



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:10 AM UTC

PDB ID : 5LB5 / pdb_00005lb5
Title : Crystal structure of human RECQL5 helicase in complex with ADP/Mg (triclinic form).
Authors : Newman, J.A.; Aitkenhead, H.; Savitsky, P.; Krojer, T.; von Delft, F.; Arrow-smith, C.H.; Edwards, A.M.; Bountra, C.; Gileadi, O.; Structural Genomics Consortium (SGC)
Deposited on : 2016-06-15
Resolution : 2.00 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](#) ①) 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

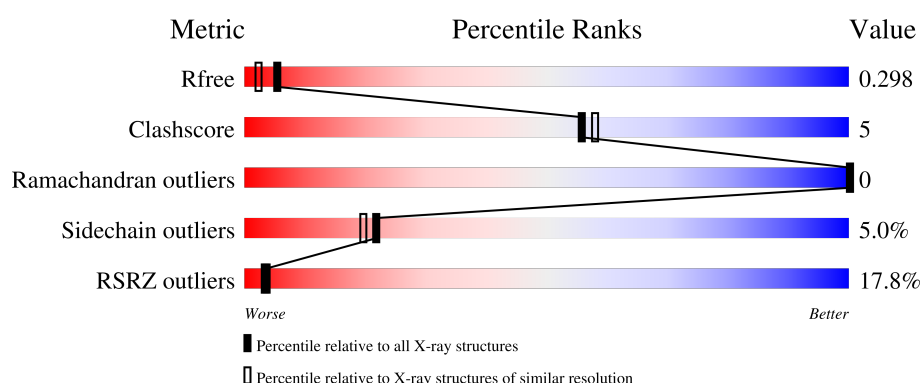
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	445	15% 87% 9% .
1	B	445	17% 86% 10% ..
1	C	445	21% 83% 11% ..
1	D	445	17% 84% 12% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13859 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 ATP-dependent DNA helicase Q5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	3	0
			3354	2117	600	615	22			
1	B	433	Total	C	N	O	S	0	3	0
			3352	2119	595	613	25			
1	C	426	Total	C	N	O	S	0	1	0
			3273	2070	576	605	22			
1	D	434	Total	C	N	O	S	0	2	0
			3353	2120	593	618	22			

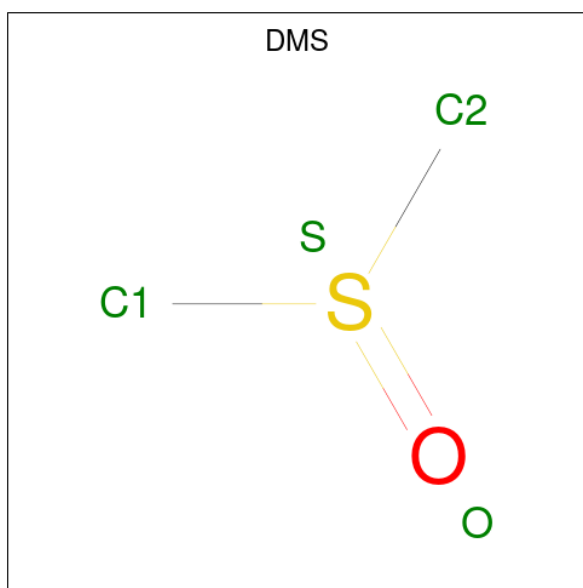
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	SER	-	expression tag	UNP O94762
A	10	MET	PHE	conflict	UNP O94762
B	9	SER	-	expression tag	UNP O94762
B	10	MET	PHE	conflict	UNP O94762
C	9	SER	-	expression tag	UNP O94762
C	10	MET	PHE	conflict	UNP O94762
D	9	SER	-	expression tag	UNP O94762
D	10	MET	PHE	conflict	UNP O94762

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).

