



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:30 AM UTC

PDB ID : 1TYQ / pdb_00001tyq
Title : Crystal structure of Arp2/3 complex with bound ATP and calcium
Authors : Nolen, B.J.; Littlefield, R.S.; Pollard, T.D.
Deposited on : 2004-07-08
Resolution : 2.55 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:

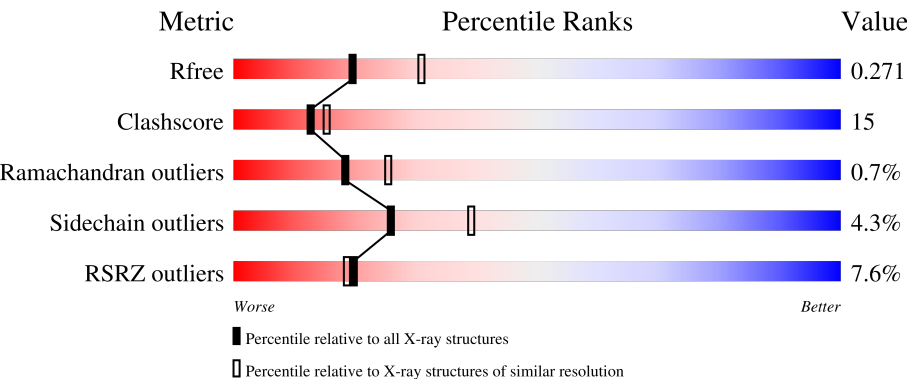
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal 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 i

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

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	6% 67% 26% • 5%
2	B	394	11% 31% 18% • 47%
3	C	372	3% 61% 27% • 8%
4	D	300	3% 68% 22% • 9%
5	E	178	8% 58% 30% 6% 5%

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Mol	Chain	Length	Quality of chain
6	F	168	
7	G	151	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 13586 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 Actin-related protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	0	0
			3166	2031	527	594	14			

- Molecule 2 is a protein called Actin-related Protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	208	Total	C	N	O	S	0	0	0
			1558	998	267	289	4			

- Molecule 3 is a protein called Arp2/3 complex 41kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	342	Total	C	N	O	S	0	0	0
			2641	1674	464	484	19			

- Molecule 4 is a protein called Arp2/3 complex 34kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	274	Total	C	N	O	S	0	0	0
			2219	1411	386	414	8			

- Molecule 5 is a protein called Arp2/3 complex 21kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	169	Total	C	N	O	S	0	0	0
			1379	888	229	253	9			

- Molecule 6 is a protein called Arp2/3 complex 20kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	166	Total	C	N	O	S	0	0	0
			1364	871	238	246	9			

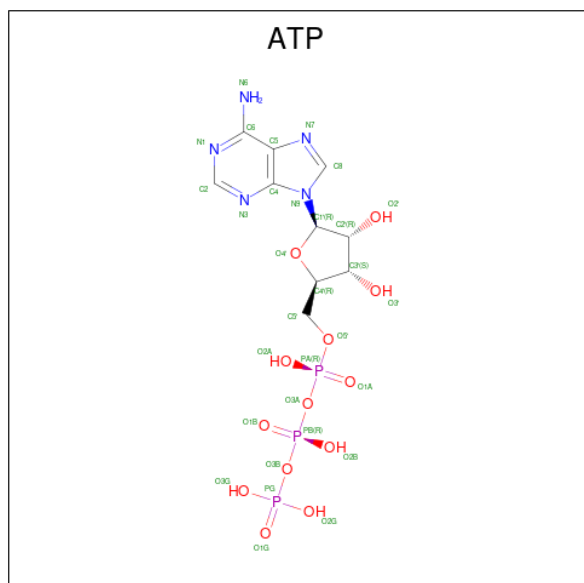
- Molecule 7 is a protein called Arp2/3 Complex 16kDa Subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	134	Total	C	N	O	S	0	0	0
			1014	637	174	200	3			

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

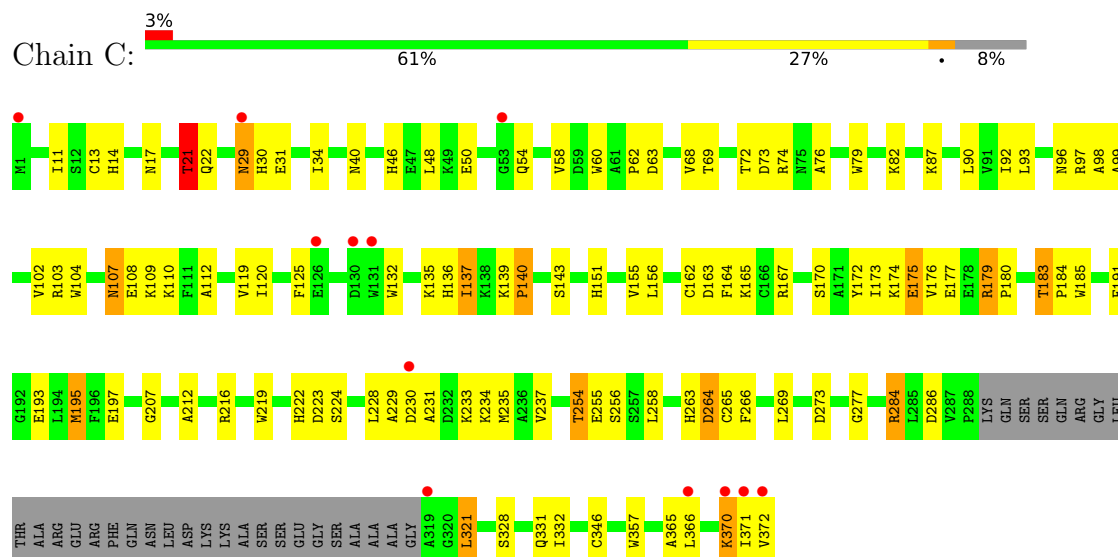
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Ca	0	0
			1	1		
8	B	1	Total	Ca	0	0
			1	1		

- Molecule 9 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

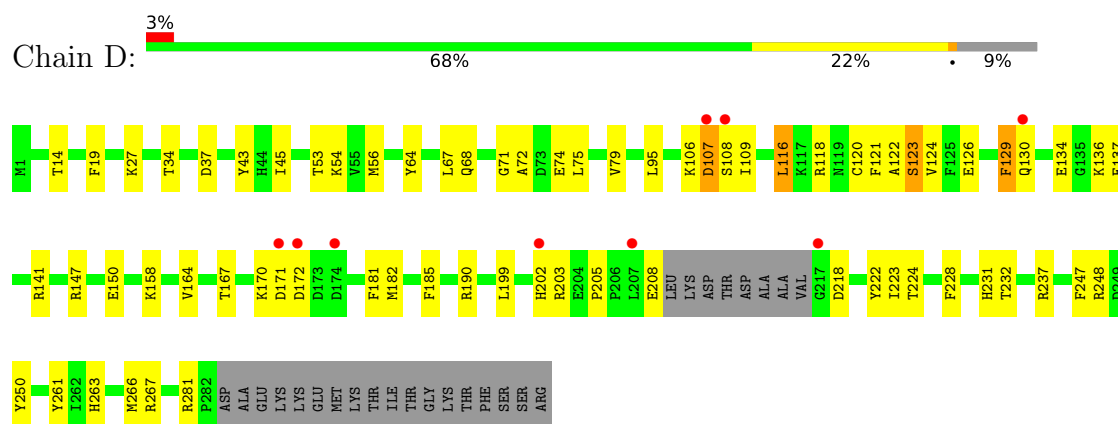


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	22	Total 22	O 22	0	0
10	B	13	Total 13	O 13	0	0
10	C	59	Total 59	O 59	0	0
10	D	41	Total 41	O 41	0	0
10	E	2	Total 2	O 2	0	0
10	F	37	Total 37	O 37	0	0
10	G	7	Total 7	O 7	0	0

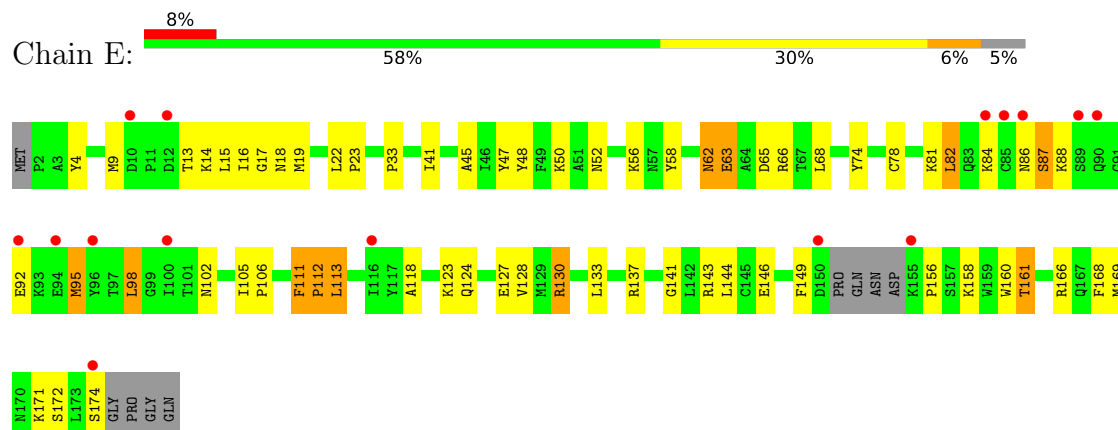
• Molecule 3: Arp2/3 complex 41kDa subunit



