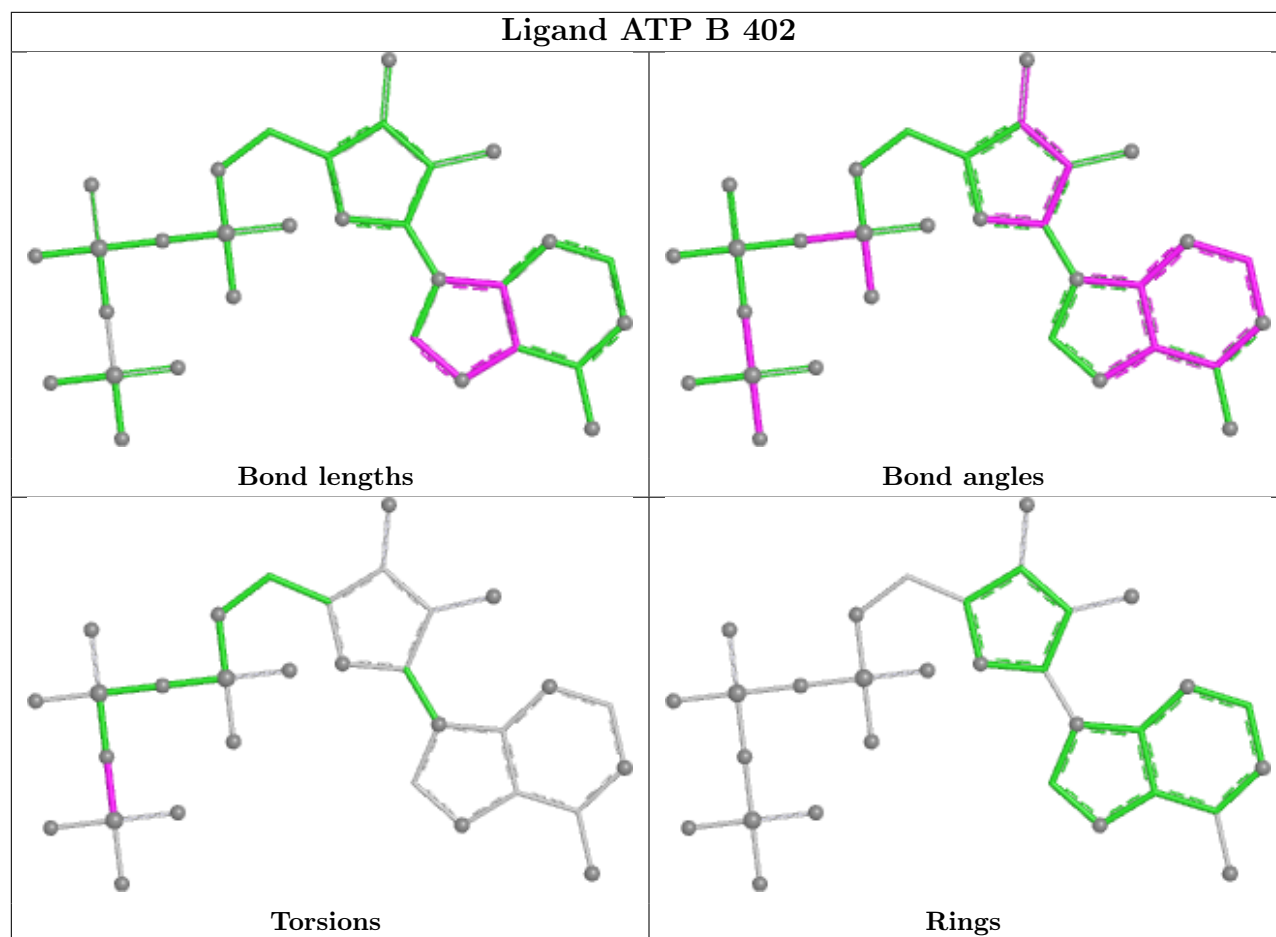
Mol	Chain	Res	Type	Atoms
5	B	402	ATP	PB-O3B-PG-O2G
6	B	403	LAR	O3-C17-C18-C19
6	B	403	LAR	C14-C15-O2-C1
6	B	403	LAR	C6-C7-C8-C9
6	B	403	LAR	C3-C4-C5-C6
6	B	403	LAR	O2-C1-C2-C3
6	B	403	LAR	O1-C1-C2-C3
5	B	402	ATP	PB-O3B-PG-O3G
6	B	403	LAR	C22-C10-C9-C8
6	B	403	LAR	C11-C10-C9-C8
6	B	403	LAR	O1-C1-O2-C15
6	B	403	LAR	C10-C11-C12-C13
6	B	403	LAR	C9-C10-C11-C12