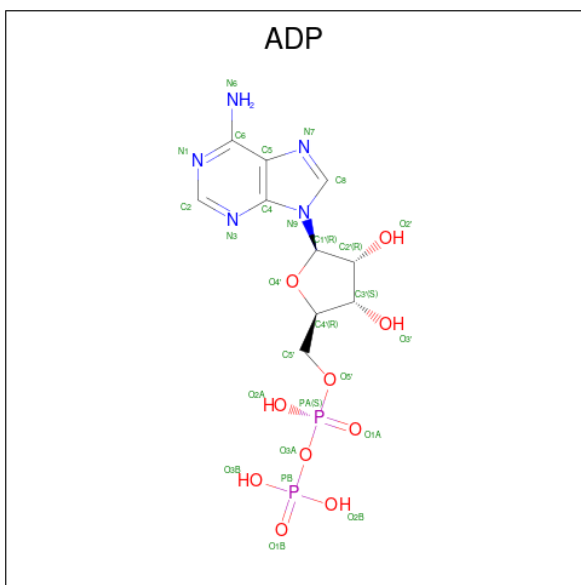


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	B	1	Total	C	O	S	0	0
			4	2	1	1		
3	D	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 27	C 10	N 5	O 10	P 2	0	0
5	B	1	Total 27	C 10	N 5	O 10	P 2	0	0
5	C	1	Total 27	C 10	N 5	O 10	P 2	0	0
5	D	1	Total 27	C 10	N 5	O 10	P 2	0	0

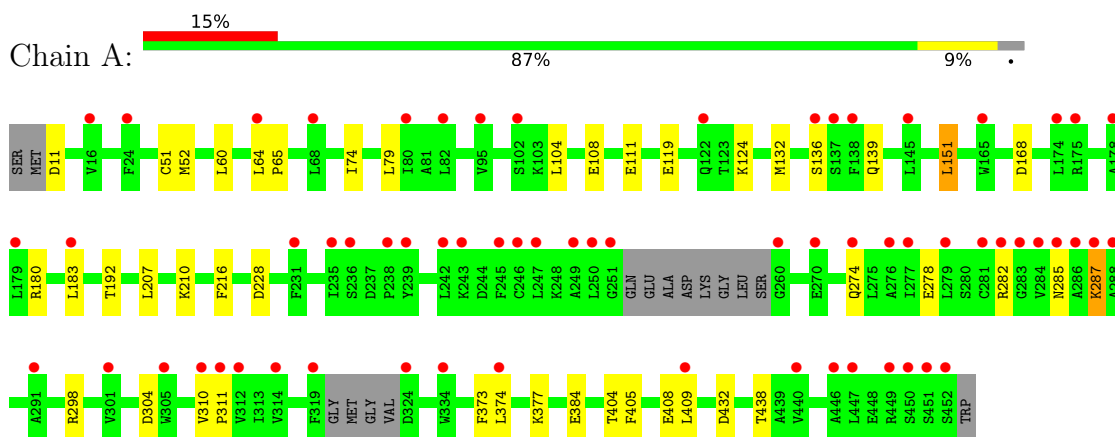
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	115	Total O 115 115	0	0
6	B	113	Total O 113 113	0	0
6	C	93	Total O 93 93	0	0
6	D	78	Total O 78 78	0	0

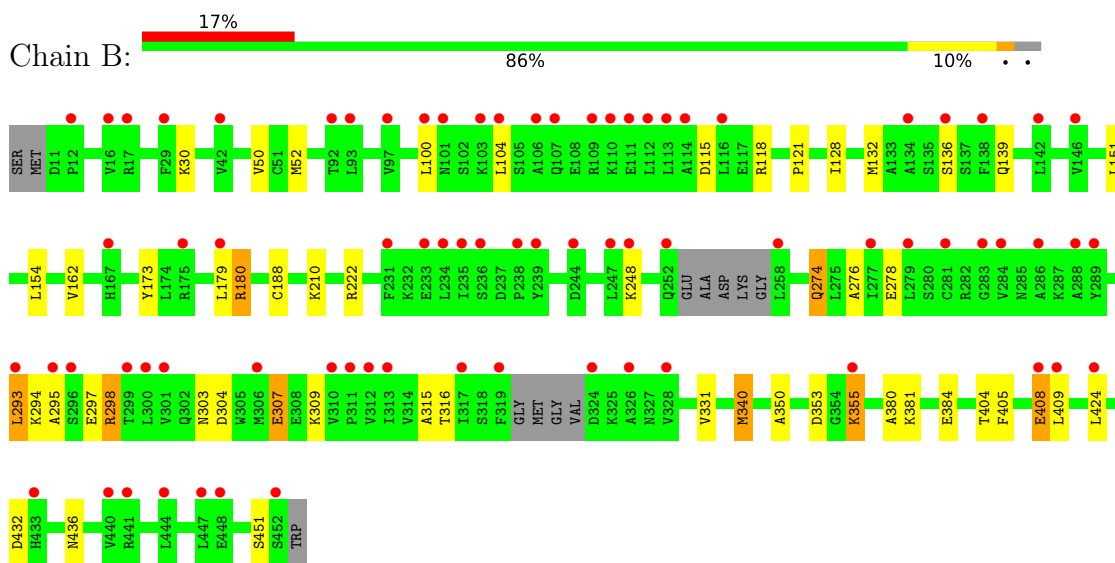
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