• Molecule 4: Arp2/3 complex 34kDa subunit

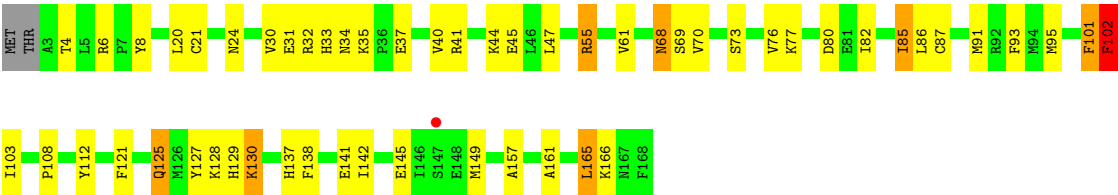


• Molecule 5: Arp2/3 complex 21kDa subunit

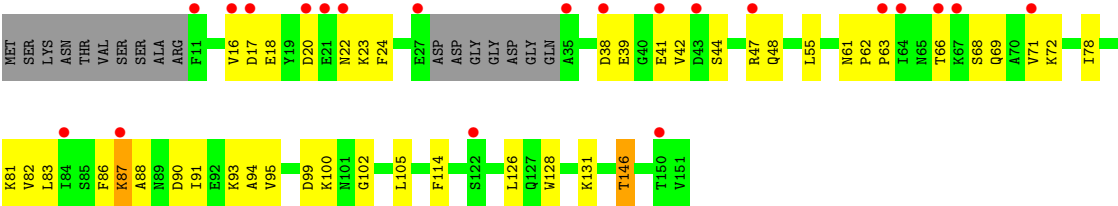


• Molecule 6: Arp2/3 complex 20kDa subunit





● Molecule 7: Arp2/3 Complex 16kDa Subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	111.37Å 129.39Å 199.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.55 30.00 – 2.56	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.55) 78.3 (30.00-2.56)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.57Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.272 0.232 , 0.271	Depositor DCC
R_{free} test set	3662 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.170	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13586	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.45	0/3247	0.90	10/4411 (0.2%)
2	B	0.46	0/1586	0.94	5/2157 (0.2%)
3	C	0.46	1/2708 (0.0%)	1.00	16/3675 (0.4%)
4	D	0.44	0/2267	0.92	7/3058 (0.2%)
5	E	0.40	0/1411	0.96	7/1900 (0.4%)
6	F	0.49	0/1386	0.91	2/1858 (0.1%)
7	G	0.42	0/1026	0.90	2/1382 (0.1%)
All	All	0.45	1/13631 (0.0%)	0.94	49/18441 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	195	MET	SD-CE	-5.55	1.65	1.79

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	111	PHE	CA-C-N	9.09	129.28	119.28
5	E	111	PHE	C-N-CA	9.09	129.28	119.28
5	E	17	GLY	N-CA-C	-8.61	98.41	111.24
3	C	30	HIS	N-CA-C	-7.75	103.84	113.38
1	A	178	ILE	N-CA-C	7.18	115.91	107.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	347	PRO	CA-C-N	7.01	126.83	119.05
2	B	347	PRO	C-N-CA	7.01	126.83	119.05
4	D	129	PHE	N-CA-C	-6.86	103.86	111.82
4	D	122	ALA	N-CA-C	6.69	119.18	111.02
3	C	11	ILE	N-CA-C	-6.68	97.37	106.85
3	C	29	ASN	N-CA-C	6.54	119.86	109.65
3	C	163	ASP	N-CA-C	-6.49	105.66	112.93
1	A	97	ILE	N-CA-C	6.26	116.43	110.74
3	C	99	ALA	N-CA-C	-6.18	101.34	110.48
2	B	225	TYR	N-CA-C	-6.14	105.44	113.12
6	F	55	ARG	N-CA-C	-6.07	104.22	111.69
2	B	349	ARG	N-CA-C	5.99	119.42	109.96
1	A	76	TRP	CA-C-N	5.96	125.66	119.82
1	A	76	TRP	C-N-CA	5.96	125.66	119.82
3	C	328	SER	N-CA-C	5.95	118.99	110.24
5	E	112	PRO	N-CA-C	5.82	121.51	113.65
1	A	402	GLU	N-CA-C	5.71	117.58	111.36
4	D	64	TYR	N-CA-C	5.63	118.14	111.33
4	D	190	ARG	N-CA-C	-5.45	106.70	113.19
4	D	123	SER	N-CA-C	5.45	117.92	111.33
3	C	151	HIS	N-CA-C	-5.44	102.30	110.24
3	C	137	ILE	N-CA-C	-5.44	99.41	107.51
1	A	115	PRO	N-CA-C	-5.43	104.08	110.70
3	C	165	LYS	N-CA-C	5.43	118.91	110.17
1	A	109	TYR	N-CA-C	-5.43	102.45	110.48
3	C	179	ARG	CA-C-N	5.39	125.33	119.78
3	C	179	ARG	C-N-CA	5.39	125.33	119.78
3	C	21	THR	N-CA-C	-5.39	106.87	113.50
6	F	102	PHE	N-CA-C	5.38	122.27	110.80
3	C	63	ASP	N-CA-C	5.36	116.80	111.07
1	A	78	ILE	N-CA-C	5.36	115.57	107.75
4	D	79	VAL	N-CA-C	5.28	115.50	110.53
2	B	300	HIS	N-CA-C	5.27	116.63	110.41
1	A	373	GLN	N-CA-C	5.27	117.03	111.28
4	D	185	PHE	N-CA-C	-5.27	105.62	111.36
5	E	113	LEU	N-CA-C	5.24	116.73	110.44
3	C	170	SER	N-CA-C	-5.22	100.72	109.24
5	E	160	TRP	N-CA-C	-5.19	106.89	113.43
5	E	19	MET	N-CA-C	-5.16	102.89	110.52
1	A	238	LEU	N-CA-C	5.08	116.51	110.97
7	G	61	ASN	CA-C-N	5.07	123.31	119.66
7	G	61	ASN	C-N-CA	5.07	123.31	119.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	254	THR	N-CA-C	-5.03	101.26	108.60
3	C	264	ASP	N-CA-C	-5.01	106.68	112.89

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	261	TYR	Sidechain

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	3166	0	3062	84	0
2	B	1558	0	1506	69	0
3	C	2641	0	2597	85	0
4	D	2219	0	2180	60	0
5	E	1379	0	1387	51	0
6	F	1364	0	1403	42	0
7	G	1014	0	1021	30	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	31	0	12	4	0
9	B	31	0	12	4	0
10	A	22	0	0	2	0
10	B	13	0	0	0	0
10	C	59	0	0	1	0
10	D	41	0	0	1	0
10	E	2	0	0	0	0
10	F	37	0	0	3	0
10	G	7	0	0	0	0
All	All	13586	0	13180	405	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 15.

