



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:39 AM UTC

PDB ID : 5NBL / pdb_00005nbl
Title : Crystal structure of the Arp4-N-actin(APO-state) heterodimer bound by a nanobody
Authors : Knoll, K.R.; Eustermann, S.; Hopfner, K.P.
Deposited on : 2017-03-02
Resolution : 2.80 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:

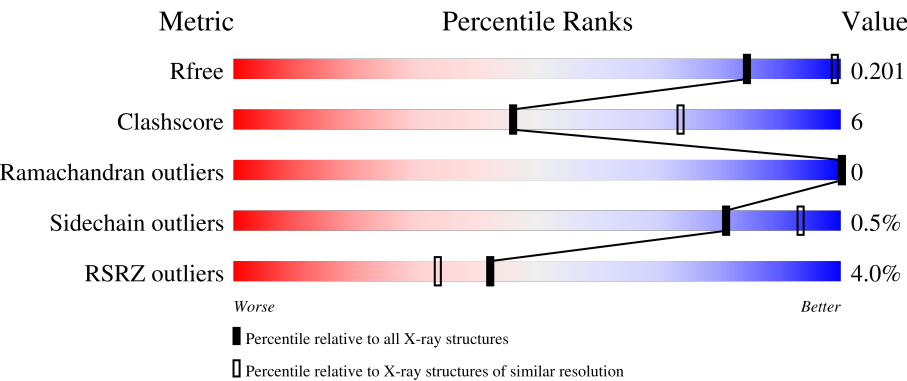
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	489	4% 68%13%19%
1	B	489	3% 72%9%19%
2	C	375	2% 83%14%..
2	D	375	% 86%11%..
3	E	159	8% 60%17%23%

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Mol	Chain	Length	Quality of chain
3	F	159	
4	G	20	
4	H	20	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14207 atoms, of which 24 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 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	0	0	0
			3098	1977	510	600	11			
1	B	397	Total	C	N	O	S	0	0	0
			3094	1975	509	599	11			

- Molecule 2 is a protein called Actin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	366	Total	C	N	O	S	0	0	0
			2854	1807	482	548	17			
2	D	366	Total	C	N	O	S	0	0	0
			2854	1807	482	548	17			

- Molecule 3 is a protein called nAct-Nanobody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	122	Total	C	N	O	S	0	0	0
			949	596	168	181	4			
3	F	124	Total	C	N	O	S	0	0	0
			961	602	170	185	4			

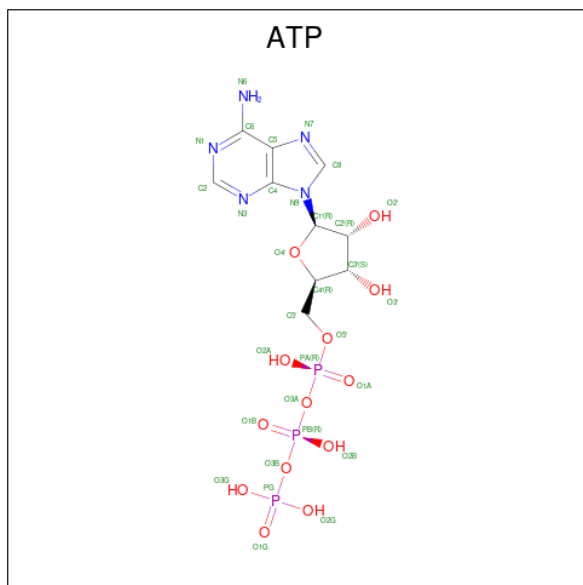
- Molecule 4 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	18	Total	C	N	O	0	0	0
			90	54	18	18			
4	H	20	Total	C	N	O	0	0	0
			100	60	20	20			

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 6 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

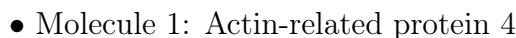


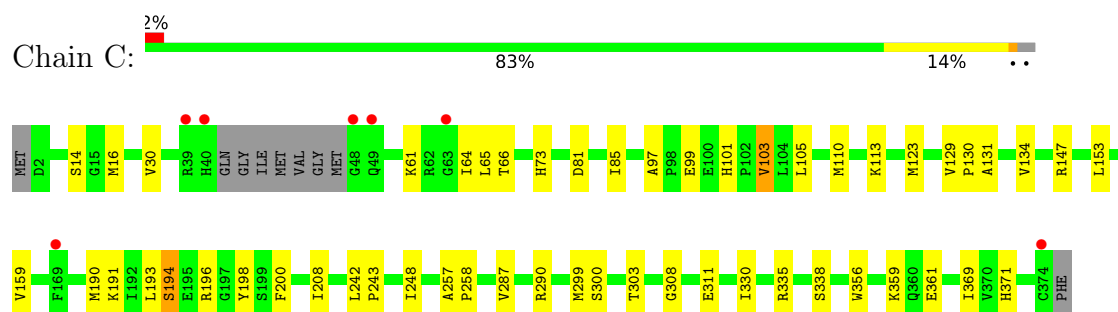
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total 43	C 10	H 12	N 5	O 13	P 3	0	0
6	B	1	Total 43	C 10	H 12	N 5	O 13	P 3	0	0

- Molecule 7 is water.