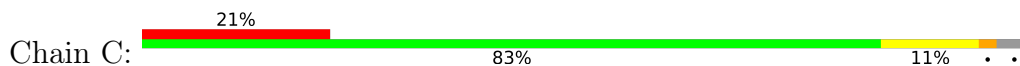
• Molecule 1: ATP-dependent DNA helicase Q5

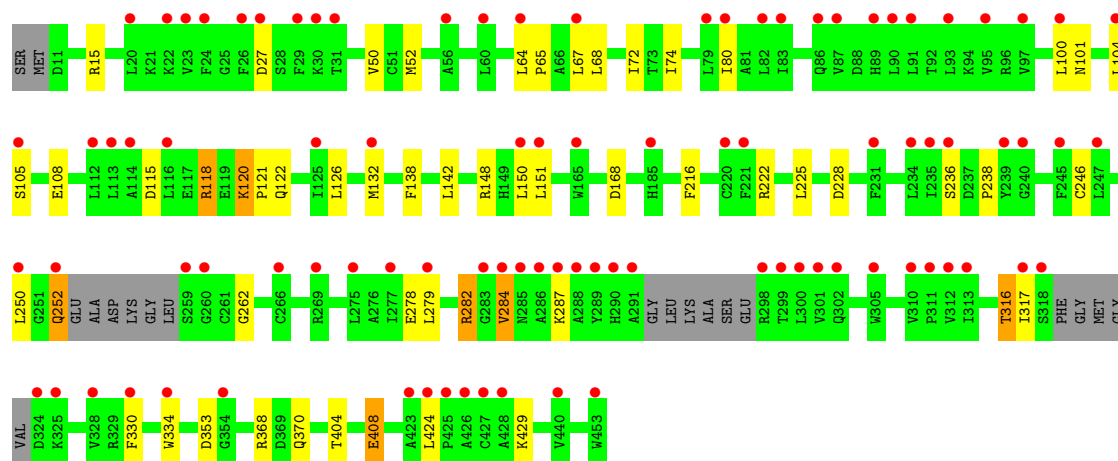


• Molecule 1: ATP-dependent DNA helicase Q5

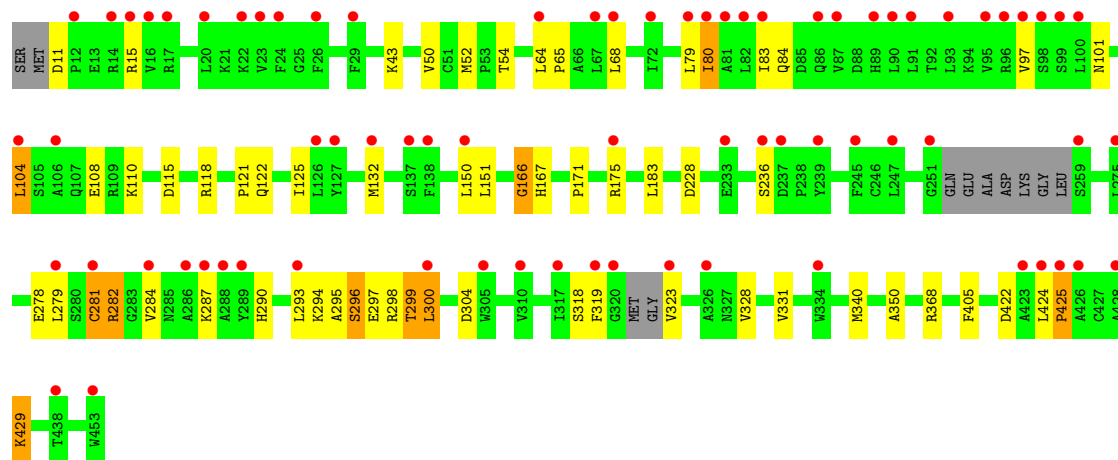
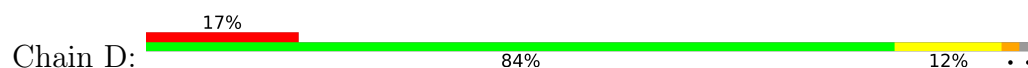


• Molecule 1: ATP-dependent DNA helicase Q5





• Molecule 1: ATP-dependent DNA helicase Q5



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.59Å 84.75Å 106.69Å 108.82° 90.06° 96.86°	Depositor
Resolution (Å)	100.90 – 2.00 100.90 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.3 (100.90-2.00) 98.2 (100.90-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.00Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.244 , 0.282 0.258 , 0.298	Depositor DCC
R_{free} test set	6995 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	37.1	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13859	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.70% 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: DMS, ADP, ZN, MG

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	0.91	1/3418 (0.0%)	1.35	6/4624 (0.1%)
1	B	0.93	1/3416 (0.0%)	1.38	14/4624 (0.3%)
1	C	0.88	0/3337	1.36	10/4526 (0.2%)
1	D	0.91	0/3418	1.40	12/4631 (0.3%)
All	All	0.91	2/13589 (0.0%)	1.38	42/18405 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	52	MET	SD-CE	-6.27	1.63	1.79
1	B	340	MET	SD-CE	-5.04	1.67	1.79

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	228	ASP	CA-CB-CG	8.90	121.50	112.60
1	C	168	ASP	CA-CB-CG	7.27	119.87	112.60
1	A	432	ASP	CA-CB-CG	6.56	119.16	112.60