All (405) 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)
6:F:130:LYS:HA	6:F:130:LYS:HE2	1.40	1.00
4:D:170:LYS:HE2	4:D:170:LYS:HA	1.44	0.99
3:C:223:ASP:HB3	7:G:146:THR:HG21	1.43	0.99
3:C:216:ARG:HG2	3:C:230:ASP:HB3	1.47	0.97
2:B:205:ASN:HD22	2:B:208:ALA:H	1.13	0.97
1:A:191:LYS:HE2	1:A:303:VAL:HG22	1.45	0.96
6:F:4:THR:HG23	6:F:55:ARG:HE	1.29	0.95
3:C:371:ILE:HG22	3:C:372:VAL:HG23	1.50	0.94
1:A:257:THR:HG22	1:A:268:SER:HB3	1.50	0.93
6:F:86:LEU:HD22	6:F:149:MET:HE3	1.49	0.91
3:C:183:THR:HG22	3:C:185:TRP:H	1.33	0.91
2:B:166:ILE:HD12	2:B:281:LEU:HD22	1.53	0.89
3:C:155:VAL:HG21	3:C:180:PRO:HG3	1.54	0.87
2:B:326:LEU:HD12	2:B:337:LEU:HD12	1.57	0.87
3:C:370:LYS:HD2	3:C:370:LYS:O	1.79	0.83
2:B:302:VAL:HG22	2:B:350:ARG:HH22	1.45	0.81
1:A:309:ILE:HD13	1:A:312:ARG:CZ	2.11	0.80
6:F:37:GLU:H	6:F:68:ASN:HD21	1.30	0.80
2:B:194:ILE:HG12	2:B:213:VAL:HG21	1.63	0.80
3:C:14:HIS:H	3:C:331:GLN:HE22	1.29	0.79
3:C:223:ASP:CB	7:G:146:THR:HG21	2.14	0.77
1:A:248:ASP:O	1:A:250:SER:N	2.18	0.76
2:B:314:PRO:O	2:B:318:GLU:HG3	1.86	0.75
2:B:205:ASN:HD22	2:B:208:ALA:N	1.84	0.74
7:G:62:PRO:CG	7:G:105:LEU:HD21	2.17	0.74
2:B:349:ARG:O	2:B:350:ARG:HB2	1.87	0.72
3:C:107:ASN:C	3:C:107:ASN:HD22	1.97	0.72
2:B:239:VAL:HG23	2:B:240:LEU:HD13	1.72	0.72
3:C:183:THR:HG22	3:C:185:TRP:N	2.05	0.71
2:B:157:VAL:HB	2:B:303:LEU:HD13	1.71	0.71
1:A:289:ASN:C	1:A:289:ASN:HD22	1.99	0.71
6:F:130:LYS:HA	6:F:130:LYS:CE	2.21	0.71
5:E:62:ASN:C	5:E:62:ASN:HD22	1.99	0.70
5:E:48:TYR:HB3	5:E:52:ASN:ND2	2.07	0.70
7:G:87:LYS:HZ3	7:G:87:LYS:HB2	1.57	0.70
2:B:304:SER:HB3	2:B:350:ARG:NH1	2.07	0.69
7:G:62:PRO:HG2	7:G:105:LEU:HD21	1.73	0.69
2:B:184:ILE:HD12	2:B:188:ASP:HB2	1.75	0.68
5:E:9:MET:CE	5:E:13:THR:HB	2.23	0.68
3:C:321:LEU:N	3:C:321:LEU:HD12	2.09	0.68
5:E:123:LYS:O	5:E:127:GLU:HG3	1.93	0.68
3:C:155:VAL:HG21	3:C:180:PRO:CG	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:166:ILE:O	2:B:168:PRO:HD3	1.94	0.68
2:B:313:LEU:HB3	2:B:314:PRO:HD3	1.76	0.68
5:E:88:LYS:O	5:E:92:GLU:HG3	1.94	0.68
3:C:21:THR:HG22	3:C:22:GLN:HG3	1.77	0.67
3:C:107:ASN:ND2	3:C:109:LYS:H	1.92	0.67
3:C:119:VAL:HG23	3:C:137:ILE:O	1.94	0.67
4:D:203:ARG:NH1	4:D:218:ASP:HA	2.11	0.66
6:F:101:PHE:O	6:F:103:ILE:N	2.28	0.66
2:B:345:GLU:C	2:B:347:PRO:HD3	2.21	0.66
4:D:137:GLU:CD	4:D:158:LYS:HE2	2.21	0.66
1:A:194:PRO:O	1:A:195:ILE:HD12	1.96	0.66
3:C:76:ALA:HB2	3:C:93:LEU:HD11	1.77	0.65
4:D:203:ARG:NH2	4:D:218:ASP:OD1	2.27	0.65
2:B:215:MET:HA	2:B:215:MET:HE2	1.78	0.65
7:G:86:PHE:C	7:G:87:LYS:HD3	2.22	0.65
2:B:261:ALA:HB3	2:B:262:PRO:HD3	1.78	0.65
3:C:229:ALA:HB2	3:C:237:VAL:HG22	1.78	0.65
1:A:91:ARG:O	1:A:94:GLU:HB2	1.97	0.64
6:F:4:THR:CG2	6:F:55:ARG:HE	2.08	0.64
7:G:95:VAL:HG21	7:G:131:LYS:HB3	1.80	0.64
6:F:68:ASN:C	6:F:68:ASN:HD22	2.06	0.64
2:B:282:LEU:HD21	2:B:301:ILE:HD13	1.81	0.63
1:A:243:ASN:ND2	5:E:47:TYR:HE1	1.96	0.63
4:D:129:PHE:HD2	4:D:237:ARG:HG3	1.65	0.62
2:B:218:GLU:HG2	9:B:1002:ATP:C5	2.34	0.62
2:B:219:LYS:HG2	2:B:220:LEU:HD13	1.80	0.62
3:C:193:GLU:HG3	3:C:195:MET:CE	2.30	0.62
5:E:62:ASN:ND2	5:E:65:ASP:H	1.98	0.62
2:B:184:ILE:HD12	2:B:185:ALA:N	2.14	0.61
5:E:95:MET:HE3	5:E:95:MET:HA	1.81	0.61
5:E:130:ARG:HG3	5:E:130:ARG:HH11	1.65	0.61
3:C:14:HIS:H	3:C:331:GLN:NE2	1.98	0.61
6:F:127:TYR:HB3	6:F:129:HIS:CE1	2.36	0.61
5:E:168:PHE:CD2	5:E:169:MET:HE2	2.35	0.61
1:A:230:ARG:HH11	1:A:230:ARG:CB	2.14	0.61
1:A:246:ASP:OD1	5:E:50:LYS:HE3	2.01	0.61
4:D:228:PHE:H	4:D:231:HIS:HD2	1.49	0.61
1:A:111:LEU:HD23	1:A:111:LEU:C	2.26	0.60
6:F:145:GLU:O	6:F:149:MET:HG3	2.01	0.60
1:A:120:PRO:HB2	1:A:409:ARG:HG2	1.83	0.60
2:B:180:ARG:CB	2:B:281:LEU:HD21	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:20:LEU:HD23	6:F:70:VAL:HG21	1.84	0.60
1:A:229:GLU:HG2	9:A:1001:ATP:C5	2.36	0.60
3:C:167:ARG:HG2	3:C:197:GLU:HG3	1.83	0.60
6:F:137:HIS:CE1	6:F:141:GLU:HG3	2.37	0.60
2:B:163:VAL:HG22	2:B:164:THR:N	2.17	0.60
6:F:80:ASP:OD1	6:F:82:ILE:HG22	2.02	0.60
6:F:121:PHE:O	6:F:125:GLN:HG2	2.02	0.59
1:A:384:LEU:HB3	1:A:414:PHE:CE1	2.36	0.59
3:C:193:GLU:CG	3:C:195:MET:HE1	2.32	0.59
2:B:205:ASN:ND2	2:B:208:ALA:H	1.92	0.59
7:G:62:PRO:HG3	7:G:105:LEU:HD21	1.84	0.59
3:C:119:VAL:HG22	3:C:120:ILE:N	2.17	0.58
2:B:151:LEU:HD13	2:B:300:HIS:HD2	1.68	0.58
2:B:155:VAL:HG21	2:B:286:ILE:HD11	1.84	0.58
7:G:87:LYS:HD3	7:G:87:LYS:N	2.19	0.58
1:A:230:ARG:HH11	1:A:230:ARG:HB3	1.69	0.57
2:B:326:LEU:HD12	2:B:337:LEU:CD1	2.31	0.57
2:B:205:ASN:HB3	2:B:208:ALA:HB3	1.86	0.57
2:B:182:LEU:HD22	2:B:184:ILE:HG23	1.86	0.57
6:F:45:GLU:HB3	7:G:24:PHE:CD2	2.40	0.57
3:C:29:ASN:HB3	3:C:31:GLU:H	1.69	0.57
1:A:176:HIS:HD2	1:A:192:HIS:ND1	2.02	0.57
2:B:184:ILE:CD1	2:B:188:ASP:HB2	2.35	0.57
1:A:311:VAL:C	1:A:314:PRO:HD2	2.30	0.57
3:C:107:ASN:HD22	3:C:108:GLU:N	2.02	0.56
4:D:266:MET:HE3	6:F:93:PHE:CD1	2.40	0.56
4:D:95:LEU:HD11	4:D:116:LEU:HG	1.87	0.56
3:C:143:SER:OG	3:C:162:CYS:HB2	2.05	0.56
4:D:147:ARG:HB2	4:D:150:GLU:HB2	1.88	0.56
4:D:223:ILE:HD12	4:D:223:ILE:N	2.21	0.56
7:G:62:PRO:HG2	7:G:105:LEU:CD2	2.36	0.56
1:A:239:VAL:HG13	5:E:4:TYR:CE2	2.40	0.56
2:B:306:GLY:HA2	2:B:309:MET:HE3	1.86	0.56
3:C:184:PRO:HB2	3:C:231:ALA:CB	2.35	0.56
1:A:374:ARG:NH1	9:A:1001:ATP:H8	2.02	0.56
4:D:37:ASP:HB2	4:D:43:TYR:CE1	2.41	0.56
1:A:339:LEU:O	1:A:343:VAL:HG12	2.06	0.56
2:B:156:VAL:HG22	2:B:302:VAL:HG12	1.88	0.56
1:A:223:THR:HG23	1:A:256:TYR:CE2	2.41	0.55
4:D:121:PHE:O	4:D:124:VAL:HG12	2.06	0.55
4:D:118:ARG:HD3	4:D:118:ARG:C	2.30	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:44:SER:O	7:G:47:ARG:HG2	2.06	0.55
5:E:16:ILE:HG23	5:E:16:ILE:O	2.07	0.55
4:D:53:THR:C	4:D:54:LYS:HD2	2.31	0.55
4:D:202:HIS:C	4:D:203:ARG:HG3	2.32	0.55
1:A:36:ALA:HB1	1:A:72:TYR:HB3	1.88	0.54
1:A:191:LYS:HZ1	1:A:306:ASN:HD22	1.55	0.54
1:A:389:GLU:CD	1:A:414:PHE:HB2	2.31	0.54
7:G:47:ARG:HG3	7:G:48:GLN:HG3	1.90	0.54
1:A:93:MET:HE2	1:A:130:MET:HE1	1.90	0.54
5:E:56:LYS:HA	5:E:169:MET:HA	1.89	0.54
3:C:72:THR:HA	3:C:98:ALA:HB1	1.90	0.54
3:C:183:THR:CG2	3:C:185:TRP:H	2.12	0.54