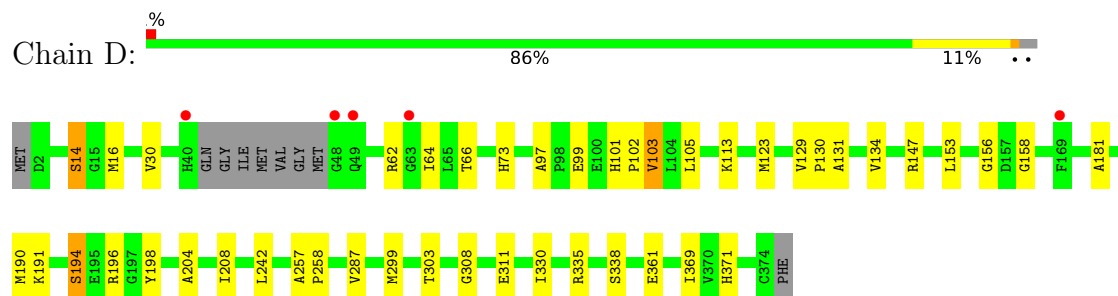
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	32	Total O 32 32	0	0
7	B	32	Total O 32 32	0	0
7	C	19	Total O 19 19	0	0
7	D	24	Total O 24 24	0	0
7	E	7	Total O 7 7	0	0
7	F	5	Total O 5 5	0	0

- Molecule 1: Actin-related protein 4

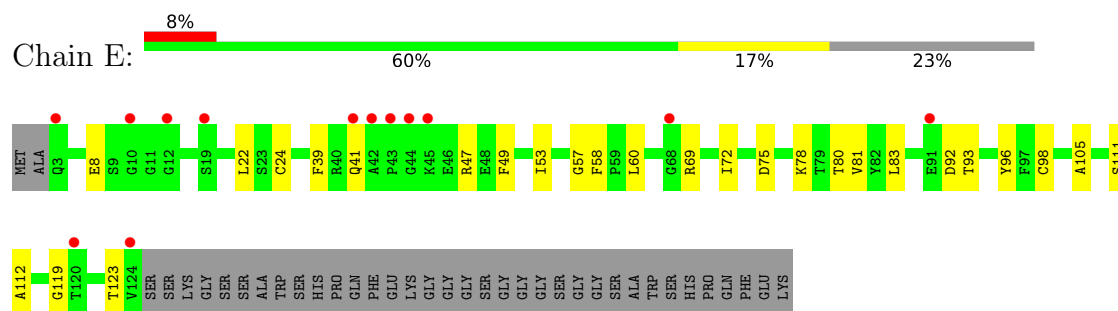




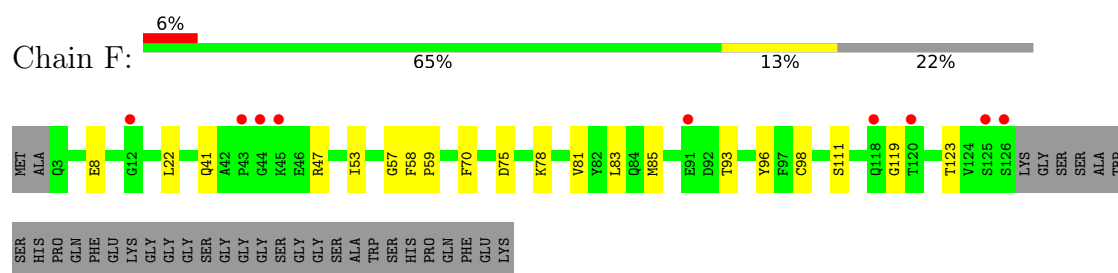
- Molecule 2: Actin



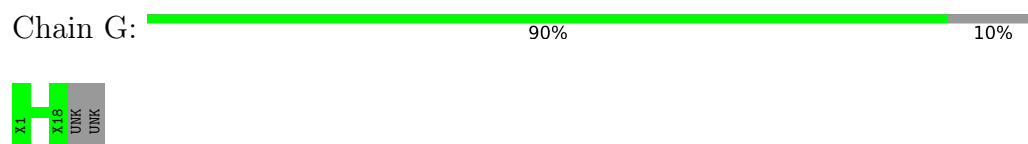
- Molecule 3: nAct-Nanobody



- Molecule 3: nAct-Nanobody



- Molecule 4: Unknown peptide



- Molecule 4: Unknown peptide

Chain H:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	191.22Å 191.22Å 221.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.43 – 2.80 49.43 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.43-2.80) 99.6 (49.43-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.171 , 0.204 0.171 , 0.201	Depositor DCC
R_{free} test set	5684 reflections (3.58%)	wwPDB-VP
Wilson B-factor (Å ²)	57.5	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.031 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14207	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% 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: ATP, CA, HIC

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	0.17	0/3167	0.41	0/4304
1	B	0.17	0/3163	0.41	0/4299
2	C	0.17	0/2902	0.39	0/3928
2	D	0.17	0/2902	0.39	0/3928
3	E	0.16	0/971	0.41	0/1314
3	F	0.18	0/983	0.42	0/1330
All	All	0.17	0/14088	0.40	0/19103

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	3098	0	3028	37	0
1	B	3094	0	3022	34	0
2	C	2854	0	2817	37	0
2	D	2854	0	2817	31	0
3	E	949	0	903	16	0
3	F	961	0	913	15	0
4	G	90	0	20	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	100	0	22	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	31	12	12	0	0
6	B	31	12	12	0	0
7	A	32	0	0	1	0
7	B	32	0	0	1	0
7	C	19	0	0	1	0
7	D	24	0	0	2	0
7	E	7	0	0	0	0
7	F	5	0	0	0	0
All	All	14183	24	13566	160	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 6.