1	B	295	ALA	N-CA-C	6.21	118.05	111.28
1	B	222	ARG	CA-C-N	6.12	128.76	120.38
1	B	222	ARG	C-N-CA	6.12	128.76	120.38
1	B	432	ASP	CA-CB-CG	5.95	118.55	112.60
1	A	228	ASP	CA-CB-CG	5.87	118.47	112.60
1	C	216	PHE	CA-CB-CG	-5.81	107.99	113.80
1	D	228	ASP	CA-CB-CG	5.73	118.33	112.60
1	D	422	ASP	N-CA-C	-5.68	101.61	110.42
1	D	183	LEU	CA-C-N	5.67	126.40	119.99
1	D	183	LEU	C-N-CA	5.67	126.40	119.99
1	A	405	PHE	CA-CB-CG	5.66	119.46	113.80
1	D	122	GLN	N-CA-C	5.63	117.50	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	380	ALA	CA-C-N	5.61	128.36	120.28
1	B	380	ALA	C-N-CA	5.61	128.36	120.28
1	B	276	ALA	CA-C-N	5.61	127.62	120.56
1	B	276	ALA	C-N-CA	5.61	127.62	120.56
1	D	368	ARG	CA-C-N	5.59	127.71	120.44
1	D	368	ARG	C-N-CA	5.59	127.71	120.44
1	A	168	ASP	CA-CB-CG	5.53	118.12	112.60
1	D	319	PHE	CA-CB-CG	5.47	119.27	113.80
1	B	179	LEU	CA-C-N	5.36	127.41	120.44
1	B	179	LEU	C-N-CA	5.36	127.41	120.44
1	D	166	GLY	N-CA-C	5.17	125.44	113.18
1	D	296	SER	N-CA-C	-5.15	105.67	111.28
1	B	436	ASN	CA-CB-CG	5.14	117.74	112.60
1	A	216	PHE	CA-CB-CG	-5.12	108.68	113.80
1	B	315	ALA	N-CA-C	5.11	116.95	109.24
1	C	316	THR	N-CA-C	-5.10	107.12	113.55
1	B	355	LYS	CA-C-N	-5.09	114.52	119.76
1	B	355	LYS	C-N-CA	-5.09	114.52	119.76
1	D	171	PRO	CA-C-N	5.08	127.08	120.28
1	D	171	PRO	C-N-CA	5.08	127.08	120.28
1	C	353	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	11	ASP	CA-CB-CG	5.05	117.65	112.60
1	C	316	THR	CB-CA-C	5.03	117.13	109.34
1	C	368	ARG	CA-C-N	5.02	127.00	120.28
1	C	368	ARG	C-N-CA	5.02	127.00	120.28
1	C	120	LYS	CA-C-N	-5.01	114.20	120.51
1	C	120	LYS	C-N-CA	-5.01	114.20	120.51