6:F:95:MET:SD	6:F:108:PRO:HD3	2.48	0.54
1:A:191:LYS:HB2	1:A:303:VAL:HG22	1.89	0.53
5:E:78:CYS:O	5:E:82:LEU:HB2	2.09	0.53
4:D:106:LYS:O	4:D:109:ILE:HG12	2.08	0.53
2:B:310:TYR:CE1	9:B:1002:ATP:H2	2.26	0.53
5:E:112:PRO:HG3	5:E:172:SER:O	2.08	0.53
1:A:289:ASN:HD22	1:A:290:PRO:N	2.05	0.53
1:A:30:ILE:HG12	1:A:375:TYR:CZ	2.43	0.53
1:A:395:HIS:HB3	1:A:407:ILE:HD12	1.90	0.53
2:B:302:VAL:HG22	2:B:350:ARG:NH2	2.20	0.53
4:D:137:GLU:OE2	4:D:158:LYS:HE2	2.09	0.53
4:D:171:ASP:OD2	4:D:172:ASP:N	2.42	0.53
1:A:189:CYS:O	1:A:303:VAL:HG13	2.09	0.53
4:D:71:GLY:HA2	4:D:74:GLU:OE1	2.09	0.53
3:C:135:LYS:HB3	3:C:191:PHE:CZ	2.43	0.53
1:A:106:GLU:HG2	1:A:135:ASN:HB3	1.90	0.52
4:D:203:ARG:NH1	4:D:218:ASP:OD1	2.43	0.52
1:A:81:GLY:O	1:A:115:PRO:HG2	2.09	0.52
1:A:393:VAL:HG21	1:A:414:PHE:CD2	2.44	0.52
4:D:37:ASP:HB2	4:D:43:TYR:HE1	1.73	0.52
4:D:106:LYS:O	4:D:109:ILE:N	2.41	0.52
1:A:176:HIS:CD2	1:A:192:HIS:ND1	2.78	0.52
4:D:247:PHE:O	4:D:250:TYR:HB3	2.08	0.52
7:G:38:ASP:HB3	7:G:41:GLU:HB3	1.92	0.52
3:C:156:LEU:HD22	3:C:195:MET:HG3	1.92	0.51
2:B:304:SER:HB3	2:B:350:ARG:CZ	2.40	0.51
1:A:343:VAL:CG2	1:A:363:ILE:HD12	2.41	0.51
2:B:326:LEU:HD23	2:B:326:LEU:O	2.11	0.51
7:G:68:SER:O	7:G:71:VAL:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1022:HOH:O	4:D:34:THR:HG21	2.10	0.51
3:C:173:ILE:HG22	3:C:175:GLU:HG2	1.92	0.51
6:F:4:THR:HG23	6:F:55:ARG:NE	2.12	0.51
1:A:129:ILE:HG22	1:A:130:MET:HE2	1.92	0.51
2:B:189:ILE:HD11	2:B:265:LEU:HG	1.93	0.51
2:B:160:GLY:HA3	9:B:1002:ATP:O2G	2.11	0.51
2:B:319:ARG:NH1	7:G:17:ASP:OD2	2.44	0.51
4:D:129:PHE:CG	4:D:232:THR:HB	2.45	0.51
4:D:202:HIS:O	4:D:203:ARG:HG3	2.10	0.51
2:B:346:ASP:N	2:B:347:PRO:HD3	2.25	0.51
4:D:281:ARG:NH1	6:F:102:PHE:CZ	2.79	0.51
3:C:228:LEU:C	3:C:228:LEU:HD23	2.36	0.51
5:E:149:PHE:CE2	5:E:156:PRO:HG3	2.46	0.51
2:B:326:LEU:HD23	2:B:326:LEU:C	2.36	0.51
1:A:349:LEU:O	1:A:353:LEU:HD23	2.10	0.51
2:B:155:VAL:HG21	2:B:286:ILE:CD1	2.41	0.50
4:D:75:LEU:HD13	4:D:123:SER:N	2.26	0.50
3:C:48:LEU:HG	3:C:79:TRP:CE3	2.47	0.50
5:E:124:GLN:O	5:E:128:VAL:HG23	2.12	0.50
1:A:157:GLN:HB2	1:A:368:ILE:HD12	1.93	0.50
1:A:168:ILE:CD1	1:A:335:LEU:HD11	2.41	0.50
1:A:191:LYS:HB2	1:A:303:VAL:CG2	2.42	0.50
1:A:370:HIS:HD2	1:A:372:MET:N	2.10	0.50
2:B:302:VAL:CG2	2:B:350:ARG:HH22	2.18	0.50
4:D:150:GLU:HG2	4:D:167:THR:HA	1.92	0.50
5:E:62:ASN:C	5:E:62:ASN:ND2	2.65	0.50
3:C:193:GLU:CG	3:C:195:MET:CE	2.90	0.50
1:A:374:ARG:NH1	9:A:1001:ATP:C8	2.80	0.50
6:F:68:ASN:HD22	6:F:69:SER:N	2.08	0.50
7:G:20:ASP:OD1	7:G:22:ASN:HB2	2.11	0.50
1:A:192:HIS:CD2	1:A:192:HIS:N	2.80	0.50
6:F:87:CYS:O	6:F:91:MET:HG2	2.11	0.50
4:D:19:PHE:HB3	4:D:106:LYS:HD3	1.94	0.50
3:C:184:PRO:HB2	3:C:231:ALA:HB1	1.93	0.49
4:D:263:HIS:HD2	4:D:266:MET:CE	2.24	0.49
2:B:231:GLN:O	2:B:235:LEU:HB2	2.11	0.49
2:B:182:LEU:HD22	2:B:184:ILE:CG2	2.42	0.49
3:C:212:ALA:HB3	3:C:255:GLU:OE2	2.13	0.49
3:C:125:PHE:HD2	3:C:132:TRP:CE2	2.30	0.49
4:D:182:MET:HE2	4:D:223:ILE:HG13	1.94	0.49
3:C:119:VAL:HG21	3:C:136:HIS:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:193:GLU:HG3	3:C:195:MET:HE1	1.93	0.49
4:D:199:LEU:HB2	4:D:224:THR:HB	1.95	0.49
6:F:68:ASN:C	6:F:68:ASN:ND2	2.67	0.49
3:C:254:THR:HG21	3:C:372:VAL:HG22	1.95	0.48
1:A:191:LYS:NZ	1:A:306:ASN:HD22	2.12	0.48
2:B:227:ILE:HD11	2:B:263:GLU:OE2	2.12	0.48
3:C:82:LYS:HG3	3:C:87:LYS:HG3	1.95	0.48
5:E:78:CYS:SG	5:E:95:MET:HE2	2.54	0.48
6:F:76:VAL:HG12	6:F:77:LYS:N	2.28	0.48
3:C:284:ARG:HD3	3:C:286:ASP:O	2.13	0.48
6:F:24:ASN:HD21	6:F:34:ASN:HD21	1.60	0.48
1:A:38:LYS:O	1:A:39:GLU:HB3	2.13	0.48
1:A:147:LEU:HD12	1:A:377:VAL:HG13	1.94	0.48
3:C:110:LYS:NZ	3:C:177:GLU:OE1	2.45	0.48
3:C:216:ARG:HH12	3:C:256:SER:HB3	1.79	0.48
5:E:111:PHE:HA	5:E:112:PRO:HD3	1.70	0.48
1:A:149:LEU:HD23	1:A:320:VAL:HG21	1.96	0.48
2:B:287:GLN:NE2	2:B:298:TYR:OH	2.46	0.48
1:A:260:ASN:O	1:A:264:LYS:N	2.46	0.48
5:E:58:TYR:CD1	5:E:168:PHE:HZ	2.32	0.48
3:C:102:VAL:HA	3:C:112:ALA:O	2.14	0.47
5:E:9:MET:HE3	5:E:13:THR:HB	1.93	0.47
1:A:191:LYS:HE2	1:A:303:VAL:CG2	2.31	0.47
1:A:243:ASN:ND2	5:E:47:TYR:CE1	2.81	0.47
2:B:321:LEU:HD12	2:B:342:ILE:HD11	1.95	0.47
5:E:95:MET:HG2	5:E:141:GLY:O	2.15	0.47
2:B:151:LEU:CD1	2:B:300:HIS:HD2	2.26	0.47
2:B:184:ILE:HD12	2:B:185:ALA:H	1.76	0.47
6:F:31:GLU:OE2	6:F:32:ARG:NE	2.41	0.47
1:A:135:ASN:OD1	1:A:135:ASN:O	2.33	0.47
3:C:321:LEU:HD11	6:F:129:HIS:CE1	2.50	0.47
1:A:114:GLU:O	1:A:144:GLN:HG3	2.14	0.47
3:C:119:VAL:CG2	3:C:120:ILE:N	2.78	0.47
3:C:332:ILE:HA	3:C:346:CYS:O	2.15	0.47
4:D:75:LEU:HD23	4:D:75:LEU:C	2.40	0.47
4:D:129:PHE:CD2	4:D:237:ARG:HG3	2.49	0.47
6:F:73:SER:HB3	6:F:112:TYR:CG	2.50	0.47
7:G:91:ILE:O	7:G:95:VAL:HG23	2.15	0.47
1:A:289:ASN:C	1:A:289:ASN:ND2	2.69	0.47
1:A:311:VAL:O	1:A:315:LEU:HG	2.15	0.46
2:B:155:VAL:HG21	2:B:286:ILE:CG1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:68:GLN:HA	4:D:72:ALA:HB3	1.98	0.46
1:A:61:PHE:C	1:A:66:ALA:HB2	2.41	0.46
3:C:254:THR:HG21	3:C:372:VAL:CG2	2.46	0.46
2:B:155:VAL:HG21	2:B:286:ILE:HG12	1.97	0.46
2:B:278:VAL:HG13	2:B:279:ALA:N	2.29	0.46
7:G:62:PRO:HA	7:G:63:PRO:HD3	1.72	0.46
1:A:384:LEU:HB3	1:A:414:PHE:CZ	2.50	0.46
3:C:234:LYS:O	3:C:235:MET:HB2	2.16	0.46
5:E:143:ARG:O	5:E:146:GLU:HG2	2.15	0.45
1:A:21:TYR:OH	1:A:103:ALA:HB2	2.17	0.45
4:D:67:LEU:HD13	4:D:120:CYS:O	2.16	0.45
5:E:113:LEU:HD11	5:E:169:MET:HE1	1.99	0.45
1:A:389:GLU:OE2	1:A:414:PHE:HB2	2.17	0.45
2:B:171:GLU:OE2	2:B:171:GLU:HA	2.17	0.45
3:C:109:LYS:HD3	3:C:176:VAL:O	2.16	0.45
5:E:130:ARG:HG3	5:E:130:ARG:NH1	2.31	0.45
1:A:327:MET:HE2	1:A:374:ARG:HB2	1.99	0.45
4:D:248:ARG:HD3	4:D:248:ARG:C	2.42	0.45
5:E:23:PRO:HG3	5:E:33:PRO:HB2	1.99	0.45
7:G:87:LYS:O	7:G:88:ALA:C	2.60	0.45
1:A:193:ILE:O	1:A:195:ILE:N	2.45	0.45
1:A:239:VAL:HG23	1:A:240:LYS:N	2.31	0.45
1:A:398:LYS:HD2	10:A:1020:HOH:O	2.17	0.45
3:C:73:ASP:O	3:C:74:ARG:HB2	2.16	0.45
4:D:126:GLU:O	4:D:130:GLN:HB2	2.16	0.45
7:G:78:ILE:O	7:G:82:VAL:HG23	2.16	0.45
1:A:193:ILE:C	1:A:195:ILE:H	2.23	0.45
4:D:27:LYS:HD3	4:D:27:LYS:HA	1.88	0.45
5:E:15:LEU:CD2	5:E:63:GLU:HG3	2.47	0.45