All (160) 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)
3:F:53:ILE:HD11	3:F:57:GLY:HA2	1.51	0.90
3:E:53:ILE:HD11	3:E:57:GLY:HA2	1.53	0.88
1:A:16:ALA:HB3	1:A:460:THR:HG21	1.62	0.82
2:D:16:MET:HE3	2:D:30:VAL:HG12	1.63	0.80
2:D:190:MET:HE3	3:F:59:PRO:HG3	1.64	0.80
1:B:16:ALA:HB3	1:B:460:THR:HG21	1.66	0.77
2:C:16:MET:HE3	2:C:30:VAL:HG12	1.67	0.75
2:D:196:ARG:HG2	7:D:404:HOH:O	1.92	0.69
2:C:105:LEU:HD21	2:C:123:MET:HE3	1.74	0.68
3:E:93:THR:HG23	3:E:123:THR:HA	1.75	0.68
2:C:110:MET:HA	2:C:110:MET:HE2	1.76	0.67
2:D:97:ALA:HB1	2:D:99:GLU:OE2	1.96	0.65
1:B:160:ILE:HG22	1:B:414:THR:HB	1.79	0.65
2:C:196:ARG:HG2	7:C:408:HOH:O	1.97	0.65
3:F:75:ASP:OD2	3:F:78:LYS:HE2	1.98	0.64
3:E:75:ASP:OD2	3:E:78:LYS:HE2	2.00	0.62
1:B:452:SER:HB2	7:B:612:HOH:O	2.00	0.61
2:D:105:LEU:HD21	2:D:123:MET:HE3	1.83	0.61
2:C:153:LEU:HD23	2:C:299:MET:HE3	1.84	0.59
1:A:204:ILE:HD13	1:A:218:LYS:HD3	1.85	0.58
2:C:190:MET:HE3	2:C:200:PHE:O	2.04	0.58
3:E:96:TYR:O	3:E:119:GLY:HA2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:8:GLU:HG3	3:F:98:CYS:SG	2.43	0.57
2:D:190:MET:HE3	3:F:59:PRO:CG	2.34	0.57
2:D:303:THR:HG22	2:D:303:THR:O	2.05	0.57
2:D:62:ARG:HD2	2:D:204:ALA:HA	1.86	0.57
1:B:144:THR:O	1:B:147:SER:HB3	2.04	0.57
2:C:303:THR:HG22	2:C:303:THR:O	2.05	0.57
1:A:16:ALA:HB3	1:A:460:THR:CG2	2.34	0.56
2:C:101:HIS:O	2:C:130:PRO:HD2	2.06	0.56
2:C:194:SER:HA	2:C:198:TYR:O	2.06	0.56
2:D:147:ARG:CZ	2:D:330:ILE:HD13	2.36	0.56
1:B:459:LEU:HD13	1:B:465:PHE:HZ	1.71	0.55
3:E:22:LEU:HB2	3:E:83:LEU:HB3	1.89	0.55
2:C:97:ALA:HB1	2:C:99:GLU:OE2	2.07	0.55
3:F:96:TYR:O	3:F:119:GLY:HA2	2.06	0.55
1:B:410:LEU:HG	1:B:415:SER:HB2	1.89	0.54
2:C:66:THR:HG21	3:E:111:SER:HB2	1.89	0.54
3:E:22:LEU:HD12	3:E:83:LEU:HD23	1.89	0.53
2:D:153:LEU:HD23	2:D:299:MET:HE3	1.90	0.53
2:C:147:ARG:CZ	2:C:330:ILE:HD13	2.38	0.53
2:D:194:SER:HA	2:D:198:TYR:O	2.08	0.53
1:A:108:ALA:O	1:A:137:CYS:HA	2.09	0.53
1:B:44:TYR:CD1	1:B:85:THR:HG21	2.45	0.52
3:F:93:THR:HG23	3:F:123:THR:HA	1.91	0.52
3:F:53:ILE:CD1	3:F:57:GLY:HA2	2.32	0.52
1:B:244:GLU:HB3	2:C:287:VAL:HG21	1.92	0.52
2:D:361:GLU:HB3	2:D:369:ILE:CD1	2.40	0.52
1:A:258:THR:O	1:A:258:THR:HG22	2.09	0.52
2:C:361:GLU:HB3	2:C:369:ILE:CD1	2.40	0.52
1:A:309:SER:HA	1:A:383:ILE:HG13	1.93	0.51
1:A:181:ARG:HB3	1:A:388:LEU:HD22	1.91	0.51
3:E:53:ILE:CD1	3:E:57:GLY:HA2	2.36	0.51
2:C:14:SER:HB3	2:C:159:VAL:HG12	1.93	0.51
1:B:258:THR:HG22	1:B:258:THR:O	2.11	0.50
1:A:136:ALA:HB1	1:A:469:TRP:HB3	1.92	0.50
1:B:132:MET:O	1:B:133:GLN:HB2	2.10	0.50
1:B:381:GLU:O	1:B:382:LEU:HB2	2.11	0.49
1:A:132:MET:O	1:A:133:GLN:HB2	2.12	0.49
1:B:198:LEU:HD11	1:B:238:PHE:HE2	1.77	0.49
1:A:244:GLU:HB3	2:D:287:VAL:HG21	1.95	0.49
1:B:136:ALA:HB1	1:B:469:TRP:HB3	1.95	0.49
1:B:138:TYR:CE2	1:B:465:PHE:CE1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:ALA:O	1:A:437:PHE:HA	2.13	0.49
1:B:16:ALA:HB3	1:B:460:THR:CG2	2.39	0.49
3:F:22:LEU:HB2	3:F:83:LEU:HB3	1.95	0.48
1:B:148:PHE:CD1	1:B:459:LEU:HD21	2.48	0.48
3:E:105:ALA:HB1	3:E:112:ALA:HB1	1.95	0.48
2:C:361:GLU:HB3	2:C:369:ILE:HD13	1.94	0.48
1:B:106:ILE:HD12	1:B:106:ILE:N	2.29	0.48
1:A:44:TYR:CD1	1:A:85:THR:HG21	2.49	0.48
1:A:65:PRO:HA	1:A:229:LEU:CD2	2.44	0.47
2:D:103:VAL:HG23	2:D:105:LEU:HD13	1.95	0.47
1:B:459:LEU:HD13	1:B:465:PHE:CZ	2.50	0.47
2:C:113:LYS:HG2	2:C:371:HIS:CE1	2.49	0.47
2:D:191:LYS:HD2	3:F:58:PHE:CD1	2.49	0.47
3:E:60:LEU:HD23	3:E:72:ILE:CG2	2.45	0.47
1:A:269:SER:HB3	1:A:279:VAL:HG22	1.97	0.47
1:B:148:PHE:CE1	1:B:459:LEU:HD21	2.50	0.47
2:D:308:GLY:HA2	2:D:311:GLU:OE1	2.15	0.47
1:A:148:PHE:CE1	1:A:459:LEU:HD21	2.50	0.47
2:C:110:MET:HE2	2:C:110:MET:CA	2.42	0.46
1:B:198:LEU:O	1:B:201:LYS:HB2	2.15	0.46
2:C:308:GLY:HA2	2:C:311:GLU:OE1	2.15	0.46
2:D:14:SER:HB2	2:D:158:GLY:H	1.80	0.46
1:A:207:PHE:CD1	1:A:207:PHE:C	2.94	0.46
1:A:308:ASN:O	1:A:309:SER:OG	2.23	0.46