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	3354	0	3334	13	0
1	B	3352	0	3330	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3273	0	3211	38	0
1	D	3353	0	3312	40	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	4	0	6	0	0
3	B	4	0	6	0	0
3	D	4	0	6	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	27	0	12	0	0
5	B	27	0	12	0	0
5	C	27	0	12	0	0
5	D	27	0	12	0	0
6	A	115	0	0	0	0
6	B	113	0	0	2	0
6	C	93	0	0	0	0
6	D	78	0	0	0	0
All	All	13859	0	13253	126	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 5.

All (126) 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:D:278:GLU:O	1:D:282:ARG:CD	1.96	1.13
1:D:278:GLU:O	1:D:282:ARG:CG	1.98	1.11
1:C:118:ARG:HD3	1:C:121:PRO:HA	1.38	1.04
1:D:278:GLU:O	1:D:282:ARG:HG2	1.59	1.02
1:C:118:ARG:HH11	1:C:118:ARG:HG3	1.23	0.98
1:D:293:LEU:O	1:D:298:ARG:NH2	1.98	0.96
1:C:279:LEU:HB3	1:C:284:VAL:HG13	1.48	0.95
1:B:293:LEU:HB2	1:B:297:GLU:OE2	1.77	0.85
1:C:278:GLU:O	1:C:282:ARG:CD	2.24	0.85
1:B:180:ARG:HD3	1:B:188:CYS:HB2	1.61	0.81
1:D:278:GLU:O	1:D:282:ARG:HD2	1.81	0.81
1:C:118:ARG:HG3	1:C:118:ARG:NH1	1.93	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:429:LYS:HD3	1:D:429:LYS:C	2.07	0.79
1:C:278:GLU:O	1:C:282:ARG:HD3	1.86	0.74
1:D:290:HIS:H	1:D:293:LEU:HD12	1.52	0.73
1:D:295:ALA:O	1:D:299:THR:OG1	2.07	0.73
1:C:72:ILE:HD11	1:C:121:PRO:HG2	1.70	0.72
1:C:279:LEU:HB3	1:C:284:VAL:CG1	2.19	0.72
1:B:298:ARG:HG2	1:B:298:ARG:NH1	2.06	0.70
1:B:298:ARG:HG2	1:B:298:ARG:HH11	1.57	0.69
1:D:279:LEU:HA	1:D:282:ARG:HG3	1.74	0.69
1:B:180:ARG:HH22	1:B:210:LYS:HG3	1.58	0.69
1:C:279:LEU:O	1:C:284:VAL:HG12	1.93	0.68
1:C:279:LEU:O	1:C:284:VAL:CG1	2.44	0.66
1:D:278:GLU:O	1:D:282:ARG:HD3	1.94	0.66
1:B:293:LEU:HG	1:B:297:GLU:HB3	1.78	0.65
1:A:180:ARG:HG2	1:A:207:LEU:O	1.96	0.65
1:C:278:GLU:O	1:C:282:ARG:HG2	1.98	0.63
1:D:80:ILE:HA	1:D:83:ILE:HD12	1.80	0.63
1:C:278:GLU:O	1:C:282:ARG:CG	2.46	0.63
1:C:105:SER:HB3	1:C:108:GLU:HG3	1.81	0.63
1:C:246:CYS:O	1:C:250:LEU:HD12	1.99	0.62
1:C:279:LEU:CB	1:C:284:VAL:HG13	2.28	0.61
1:C:262:GLY:HA3	1:C:330:PHE:CE2	2.37	0.60
1:B:128:ILE:HD11	1:B:132[A]:MET:HG3	1.82	0.60
1:B:298:ARG:HH11	1:B:298:ARG:CG	2.14	0.59
1:B:180:ARG:NH2	1:B:210:LYS:HG3	2.18	0.59