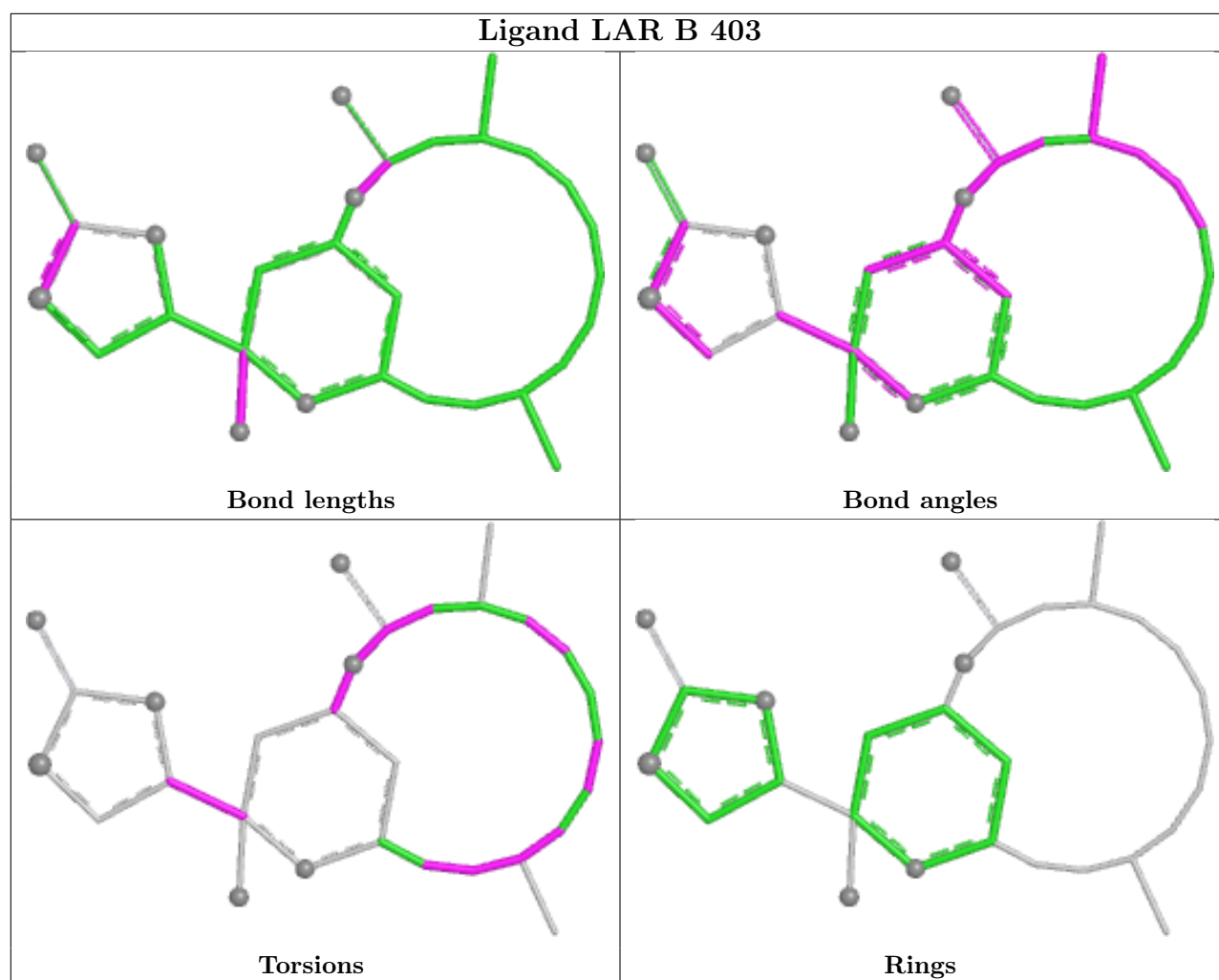
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	PO4	1	0
5	B	402	ATP	2	0
6	B	403	LAR	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	411/418 (98%)	-0.41	2 (0%) 87 86	17, 31, 55, 81	0
2	B	360/375 (96%)	-0.26	22 (6%) 27 24	13, 26, 86, 158	0
All	All	771/793 (97%)	-0.34	24 (3%) 51 48	13, 29, 62, 158	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	38	PRO	5.9
2	B	64	ILE	5.3
2	B	66	THR	5.0
2	B	50	LYS	4.9
2	B	374	CYS	4.6
2	B	36	GLY	4.4
1	A	413	ASN	4.2
2	B	37	ARG	4.1
2	B	39	ARG	3.9
2	B	63	GLY	3.8
2	B	60	SER	3.8
2	B	65	LEU	3.6
2	B	53	TYR	3.6
2	B	61	LYS	3.5
2	B	56	ASP	3.3
2	B	373	LYS	2.9
2	B	5	THR	2.9
1	A	109	GLU	2.8
2	B	52	SER	2.5
2	B	58	ALA	2.5
2	B	67	LEU	2.4
2	B	51	ASP	2.4
2	B	372	ARG	2.4
2	B	35	VAL	2.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