2:C:131:ALA:HB1	2:C:356:TRP:HB3	1.97	0.46
2:D:303:THR:O	2:D:303:THR:CG2	2.63	0.46
3:F:70:PHE:CZ	3:F:85:MET:HE2	2.51	0.46
1:B:240:GLN:OE1	1:B:244:GLU:HG3	2.15	0.46
1:A:250:CYS:O	1:A:423:ARG:HD3	2.17	0.45
1:A:253:LYS:HB2	1:A:257:GLU:OE1	2.15	0.45
2:C:303:THR:O	2:C:303:THR:CG2	2.63	0.45
1:A:20:ASP:HA	1:A:111:THR:OG1	2.16	0.45
1:A:240:GLN:NE2	1:A:244:GLU:HG3	2.31	0.45
1:B:304:TRP:CD1	1:B:305:PRO:HD2	2.51	0.45
3:E:69:ARG:HH22	3:E:92:ASP:CG	2.24	0.45
1:B:428:LEU:HD13	1:B:437:PHE:CE1	2.52	0.45
3:F:22:LEU:HD12	3:F:83:LEU:HD23	1.97	0.45
1:B:42:SER:C	1:B:43:VAL:HG23	2.42	0.44
2:C:242:LEU:HB3	2:C:243:PRO:CD	2.48	0.44
3:E:8:GLU:HG3	3:E:98:CYS:SG	2.57	0.44
2:D:123:MET:O	2:D:129:VAL:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:PHE:CE2	1:A:193:LEU:HD11	2.52	0.44
1:A:144:THR:O	1:A:147:SER:HB3	2.18	0.43
1:B:108:ALA:O	1:B:137:CYS:HA	2.18	0.43
3:F:41:GLN:OE1	3:F:47:ARG:HG3	2.16	0.43
2:D:101:HIS:O	2:D:130:PRO:HD2	2.17	0.43
3:E:39:PHE:CD2	3:E:49:PHE:HA	2.53	0.43
1:A:42:SER:C	1:A:43:VAL:HG23	2.44	0.43
1:A:95:GLN:HG3	7:A:628:HOH:O	2.19	0.43
1:A:212:ARG:NH1	1:A:213:LYS:HE3	2.33	0.43
1:A:239:PHE:O	1:A:243:LYS:HG3	2.18	0.43
2:C:103:VAL:HG23	2:C:105:LEU:HD13	2.00	0.43
2:D:64:ILE:HG22	2:D:64:ILE:O	2.18	0.43
3:E:24:CYS:O	3:E:80:THR:HA	2.19	0.43
1:A:160:ILE:HG22	1:A:414:THR:HB	2.00	0.43
1:B:244:GLU:CD	2:C:290:ARG:HH22	2.27	0.43
2:D:113:LYS:HG2	2:D:371:HIS:CE1	2.53	0.43
2:C:335:ARG:HA	2:C:338:SER:OG	2.18	0.43
2:D:208:ILE:HG21	2:D:242:LEU:HD22	2.01	0.43
2:C:257:ALA:HB3	2:C:258:PRO:CD	2.50	0.42
1:A:106:ILE:N	1:A:106:ILE:HD12	2.34	0.42
2:C:64:ILE:HG22	2:C:64:ILE:O	2.19	0.42
2:C:105:LEU:O	2:C:134:VAL:HA	2.19	0.42
1:A:381:GLU:O	1:A:382:LEU:HB2	2.19	0.42
1:B:459:LEU:HB3	1:B:465:PHE:CE2	2.54	0.42
1:B:207:PHE:CD1	1:B:207:PHE:C	2.98	0.42
2:C:300:SER:HB2	2:C:338:SER:HB2	2.01	0.42
2:C:208:ILE:HG21	2:C:242:LEU:HD22	2.02	0.42
2:C:123:MET:O	2:C:129:VAL:HG22	2.20	0.42
3:E:41:GLN:HB2	3:E:47:ARG:HA	2.01	0.42
1:B:181:ARG:HB3	1:B:388:LEU:HD22	2.00	0.41
2:D:64:ILE:HG22	7:D:417:HOH:O	2.20	0.41
2:D:102:PRO:HB3	2:D:131:ALA:HB3	2.02	0.41
1:A:260:THR:HG22	1:A:260:THR:O	2.21	0.41
1:A:410:LEU:HG	1:A:415:SER:HB2	2.02	0.41
1:B:390:TYR:HB2	1:B:431:ILE:HD12	2.03	0.41
1:B:420:LEU:C	1:B:420:LEU:HD23	2.46	0.41
2:C:81:ASP:O	2:C:85:ILE:HG13	2.20	0.41
3:F:41:GLN:HB2	3:F:47:ARG:HA	2.02	0.41
2:C:61:LYS:O	2:C:65:LEU:HD12	2.21	0.41
1:B:405:ALA:O	1:B:437:PHE:HA	2.20	0.41
1:A:138:TYR:CD2	1:A:465:PHE:CE1	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ASN:OD1	1:A:183:ASN:C	2.64	0.41
1:A:112:GLU:O	1:A:142:THR:HG23	2.21	0.41
2:D:66:THR:HG21	3:F:111:SER:HB2	2.02	0.41
2:D:156:GLY:O	2:D:181:ALA:HB1	2.21	0.41
1:B:454:LEU:HD12	1:B:454:LEU:HA	1.90	0.41
2:D:105:LEU:O	2:D:134:VAL:HA	2.21	0.41
2:D:335:ARG:HA	2:D:338:SER:OG	2.21	0.41
1:A:463:GLY:HA3	2:C:359:LYS:NZ	2.36	0.40
1:B:188:LYS:O	1:B:191:ASN:HB2	2.22	0.40
2:C:191:LYS:HD2	3:E:58:PHE:CD1	2.56	0.40
2:C:193:LEU:HD23	2:C:193:LEU:HA	1.96	0.40
2:C:198:TYR:CZ	2:C:248:ILE:HB	2.56	0.40
2:D:257:ALA:HB3	2:D:258:PRO:CD	2.51	0.40
1:A:390:TYR:CD2	1:A:431:ILE:HD12	2.57	0.40
2:D:361:GLU:HB3	2:D:369:ILE:HD13	2.03	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	393/489 (80%)	380 (97%)	13 (3%)	0	100	100
1	B	393/489 (80%)	382 (97%)	11 (3%)	0	100	100
2	C	361/375 (96%)	354 (98%)	7 (2%)	0	100	100
2	D	361/375 (96%)	354 (98%)	7 (2%)	0	100	100
3	E	120/159 (76%)	113 (94%)	7 (6%)	0	100	100
3	F	122/159 (77%)	113 (93%)	9 (7%)	0	100	100
All	All	1750/2046 (86%)	1696 (97%)	54 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	340/434 (78%)	339 (100%)	1 (0%)	86	95
1	B	339/434 (78%)	339 (100%)	0	100	100
2	C	311/319 (98%)	309 (99%)	2 (1%)	78	92
2	D	311/319 (98%)	308 (99%)	3 (1%)	68	88
3	E	97/122 (80%)	96 (99%)	1 (1%)	68	88
3	F	99/122 (81%)	98 (99%)	1 (1%)	68	88
All	All	1497/1750 (86%)	1489 (100%)	8 (0%)	81	93