6:F:44:LYS:HG2	10:F:193:HOH:O	2.17	0.45
6:F:76:VAL:HG13	10:F:188:HOH:O	2.17	0.45
3:C:172:TYR:C	3:C:172:TYR:CD2	2.92	0.44
5:E:82:LEU:HD13	5:E:95:MET:SD	2.57	0.44
5:E:166:ARG:HG2	5:E:166:ARG:HH11	1.82	0.44
3:C:107:ASN:HD22	3:C:109:LYS:H	1.65	0.44
2:B:347:PRO:HA	2:B:348:PRO:HD3	1.75	0.44
3:C:184:PRO:HB2	3:C:231:ALA:HB3	2.00	0.44
4:D:106:LYS:O	4:D:107:ASP:C	2.60	0.44
6:F:125:GLN:HG2	6:F:125:GLN:H	1.59	0.44
3:C:40:ASN:ND2	10:C:405:HOH:O	2.50	0.44
5:E:113:LEU:HD21	5:E:171:LYS:HG3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:45:ILE:HA	4:D:56:MET:O	2.17	0.44
2:B:310:TYR:CZ	9:B:1002:ATP:H2	2.36	0.44
3:C:68:VAL:HG12	3:C:104:TRP:NE1	2.32	0.44
2:B:146:LEU:CD1	2:B:169:VAL:HB	2.48	0.44
3:C:162:CYS:C	3:C:164:PHE:H	2.25	0.44
3:C:263:HIS:CD2	6:F:21:CYS:HB3	2.53	0.43
5:E:41:ILE:O	5:E:41:ILE:HG13	2.18	0.43
2:B:329:VAL:C	2:B:331:LYS:H	2.25	0.43
3:C:174:LYS:HG3	3:C:175:GLU:N	2.33	0.43
4:D:203:ARG:HH12	4:D:218:ASP:HA	1.79	0.43
5:E:86:ASN:O	5:E:87:SER:HB3	2.18	0.43
3:C:96:ASN:OD1	3:C:97:ARG:HG2	2.18	0.43
3:C:183:THR:HG23	3:C:184:PRO:HD2	1.99	0.43
3:C:193:GLU:HG2	3:C:195:MET:HE1	1.99	0.43
2:B:239:VAL:HG23	2:B:240:LEU:CD1	2.46	0.43
3:C:222:HIS:C	3:C:224:SER:H	2.27	0.43
4:D:170:LYS:HE2	4:D:170:LYS:CA	2.31	0.43
4:D:208:GLU:HB3	10:D:327:HOH:O	2.18	0.43
6:F:41:ARG:HB3	6:F:47:LEU:HD11	2.01	0.43
1:A:263:SER:C	1:A:265:LYS:N	2.75	0.43
3:C:258:LEU:O	3:C:269:LEU:HD12	2.19	0.43
1:A:229:GLU:HG2	9:A:1001:ATP:C4	2.53	0.43
4:D:14:THR:HG21	4:D:45:ILE:HG21	2.01	0.43
4:D:137:GLU:OE1	4:D:158:LYS:HB2	2.19	0.43
4:D:164:VAL:HG22	4:D:224:THR:HG23	2.00	0.43
3:C:185:TRP:CD2	3:C:231:ALA:HB2	2.54	0.43
5:E:84:LYS:HA	5:E:84:LYS:HD3	1.91	0.43
7:G:83:LEU:HD22	7:G:128:TRP:CD2	2.53	0.43
2:B:163:VAL:CG2	2:B:164:THR:N	2.81	0.43
3:C:13:CYS:SG	3:C:58:VAL:HG23	2.58	0.43
3:C:321:LEU:N	3:C:321:LEU:CD1	2.81	0.43
6:F:85:ILE:HG13	6:F:86:LEU:N	2.33	0.43
7:G:55:LEU:HD22	7:G:94:ALA:HB1	2.01	0.42
5:E:14:LYS:O	5:E:15:LEU:HD23	2.19	0.42
6:F:8:TYR:OH	6:F:61:VAL:HG23	2.19	0.42
1:A:289:ASN:ND2	1:A:291:ASP:H	2.16	0.42
3:C:264:ASP:O	3:C:265:CYS:HB2	2.19	0.42
5:E:9:MET:SD	5:E:63:GLU:HG2	2.59	0.42
1:A:38:LYS:HE2	1:A:72:TYR:CZ	2.55	0.42
4:D:223:ILE:HG21	4:D:247:PHE:CE2	2.54	0.42
7:G:18:GLU:OE1	7:G:23:LYS:NZ	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:38:ASP:O	7:G:42:VAL:HG23	2.18	0.42
3:C:230:ASP:OD2	3:C:233:LYS:HG3	2.19	0.42
1:A:117:LEU:HD11	1:A:192:HIS:HE1	1.85	0.42
4:D:106:LYS:O	4:D:108:SER:N	2.52	0.42
5:E:18:ASN:O	5:E:63:GLU:HB3	2.20	0.42
5:E:105:ILE:HB	5:E:106:PRO:HD2	2.02	0.42
1:A:239:VAL:HG13	5:E:4:TYR:CZ	2.55	0.42
2:B:177:HIS:ND1	2:B:178:LEU:HG	2.35	0.42
2:B:246:LEU:HB3	2:B:247:PRO:HD2	2.01	0.42
3:C:266:PHE:CE1	3:C:284:ARG:HG3	2.55	0.42
5:E:172:SER:C	5:E:174:SER:N	2.76	0.42
1:A:2:ALA:HB2	1:A:391:TYR:CE1	2.55	0.42
1:A:19:LEU:HD23	1:A:19:LEU:N	2.34	0.42
3:C:179:ARG:HA	3:C:180:PRO:HD3	1.80	0.42
4:D:202:HIS:O	4:D:202:HIS:CG	2.73	0.42
4:D:205:PRO:HG3	4:D:222:TYR:CZ	2.55	0.42
4:D:223:ILE:HG21	4:D:247:PHE:CZ	2.54	0.42
7:G:99:ASP:O	7:G:102:GLY:N	2.52	0.42
1:A:234:VAL:HG11	1:A:334:ARG:HG2	2.01	0.42
1:A:237:ASP:OD2	1:A:240:LYS:HG3	2.20	0.41
3:C:365:ALA:C	3:C:366:LEU:HD12	2.46	0.41
1:A:319:ILE:HB	1:A:367:VAL:HG22	2.02	0.41
2:B:295:SER:O	2:B:299:LYS:HG2	2.21	0.41
3:C:366:LEU:HD12	3:C:366:LEU:N	2.35	0.41
4:D:118:ARG:C	4:D:118:ARG:CD	2.94	0.41
5:E:66:ARG:HH11	5:E:66:ARG:HG3	1.85	0.41
1:A:152:SER:HB3	1:A:320:VAL:CG1	2.51	0.41
2:B:161:ASP:OD1	2:B:187:ARG:HG3	2.20	0.41
5:E:74:TYR:CE1	5:E:137:ARG:HD2	2.55	0.41
5:E:9:MET:HB2	5:E:62:ASN:OD1	2.20	0.41
7:G:55:LEU:CD2	7:G:94:ALA:HB1	2.51	0.41
7:G:100:LYS:HA	7:G:100:LYS:HD3	1.76	0.41
1:A:242:PHE:CE1	5:E:50:LYS:HB3	2.56	0.41
2:B:155:VAL:O	2:B:301:ILE:HA	2.20	0.41
4:D:54:LYS:HD2	4:D:54:LYS:N	2.33	0.41
1:A:177:VAL:HG11	1:A:300:VAL:HA	2.01	0.41
1:A:329:ARG:O	1:A:330:ASP:HB2	2.20	0.41
2:B:153:THR:HA	2:B:169:VAL:O	2.21	0.41
4:D:134:GLU:HB2	4:D:136:LYS:HG3	2.03	0.41
3:C:102:VAL:O	3:C:103:ARG:NH1	2.54	0.41
3:C:286:ASP:HB2	3:C:357:TRP:CH2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:159:SER:HB2	2:B:164:THR:HG23	2.03	0.41
3:C:34:ILE:HB	3:C:46:HIS:HB2	2.02	0.41
3:C:92:ILE:HD12	3:C:92:ILE:N	2.36	0.41
3:C:139:LYS:HA	3:C:140:PRO:HA	1.85	0.41
3:C:183:THR:HG21	3:C:185:TRP:HD1	1.85	0.41
4:D:263:HIS:HD2	4:D:266:MET:HE2	1.84	0.41
4:D:263:HIS:O	4:D:267:ARG:HG3	2.20	0.41
5:E:144:LEU:HD13	5:E:144:LEU:O	2.21	0.41
6:F:40:VAL:O	6:F:41:ARG:C	2.64	0.41
6:F:161:ALA:O	6:F:165:LEU:HB2	2.20	0.41
7:G:114:PHE:CZ	7:G:126:LEU:HD23	2.56	0.41
3:C:17:ASN:HB3	3:C:60:TRP:CZ2	2.56	0.41
3:C:69:THR:O	3:C:76:ALA:HA	2.21	0.41
4:D:181:PHE:CE2	6:F:157:ALA:HA	2.55	0.41
6:F:33:HIS:ND1	6:F:35:LYS:HE2	2.35	0.41
7:G:66:THR:O	7:G:72:LYS:HE3	2.21	0.41
4:D:267:ARG:HG2	6:F:93:PHE:HZ	1.86	0.40
5:E:81:LYS:HE2	5:E:98:LEU:HD21	2.03	0.40
1:A:340:LYS:HE3	1:A:340:LYS:HB3	1.95	0.40
2:B:317:LEU:HB2	2:B:344:ILE:HD12	2.03	0.40
6:F:35:LYS:NZ	10:F:171:HOH:O	2.54	0.40
1:A:129:ILE:O	1:A:133:SER:HB2	2.21	0.40
1:A:157:GLN:HB3	1:A:366:GLN:NE2	2.36	0.40
1:A:247:THR:O	1:A:247:THR:HG22	2.20	0.40
2:B:319:ARG:O	2:B:323:GLN:HG3	2.22	0.40
3:C:29:ASN:O	3:C:54:GLN:HA	2.21	0.40
3:C:273:ASP:O	3:C:277:GLY:N	2.51	0.40
6:F:30:VAL:HG11	6:F:33:HIS:CE1	2.56	0.40
6:F:138:PHE:O	6:F:142:ILE:HG23	2.22	0.40
1:A:128:GLU:HG3	1:A:132:GLU:HG3	2.03	0.40
3:C:207:GLY:O	3:C:219:TRP:HA	2.22	0.40
1:A:311:VAL:O	1:A:311:VAL:HG22	2.21	0.40
5:E:18:ASN:ND2	5:E:118:ALA:HB2	2.37	0.40
5:E:45:ALA:HA	5:E:68:LEU:HD11	2.03	0.40
5:E:158:LYS:HA	5:E:161:THR:OG1	2.21	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	393/418 (94%)	371 (94%)	20 (5%)	2 (0%)	24	34
2	B	206/394 (52%)	184 (89%)	18 (9%)	4 (2%)	6	7
3	C	338/372 (91%)	312 (92%)	24 (7%)	2 (1%)	21	29
4	D	270/300 (90%)	260 (96%)	9 (3%)	1 (0%)	30	39
5	E	165/178 (93%)	152 (92%)	12 (7%)	1 (1%)	21	29
6	F	164/168 (98%)	160 (98%)	3 (2%)	1 (1%)	21	29
7	G	130/151 (86%)	123 (95%)	6 (5%)	1 (1%)	16	22
All	All	1666/1981 (84%)	1562 (94%)	92 (6%)	12 (1%)	18	25