1:C:118:ARG:HH11	1:C:118:ARG:CG	2.09	0.58
1:D:115:ASP:O	1:D:118:ARG:HB2	2.03	0.57
1:B:293:LEU:HB2	1:B:297:GLU:CD	2.30	0.57
1:B:294:LYS:O	1:B:297:GLU:HB2	2.05	0.56
1:C:279:LEU:HD22	1:C:284:VAL:HG11	1.88	0.56
1:D:278:GLU:OE1	1:D:282:ARG:NH1	2.37	0.56
1:C:279:LEU:C	1:C:284:VAL:HG13	2.30	0.56
1:B:293:LEU:C	1:B:293:LEU:HD23	2.31	0.56
1:B:293:LEU:HD23	1:B:293:LEU:O	2.06	0.55
1:D:50:VAL:HG13	1:D:52:MET:HE3	1.88	0.55
1:D:79:LEU:O	1:D:83:ILE:HG13	2.07	0.55
1:B:303:ASN:O	1:B:307:GLU:HG2	2.07	0.54
1:B:304:ASP:HA	1:B:309:LYS:HD2	1.90	0.54
1:B:293:LEU:CD2	1:B:298:ARG:CD	2.85	0.54
1:C:279:LEU:CD2	1:C:284:VAL:HG11	2.38	0.53
1:D:328:VAL:HB	1:D:350:ALA:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:HIS:H	1:D:293:LEU:CD1	2.20	0.53
1:D:331:VAL:HG23	1:D:350:ALA:HB2	1.92	0.51
1:D:300:LEU:HD12	1:D:304:ASP:OD2	2.10	0.51
1:C:15:ARG:HG2	1:C:68:LEU:HD22	1.93	0.51
1:A:180:ARG:HH21	1:A:210:LYS:HG3	1.76	0.51
1:D:101:ASN:H	1:D:104:LEU:HD12	1.76	0.50
1:B:293:LEU:CD2	1:B:298:ARG:HD3	2.42	0.50
1:B:293:LEU:HD23	1:B:298:ARG:HD3	1.94	0.49
1:A:373:PHE:CZ	1:A:377:LYS:HE2	2.47	0.49
1:D:15:ARG:HE	1:D:68:LEU:HD22	1.78	0.48
1:B:293:LEU:CD2	1:B:298:ARG:HD2	2.44	0.48
1:D:101:ASN:HA	1:D:132:MET:HG3	1.95	0.48
1:D:294:LYS:O	1:D:297:GLU:N	2.46	0.48
1:D:424:LEU:HG	1:D:425:PRO:HD2	1.96	0.48
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.96	0.47
1:C:404:THR:O	1:C:408:GLU:HB2	2.13	0.47
1:C:118:ARG:O	1:C:148:ARG:NH1	2.46	0.47
1:D:318:SER:HA	3:D:502:DMS:H22	1.97	0.47
1:A:74:ILE:HG13	1:A:151:LEU:HD21	1.97	0.47
1:A:136:SER:HA	1:A:139:GLN:HG2	1.97	0.47
1:A:278:GLU:O	1:A:282:ARG:HG2	2.14	0.47
1:B:154:LEU:HD23	1:B:180:ARG:HG2	1.97	0.47
1:B:162:VAL:HG12	1:B:173:TYR:HB3	1.97	0.46
1:D:323:VAL:HG12	1:D:323:VAL:O	2.14	0.46
1:C:284:VAL:HG13	1:C:284:VAL:O	2.16	0.46
1:C:148:ARG:HB3	1:C:150:LEU:HD13	1.98	0.46
1:C:64:LEU:HB3	1:C:65:PRO:HD3	1.98	0.46
1:C:279:LEU:O	1:C:284:VAL:HG13	2.15	0.46
1:C:115:ASP:O	1:C:121:PRO:HB3	2.16	0.45
1:D:282:ARG:HG2	1:D:282:ARG:H	1.46	0.45
1:D:80:ILE:H	1:D:80:ILE:HG13	1.46	0.45
1:C:101:ASN:HA	1:C:132:MET:HG3	1.98	0.45
1:D:64:LEU:HB3	1:D:65:PRO:HD3	1.99	0.45
1:B:115:ASP:O	1:B:121:PRO:HB3	2.16	0.45
1:D:429:LYS:HD3	1:D:429:LYS:O	2.15	0.45