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	126	GLU
2	C	103	VAL
2	C	194	SER
2	D	14	SER
2	D	103	VAL
2	D	194	SER
3	E	81	VAL
3	F	81	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	101	ASN
1	A	103	ASN
1	A	248	HIS
1	B	91	GLN
1	B	103	ASN
1	B	248	HIS
1	B	275	ASN
1	B	407	ASN

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Mol	Chain	Res	Type
1	B	451	GLN
2	C	87	HIS
2	C	121	GLN
2	C	263	HIS
2	D	87	HIS
2	D	92	ASN
2	D	121	GLN
2	D	232	GLN
2	D	263	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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
2	HIC	C	73	2	10,11,12	1.55	1 (10%)	9,14,16	1.10	1 (11%)
2	HIC	D	73	2	10,11,12	1.54	1 (10%)	9,14,16	1.20	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HIC	C	73	2	-	0/5/6/8	0/1/1/1
2	HIC	D	73	2	-	0/5/6/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	73	HIC	CD2-CG	3.15	1.41	1.36
2	D	73	HIC	CD2-CG	3.13	1.41	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	73	HIC	NE2-CE1-ND1	-2.95	111.53	112.66
2	C	73	HIC	NE2-CE1-ND1	-2.51	111.70	112.66

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 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
6	ATP	B	502	5	32,33,33	1.36	5 (15%)	48,52,52	1.77	10 (20%)
6	ATP	A	502	5	32,33,33	1.43	7 (21%)	48,52,52	1.78	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
6	ATP	B	502	5	-	3/22/38/38	0/3/3/3
6	ATP	A	502	5	-	4/22/38/38	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	502	ATP	C5-C4	4.47	1.47	1.39
6	A	502	ATP	C5-C4	4.36	1.46	1.39
6	A	502	ATP	PA-O3A	2.59	1.62	1.59
6	B	502	ATP	C5-C6	2.54	1.48	1.41
6	B	502	ATP	C8-N7	2.41	1.36	1.31
6	A	502	ATP	C5-C6	2.40	1.47	1.41
6	A	502	ATP	C8-N7	2.35	1.36	1.31
6	A	502	ATP	PB-O3A	2.33	1.62	1.59
6	A	502	ATP	C5-N7	-2.25	1.35	1.39
6	B	502	ATP	C5-N7	-2.17	1.35	1.39
6	B	502	ATP	PB-O3B	2.14	1.61	1.59
6	A	502	ATP	PB-O3B	2.11	1.61	1.59