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	GLY
2	B	329	VAL
2	B	331	LYS
6	F	102	PHE
5	E	87	SER
2	B	179	THR
3	C	50	GLU
4	D	107	ASP
1	A	194	PRO
2	B	342	ILE
3	C	62	PRO
7	G	16	VAL

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	339/363 (93%)	327 (96%)	12 (4%)	32	48
2	B	154/345 (45%)	141 (92%)	13 (8%)	10	14
3	C	288/313 (92%)	279 (97%)	9 (3%)	35	53
4	D	241/264 (91%)	239 (99%)	2 (1%)	73	84
5	E	152/159 (96%)	142 (93%)	10 (7%)	15	21
6	F	153/155 (99%)	144 (94%)	9 (6%)	18	27
7	G	109/124 (88%)	102 (94%)	7 (6%)	16	23
All	All	1436/1723 (83%)	1374 (96%)	62 (4%)	26	39

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	GLU
1	A	88	LEU
1	A	143	VAL
1	A	192	HIS
1	A	195	ILE
1	A	230	ARG
1	A	255	GLN
1	A	268	SER
1	A	310	ASP
1	A	335	LEU
1	A	394	CYS
1	A	402	GLU
2	B	167	CYS
2	B	182	LEU
2	B	184	ILE
2	B	200	ARG
2	B	220	LEU
2	B	235	LEU
2	B	240	LEU
2	B	274	GLU
2	B	281	LEU
2	B	320	GLU
2	B	337	LEU
2	B	342	ILE
2	B	350	ARG
3	C	21	THR

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Mol	Chain	Res	Type
3	C	90	LEU
3	C	107	ASN
3	C	140	PRO
3	C	175	GLU
3	C	183	THR
3	C	284	ARG
3	C	321	LEU
3	C	370	LYS
4	D	116	LEU
4	D	141	ARG
5	E	22	LEU
5	E	62	ASN
5	E	63	GLU
5	E	82	LEU
5	E	95	MET
5	E	98	LEU
5	E	102	ASN
5	E	130	ARG
5	E	133	LEU
5	E	161	THR
6	F	6	ARG
6	F	68	ASN
6	F	85	ILE
6	F	101	PHE
6	F	125	GLN
6	F	128	LYS
6	F	130	LYS
6	F	165	LEU
6	F	166	LYS
7	G	39	GLU
7	G	69	GLN
7	G	81	LYS
7	G	87	LYS
7	G	90	ASP
7	G	93	LYS
7	G	146	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	ASN
1	A	122	ASN

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Mol	Chain	Res	Type
1	A	157	GLN
1	A	176	HIS
1	A	205	GLN
1	A	206	GLN
1	A	255	GLN
1	A	289	ASN
1	A	306	ASN
1	A	318	ASN
1	A	366	GLN
1	A	370	HIS
1	A	395	HIS
1	A	410	HIS
2	B	205	ASN
2	B	229	GLN
2	B	231	GLN
2	B	267	GLN
2	B	284	ASN
2	B	287	GLN
2	B	300	HIS
2	B	323	GLN
3	C	4	HIS
3	C	22	GLN
3	C	29	ASN
3	C	44	GLN
3	C	46	HIS
3	C	54	GLN
3	C	65	ASN
3	C	107	ASN
3	C	331	GLN
4	D	49	ASN
4	D	140	ASN
4	D	202	HIS
4	D	231	HIS
4	D	263	HIS
5	E	62	ASN
5	E	90	GLN
6	F	24	ASN
6	F	28	GLN
6	F	68	ASN
6	F	125	GLN
6	F	129	HIS
6	F	137	HIS

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Mol	Chain	Res	Type
6	F	154	ASN
7	G	50	ASN
7	G	56	GLN
7	G	65	ASN
7	G	69	GLN
7	G	96	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
9	ATP	B	1002	8	32,33,33	1.53	5 (15%)	48,52,52	1.69	9 (18%)
9	ATP	A	1001	8	32,33,33	1.53	5 (15%)	48,52,52	1.70	10 (20%)

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
9	ATP	B	1002	8	-	2/22/38/38	0/3/3/3
9	ATP	A	1001	8	-	2/22/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1001	ATP	C2-N1	3.74	1.40	1.33
9	B	1002	ATP	C2-N1	3.69	1.40	1.33
9	B	1002	ATP	PG-O1G	3.52	1.61	1.50
9	A	1001	ATP	PG-O1G	3.52	1.61	1.50
9	A	1001	ATP	C5-N7	-3.18	1.33	1.39
9	B	1002	ATP	C5-N7	-3.09	1.33	1.39
9	A	1001	ATP	C8-N9	-2.32	1.33	1.37
9	B	1002	ATP	C8-N9	-2.28	1.33	1.37
9	B	1002	ATP	C4-N9	-2.10	1.33	1.37
9	A	1001	ATP	C4-N9	-2.04	1.33	1.37

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1001	ATP	N3-C2-N1	-5.57	120.15	128.58
9	B	1002	ATP	N3-C2-N1	-5.40	120.41	128.58
9	A	1001	ATP	C5-C4-N3	-4.27	120.83	126.72
9	B	1002	ATP	C5-C4-N3	-4.26	120.84	126.72
9	A	1001	ATP	C2-N3-C4	4.14	121.94	111.83
9	B	1002	ATP	C2-N3-C4	4.05	121.71	111.83
9	B	1002	ATP	N9-C8-N7	-3.08	109.57	113.94
9	A	1001	ATP	N3-C4-N9	3.00	132.27	127.17
9	A	1001	ATP	N9-C8-N7	-2.94	109.76	113.94
9	B	1002	ATP	N3-C4-N9	2.94	132.17	127.17
9	B	1002	ATP	C5-N7-C8	2.81	107.87	103.45
9	B	1002	ATP	C4-C5-N7	-2.76	107.42	110.58
9	A	1001	ATP	C5-N7-C8	2.70	107.69	103.45
9	A	1001	ATP	C4-C5-N7	-2.63	107.58	110.58
9	B	1002	ATP	O3G-PG-O3B	2.60	113.35	104.64
9	A	1001	ATP	O3G-PG-O3B	2.56	113.20	104.64
9	B	1002	ATP	C4-N9-C8	2.30	108.15	105.74
9	A	1001	ATP	C4-N9-C8	2.23	108.08	105.74
9	A	1001	ATP	O4'-C1'-C2'	-2.05	102.23	106.62

There are no chirality outliers.