1:A:104:LEU:HD22	1:A:108:GLU:HB3	1.99	0.44
1:D:424:LEU:HG	1:D:425:PRO:N	2.32	0.44
1:C:50:VAL:HG13	1:C:52:MET:HE3	1.99	0.44
1:A:274:GLN:O	1:A:278:GLU:HB2	2.17	0.44
1:B:118:ARG:HD3	6:B:683:HOH:O	2.16	0.44
1:B:293:LEU:C	1:B:293:LEU:CD2	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:VAL:HG13	1:B:52:MET:HE3	2.00	0.43
1:D:340:MET:HE1	1:D:405:PHE:HB2	1.99	0.43
1:C:222:ARG:HB3	1:C:225:LEU:HD13	1.99	0.43
1:C:74:ILE:HD12	1:C:126:LEU:HD23	2.01	0.43
1:C:118:ARG:HD3	1:C:120:LYS:O	2.18	0.43
1:D:294:LYS:O	1:D:297:GLU:HB2	2.19	0.43
1:C:252:GLN:HA	1:C:252:GLN:OE1	2.19	0.42
1:D:281:CYS:SG	1:D:282:ARG:N	2.92	0.42
1:C:115:ASP:O	1:C:118:ARG:HD2	2.19	0.42
1:D:424:LEU:HG	1:D:425:PRO:CD	2.50	0.42
1:B:248:LYS:HE3	6:B:690:HOH:O	2.19	0.42
1:C:279:LEU:CB	1:C:284:VAL:CG1	2.94	0.42
1:D:429:LYS:C	1:D:429:LYS:CD	2.85	0.42
1:A:404:THR:O	1:A:408:GLU:HB2	2.20	0.41
1:B:293:LEU:HD21	1:B:298:ARG:HD2	2.02	0.41
1:B:331:VAL:HG23	1:B:350:ALA:HB2	2.02	0.41
1:B:340:MET:HE1	1:B:405:PHE:HB2	2.01	0.41
1:B:353:ASP:OD1	1:B:355:LYS:HB2	2.19	0.41
1:A:287:LYS:HB2	1:A:310:VAL:HG11	2.02	0.41
1:B:274:GLN:O	1:B:278:GLU:HG2	2.19	0.41
1:B:293:LEU:HD21	1:B:298:ARG:CD	2.51	0.41
1:B:408:GLU:HG2	1:B:409:LEU:N	2.35	0.41
1:D:115:ASP:O	1:D:121:PRO:HB3	2.19	0.41
1:B:404:THR:O	1:B:408:GLU:HB3	2.21	0.41
1:A:285:ASN:HB3	1:A:311:PRO:HD2	2.03	0.41
1:B:136:SER:HA	1:B:139:GLN:HG2	2.03	0.41
1:C:138:PHE:CE2	1:C:142:LEU:HD13	2.56	0.40
1:D:424:LEU:HG	1:D:425:PRO:O	2.22	0.40
1:D:97:VAL:HG23	1:D:125:ILE:HB	2.02	0.40
1:D:166:GLY:O	1:D:167:HIS:CB	2.69	0.40
1:A:51:CYS:HA	1:A:192:THR:O	2.22	0.40
1:C:238:PRO:HB2	1:C:334:TRP:HH2	1.86	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	427/445 (96%)	418 (98%)	9 (2%)	0	100	100
1	B	430/445 (97%)	422 (98%)	8 (2%)	0	100	100
1	C	419/445 (94%)	411 (98%)	8 (2%)	0	100	100
1	D	430/445 (97%)	424 (99%)	6 (1%)	0	100	100
All	All	1706/1780 (96%)	1675 (98%)	31 (2%)	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	355/373 (95%)	340 (96%)	15 (4%)	26	25
1	B	355/373 (95%)	340 (96%)	15 (4%)	26	25
1	C	344/373 (92%)	325 (94%)	19 (6%)	19	17
1	D	353/373 (95%)	332 (94%)	21 (6%)	18	14
All	All	1407/1492 (94%)	1337 (95%)	70 (5%)	22	20