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	502	ATP	C5-C4-N3	-5.46	119.20	126.72
6	A	502	ATP	C5-C4-N3	-5.44	119.23	126.72
6	A	502	ATP	N3-C4-N9	4.59	134.98	127.17
6	B	502	ATP	N3-C4-N9	4.50	134.82	127.17
6	A	502	ATP	N3-C2-N1	-3.86	122.74	128.58
6	B	502	ATP	N3-C2-N1	-3.78	122.86	128.58
6	A	502	ATP	C2-N3-C4	3.76	121.03	111.83
6	B	502	ATP	C2-N3-C4	3.73	120.94	111.83
6	A	502	ATP	C4-N9-C8	3.35	109.26	105.74
6	B	502	ATP	C4-C5-N7	-3.27	106.84	110.58
6	B	502	ATP	C4-N9-C8	3.23	109.12	105.74
6	A	502	ATP	C4-C5-N7	-3.03	107.12	110.58
6	B	502	ATP	C5-N7-C8	2.60	107.54	103.45
6	A	502	ATP	C5-N7-C8	2.50	107.37	103.45
6	A	502	ATP	N9-C8-N7	-2.45	110.47	113.94
6	B	502	ATP	N9-C8-N7	-2.41	110.51	113.94
6	B	502	ATP	C2-N1-C6	2.16	122.28	118.73
6	B	502	ATP	C6-C5-N7	2.15	136.24	132.09
6	A	502	ATP	C2-N1-C6	2.06	122.12	118.73
6	A	502	ATP	C6-C5-N7	2.05	136.04	132.09

There are no chirality outliers.

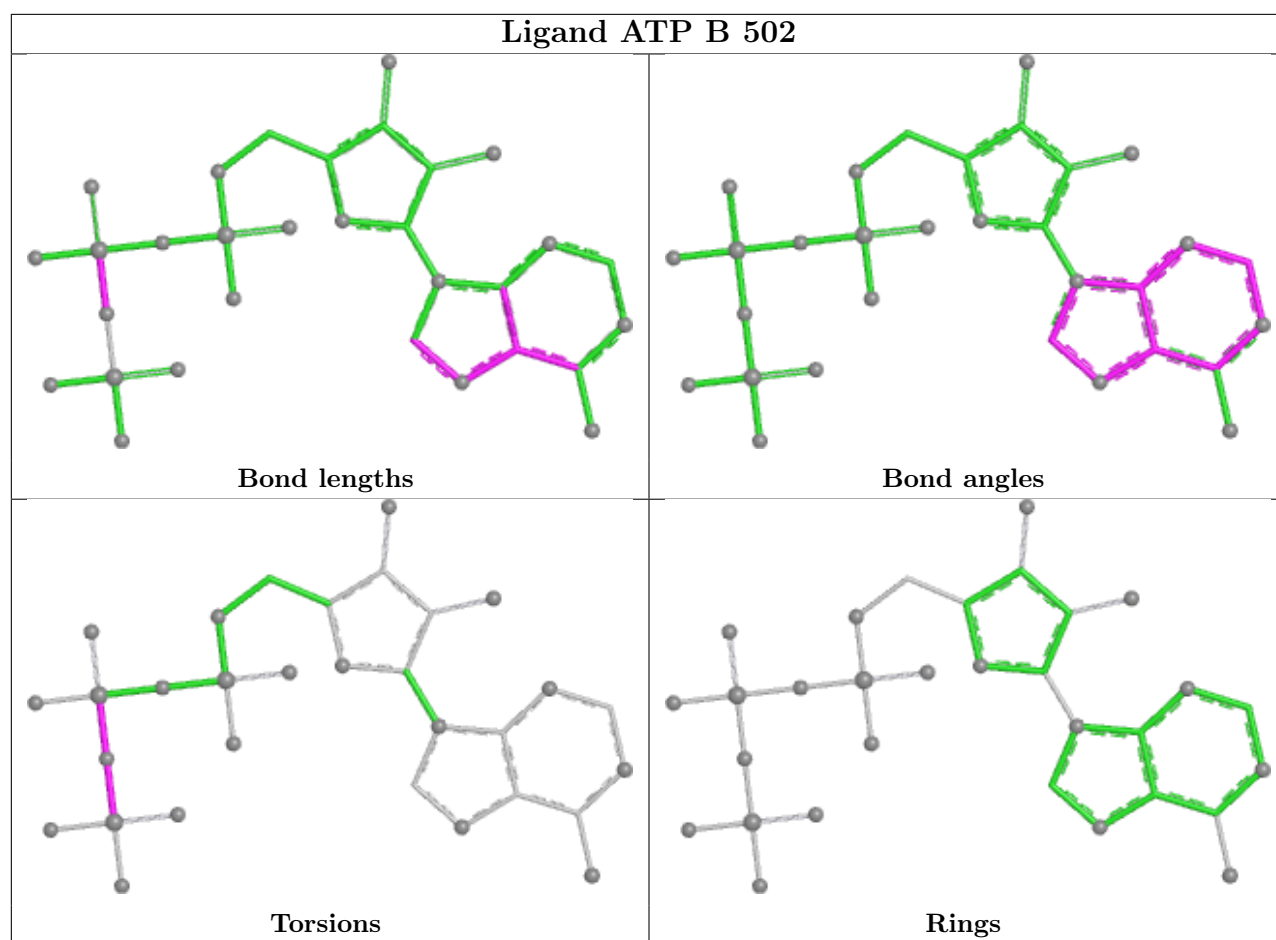
All (7) torsion outliers are listed below:

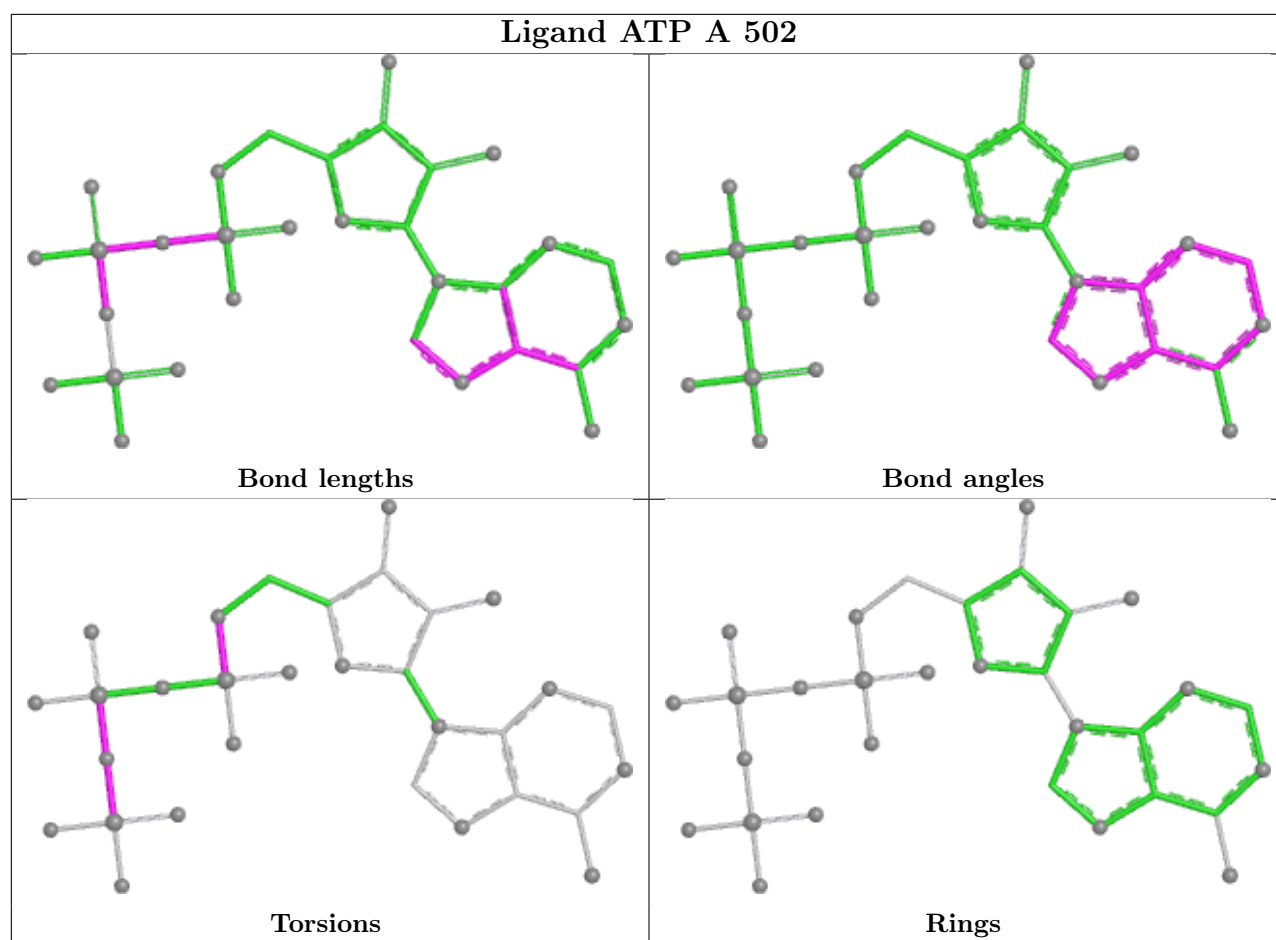
Mol	Chain	Res	Type	Atoms
6	A	502	ATP	PB-O3B-PG-O2G
6	B	502	ATP	PB-O3B-PG-O2G
6	A	502	ATP	C5'-O5'-PA-O1A
6	A	502	ATP	PG-O3B-PB-O1B
6	A	502	ATP	PG-O3B-PB-O2B
6	B	502	ATP	PB-O3B-PG-O1G
6	B	502	ATP	PG-O3B-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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	397/489 (81%)	-0.37	20 (5%) 34 26	30, 51, 96, 137	0
1	B	397/489 (81%)	-0.36	17 (4%) 40 31	28, 51, 95, 134	0
2	C	365/375 (97%)	-0.42	7 (1%) 66 57	33, 51, 85, 121	0
2	D	365/375 (97%)	-0.45	5 (1%) 73 64	33, 52, 85, 125	0
3	E	122/159 (76%)	0.43	13 (10%) 11 8	41, 70, 112, 124	0
3	F	124/159 (77%)	0.50	9 (7%) 21 15	41, 72, 116, 124	0
4	G	0/20	-	-	-	-
4	H	0/20	-	-	-	-
All	All	1770/2086 (84%)	-0.28	71 (4%) 42 33	28, 53, 96, 137	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	40	HIS	8.5
2	D	40	HIS	8.0
1	B	263	SER	6.9
1	B	308	ASN	6.0
1	A	263	SER	5.8
3	F	126	SER	5.4
1	A	308	ASN	5.3
1	B	465	PHE	4.8
1	B	138	TYR	4.6
1	A	381	GLU	4.6
1	B	479	GLY	4.5
1	B	468	LEU	4.4
1	A	468	LEU	4.4
1	A	465	PHE	4.3
3	E	91	GLU	4.2
2	C	48	GLY	4.0
2	D	48	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	466	HIS	4.0
2	D	49	GLN	4.0
2	C	169	PHE	3.8
1	B	381	GLU	3.8
1	B	467	GLN	3.8
1	B	466	HIS	3.7
3	E	12	GLY	3.7
3	F	12	GLY	3.6
3	E	45	LYS	3.5
2	C	49	GLN	3.4
1	A	312	VAL	3.4
1	A	479	GLY	3.4
1	A	256	GLU	3.4
3	F	125	SER	3.3
1	B	312	VAL	3.3
1	A	265	THR	3.2
3	F	43	PRO	3.2
1	A	15	SER	3.2
1	A	478	VAL	3.1
1	A	260	THR	3.1
3	F	44	GLY	3.1
3	F	45	LYS	3.1
2	C	63	GLY	3.0
2	D	169	PHE	3.0
1	B	256	GLU	2.9
3	F	120	THR	2.9
3	E	44	GLY	2.8
1	A	262	LEU	2.7
1	B	15	SER	2.7
1	B	478	VAL	2.7
3	F	91	GLU	2.7
1	A	138	TYR	2.6
1	B	469	TRP	2.5
1	B	261	GLU	2.5
1	B	265	THR	2.5
1	B	477	GLU	2.5
3	E	42	ALA	2.5
1	A	264	SER	2.5
3	F	118	GLN	2.5
2	D	63	GLY	2.4
3	E	3	GLN	2.3
3	E	124	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
3	E	10	GLY	2.2
3	E	41	GLN	2.2
2	C	374	CYS	2.2
3	E	43	PRO	2.2
1	A	467	GLN	2.1
3	E	120	THR	2.1
2	C	39	ARG	2.1
3	E	68	GLY	2.1
1	A	202	GLU	2.1
1	A	309	SER	2.0
3	E	19	SER	2.0
1	A	261	GLU	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
2	HIC	C	73	11/12	0.98	0.06	44,46,53,57	0
2	HIC	D	73	11/12	0.98	0.06	39,45,54,55	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