All (4) torsion outliers are listed below:

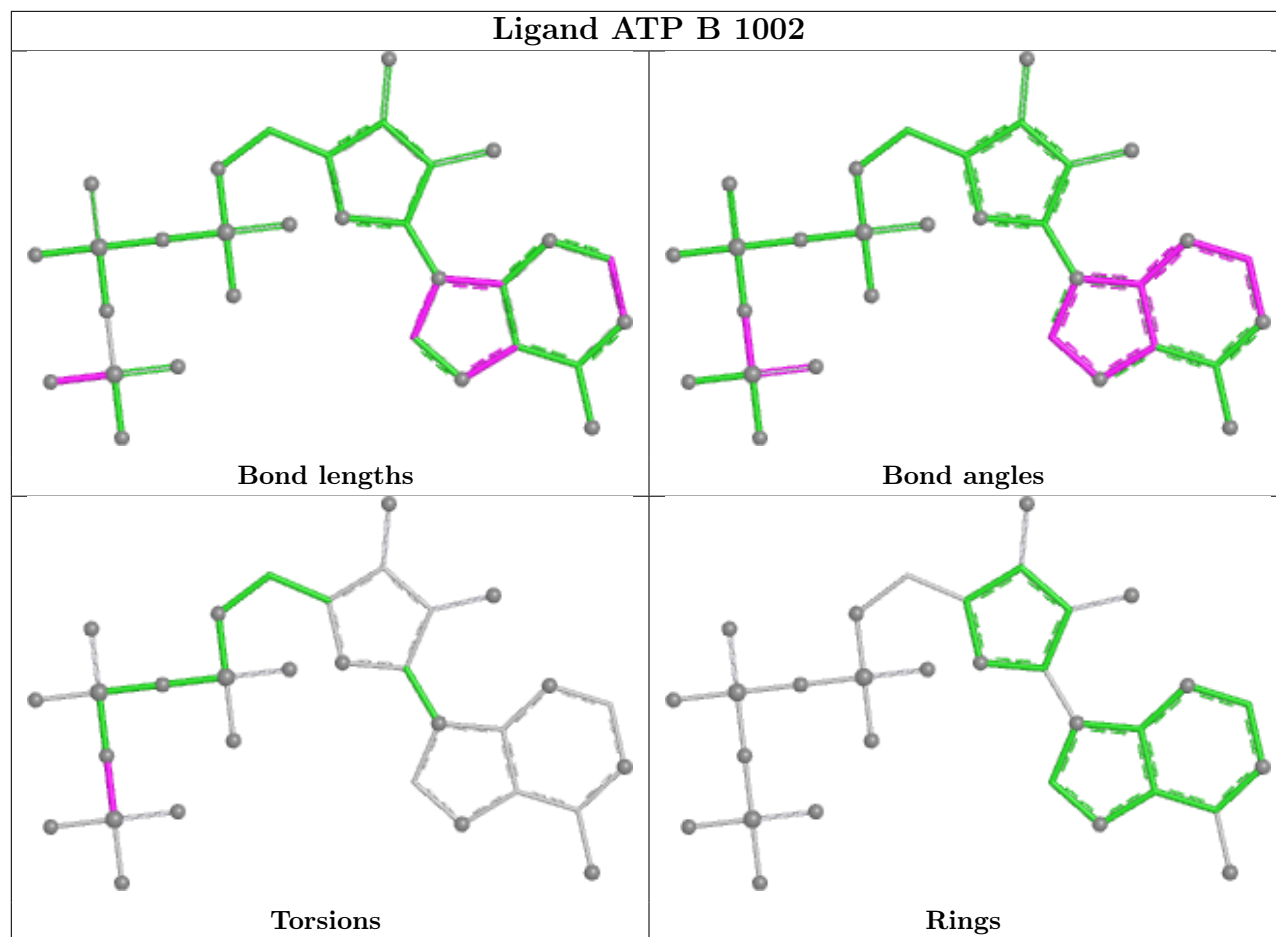
Mol	Chain	Res	Type	Atoms
9	A	1001	ATP	PB-O3B-PG-O2G
9	B	1002	ATP	PB-O3B-PG-O2G
9	A	1001	ATP	PB-O3B-PG-O1G
9	B	1002	ATP	PB-O3B-PG-O1G

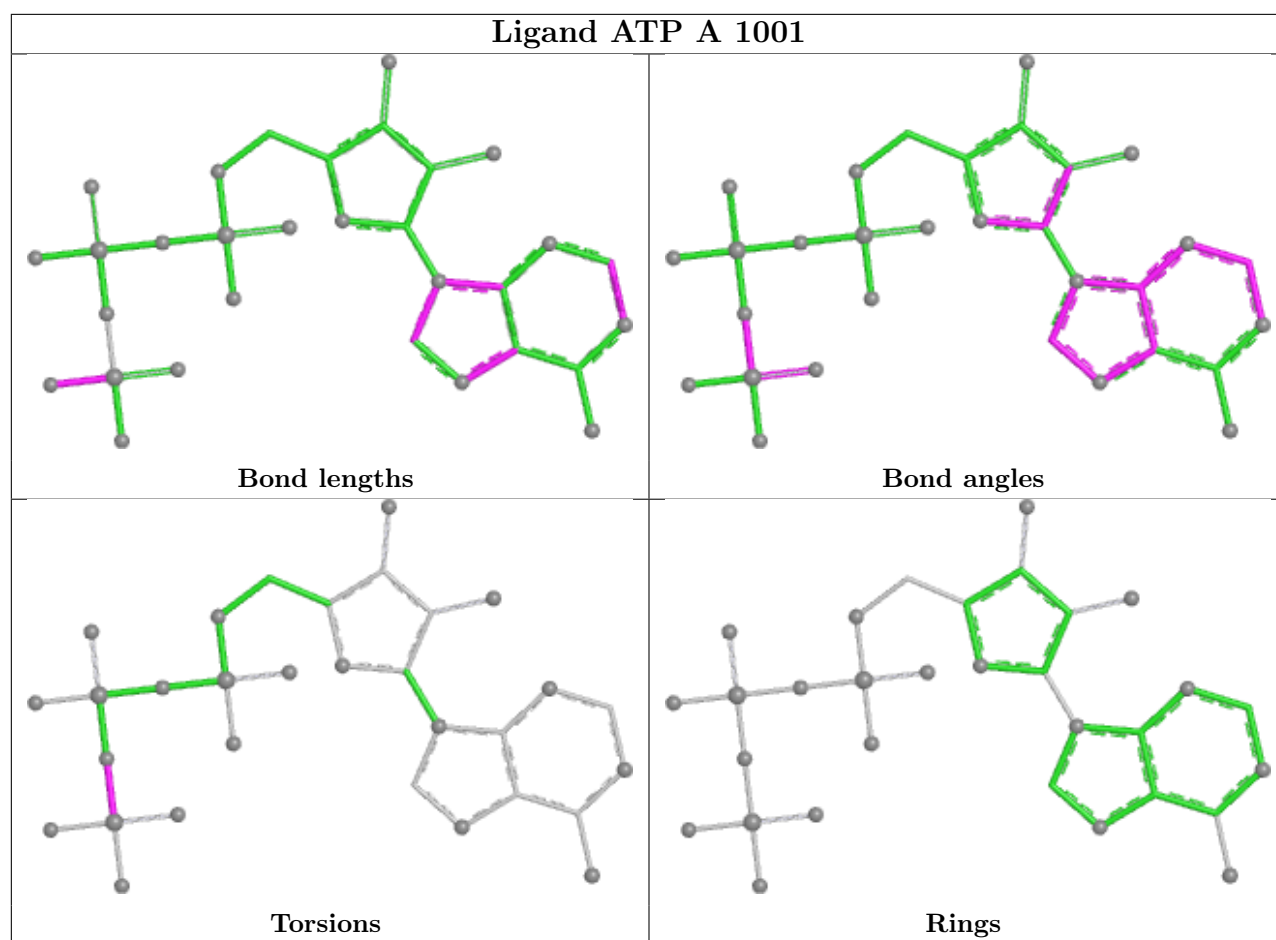
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	1002	ATP	4	0
9	A	1001	ATP	4	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	399/418 (95%)	0.46	27 (6%) 23 22	23, 49, 76, 102	0
2	B	208/394 (52%)	1.07	44 (21%) 2 2	31, 60, 92, 100	0
3	C	342/372 (91%)	0.10	12 (3%) 47 48	27, 40, 67, 89	0
4	D	274/300 (91%)	0.19	9 (3%) 49 50	26, 44, 69, 82	0
5	E	169/178 (94%)	0.73	15 (8%) 15 14	40, 57, 81, 92	0
6	F	166/168 (98%)	-0.00	1 (0%) 85 88	28, 41, 55, 73	0
7	G	134/151 (88%)	0.96	21 (15%) 5 4	32, 66, 85, 105	0
All	All	1692/1981 (85%)	0.44	129 (7%) 20 19	23, 47, 83, 105	0