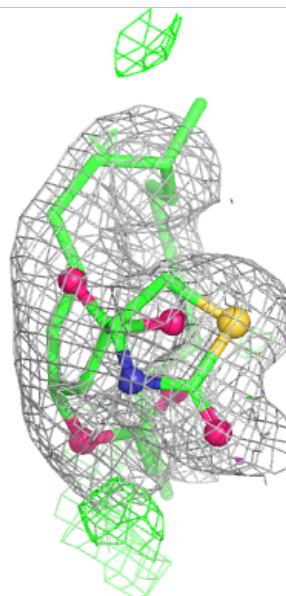
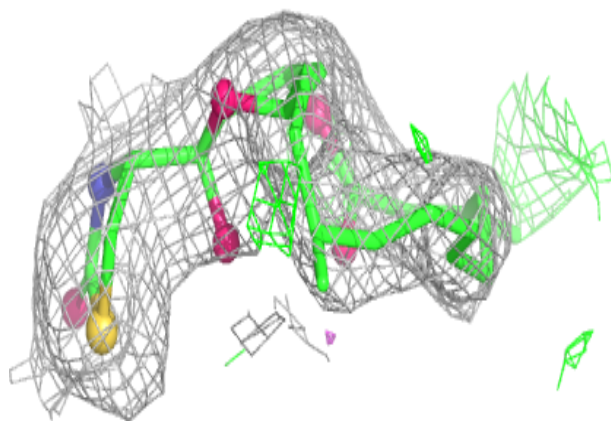
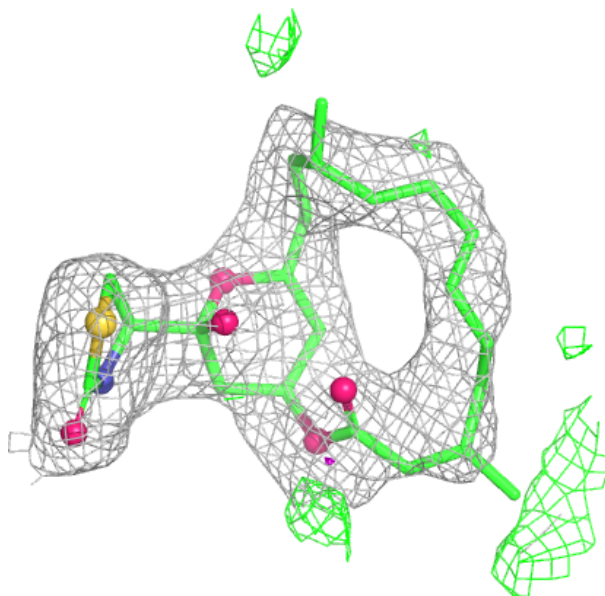
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	LAR	B	403	29/29	0.88	0.16	32,55,77,80	0
3	PO4	A	600	5/5	0.94	0.09	45,46,50,51	0
5	ATP	B	402	31/31	0.99	0.05	15,17,22,24	0
4	CA	B	401	1/1	1.00	0.01	21,21,21,21	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.

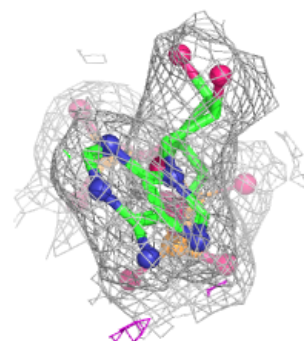
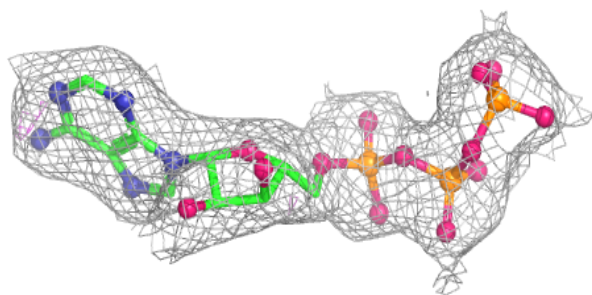
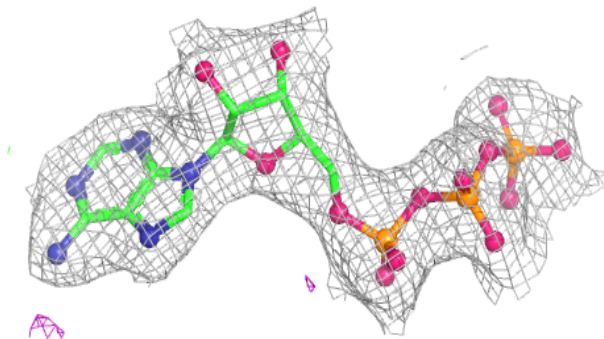
Electron density around LAR B 403:

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



Electron density around ATP B 402:

$2mF_o-DF_c$ (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.