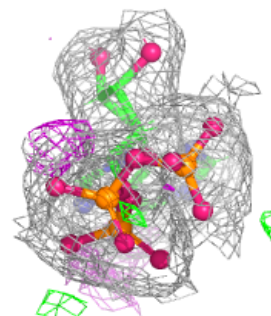
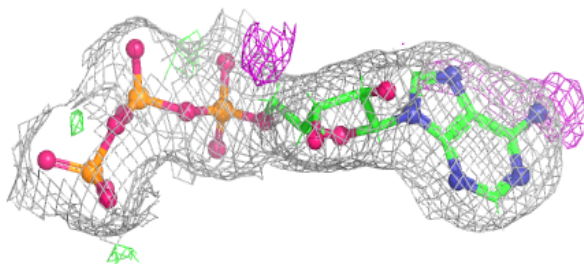
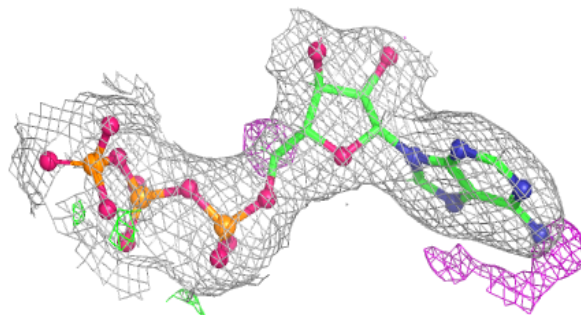
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	CA	A	501	1/1	0.98	0.05	61,61,61,61	0
5	CA	B	501	1/1	0.98	0.05	62,62,62,62	0
6	ATP	A	502	31/31	0.98	0.06	30,37,52,56	0
6	ATP	B	502	31/31	0.99	0.04	30,37,48,50	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.

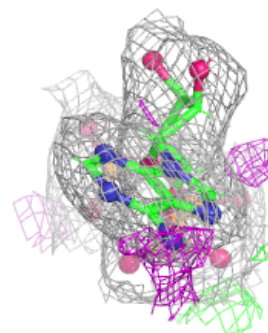
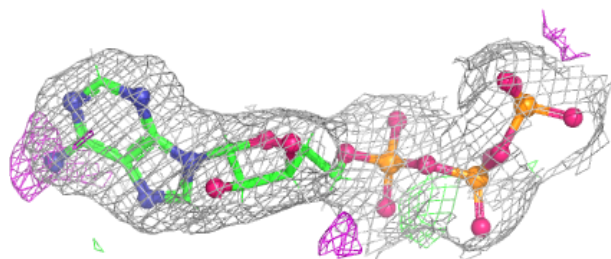
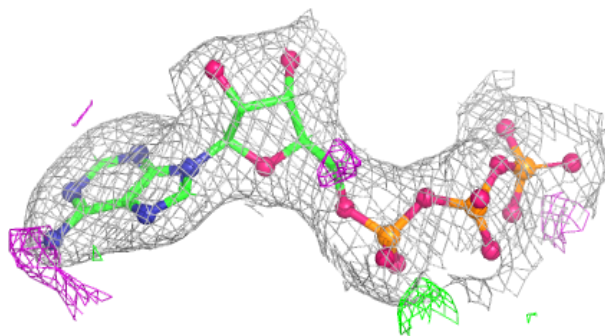
Electron density around ATP A 502:

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 502:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.