All (129) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	169	VAL	4.9
2	B	144	LEU	4.9
2	B	289	ALA	4.5
5	E	150	ASP	4.5
3	C	131	TRP	4.5
7	G	27	GLU	4.2
3	C	130	ASP	4.2
2	B	349	ARG	4.1
2	B	290	ASP	4.1
3	C	1	MET	4.1
4	D	171	ASP	4.0
4	D	217	GLY	3.9
1	A	158	VAL	3.9
2	B	154	GLY	3.8
4	D	108	SER	3.8
1	A	353	LEU	3.6
2	B	180	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
2	B	347	PRO	3.6
2	B	333	ASP	3.6
5	E	155	LYS	3.5
1	A	350	SER	3.4
2	B	291	ILE	3.4
2	B	350	ARG	3.4
2	B	329	VAL	3.4
2	B	341	LYS	3.3
1	A	310	ASP	3.3
4	D	207	LEU	3.3
7	G	22	ASN	3.3
2	B	181	ARG	3.2
2	B	294	ARG	3.2
1	A	417	MET	3.2
7	G	66	THR	3.2
1	A	262	ILE	3.2
6	F	147	SER	3.1
1	A	346	ARG	3.1
3	C	230	ASP	3.1
1	A	257	THR	3.0
4	D	107	ASP	3.0
5	E	174	SER	3.0
3	C	372	VAL	3.0
4	D	130	GLN	3.0
2	B	295	SER	3.0
2	B	178	LEU	3.0
5	E	10	ASP	3.0
3	C	371	ILE	2.9
2	B	147	TYR	2.9
3	C	29	ASN	2.9
2	B	153	THR	2.9
7	G	67	LYS	2.8
7	G	71	VAL	2.8
1	A	71	THR	2.8
5	E	92	GLU	2.8
5	E	100	ILE	2.8
5	E	96	TYR	2.7
2	B	143	VAL	2.7
7	G	38	ASP	2.7
7	G	16	VAL	2.7
2	B	292	ASP	2.7
2	B	338	SER	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	149	GLN	2.7
5	E	85	CYS	2.6
2	B	273	VAL	2.6
2	B	170	TYR	2.6
3	C	370	LYS	2.6
4	D	172	ASP	2.6
3	C	319	ALA	2.6
2	B	184	ILE	2.5
1	A	68	GLU	2.5
2	B	340	PHE	2.5
7	G	41	GLU	2.5
7	G	84	ILE	2.5
1	A	213	VAL	2.5
2	B	177	HIS	2.5
3	C	53	GLY	2.5
5	E	12	ASP	2.5
3	C	366	LEU	2.5
2	B	296	GLU	2.5
7	G	150	THR	2.5
2	B	183	ASP	2.4
2	B	326	LEU	2.4
2	B	176	PRO	2.4
3	C	126	GLU	2.4
7	G	63	PRO	2.3
1	A	418	SER	2.3
2	B	146	LEU	2.3
2	B	286	ILE	2.3
2	B	324	LEU	2.3
5	E	89	SER	2.3
7	G	122	SER	2.3
7	G	87	LYS	2.3
4	D	202	HIS	2.3
5	E	90	GLN	2.3
7	G	43	ASP	2.3
7	G	21	GLU	2.3
2	B	328	ARG	2.3
7	G	47	ARG	2.3
1	A	265	LYS	2.2
1	A	348	LYS	2.2
2	B	173	PHE	2.2
1	A	52	MET	2.2
1	A	247	THR	2.2

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Mol	Chain	Res	Type	RSRZ
5	E	116	ILE	2.2
1	A	263	SER	2.2
1	A	39	GLU	2.2
2	B	299	LYS	2.2
1	A	154	THR	2.2
2	B	305	GLY	2.2
7	G	64	ILE	2.2
1	A	343	VAL	2.1
2	B	306	GLY	2.1
1	A	202	TYR	2.1
7	G	17	ASP	2.1
5	E	94	GLU	2.1
7	G	20	ASP	2.1
5	E	84	LYS	2.1
5	E	86	ASN	2.1
1	A	230	ARG	2.1
4	D	174	ASP	2.1
1	A	159	GLY	2.1
2	B	168	PRO	2.1
2	B	276	VAL	2.0
2	B	302	VAL	2.0
1	A	375	TYR	2.0
1	A	268	SER	2.0
1	A	174	VAL	2.0
7	G	11	PHE	2.0
7	G	35	ALA	2.0
2	B	145	THR	2.0
1	A	371	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

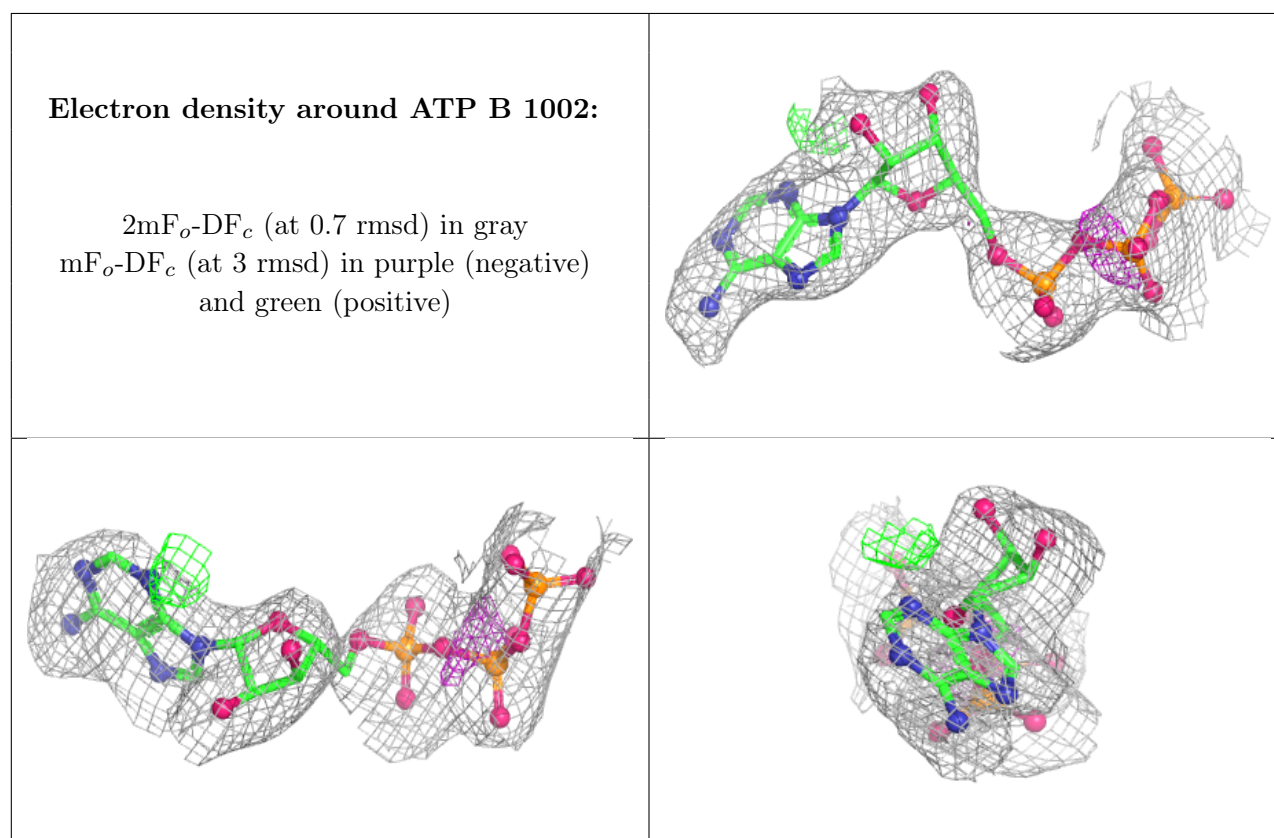
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

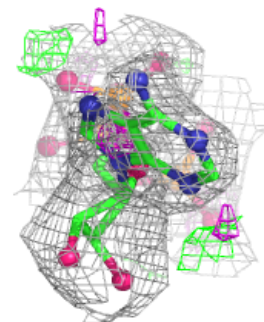
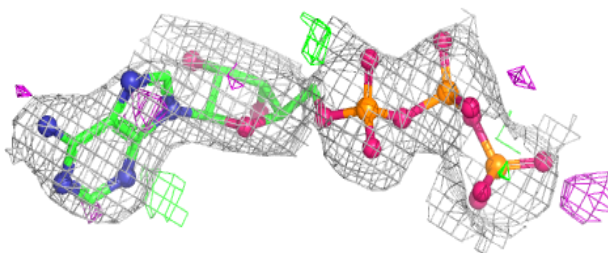
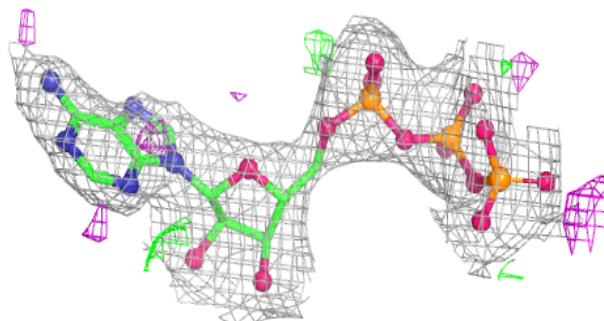
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	CA	B	501	1/1	0.84	0.14	95,95,95,95	0
8	CA	A	500	1/1	0.94	0.19	73,73,73,73	0
9	ATP	B	1002	31/31	0.95	0.09	52,59,74,76	0
9	ATP	A	1001	31/31	0.96	0.09	46,52,58,60	0

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 1001:

$2mF_o - DF_c$ (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.