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LEU
1	A	79	LEU
1	A	111	GLU
1	A	119	GLU
1	A	124	LYS
1	A	132	MET
1	A	151	LEU
1	A	183	LEU

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Mol	Chain	Res	Type
1	A	287	LYS
1	A	298	ARG
1	A	304	ASP
1	A	374	LEU
1	A	384	GLU
1	A	409	LEU
1	A	438	THR
1	B	30	LYS
1	B	100	LEU
1	B	104	LEU
1	B	151	LEU
1	B	180	ARG
1	B	274	GLN
1	B	293	LEU
1	B	298	ARG
1	B	307	GLU
1	B	316	THR
1	B	381	LYS
1	B	384	GLU
1	B	408	GLU
1	B	424	LEU
1	B	451	SER
1	C	27	ASP
1	C	67	LEU
1	C	80	ILE
1	C	100	LEU
1	C	104	LEU
1	C	118	ARG
1	C	122	GLN
1	C	151	LEU
1	C	236	SER
1	C	252	GLN
1	C	282	ARG
1	C	284	VAL
1	C	287	LYS
1	C	316	THR
1	C	317	ILE
1	C	370	GLN
1	C	408	GLU
1	C	424	LEU
1	C	429	LYS
1	D	11	ASP

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Mol	Chain	Res	Type
1	D	43	LYS
1	D	54	THR
1	D	80	ILE
1	D	84	GLN
1	D	104	LEU
1	D	108	GLU
1	D	110	LYS
1	D	150	LEU
1	D	151	LEU
1	D	175	ARG
1	D	236	SER
1	D	281	CYS
1	D	282	ARG
1	D	284	VAL
1	D	287	LYS
1	D	296	SER
1	D	299	THR
1	D	300	LEU
1	D	425	PRO
1	D	429	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	84	GLN
1	A	101	ASN
1	A	198	GLN
1	A	274	GLN
1	A	345	GLN
1	A	433	HIS
1	B	84	GLN
1	B	89	HIS
1	B	101	ASN
1	B	122	GLN
1	B	143	ASN
1	B	185	HIS
1	B	198	GLN
1	B	200	GLN
1	B	285	ASN
1	C	84	GLN
1	C	101	ASN
1	C	122	GLN

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Mol	Chain	Res	Type
1	C	198	GLN
1	C	241	ASN
1	C	274	GLN
1	C	433	HIS
1	C	436	ASN
1	D	84	GLN
1	D	101	ASN
1	D	198	GLN
1	D	241	ASN
1	D	366	ASN
1	D	370	GLN
1	D	388	ASN
1	D	433	HIS

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 15 ligands modelled in this entry, 8 are monoatomic - leaving 7 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	$\# Z > 2$
5	ADP	B	504	4	28,29,29	0.46	0	43,45,45	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ADP	C	503	4	28,29,29	0.43	0	43,45,45	0.52	0
3	DMS	A	502	-	3,3,3	0.29	0	3,3,3	0.74	0
5	ADP	D	504	4	28,29,29	0.40	0	43,45,45	0.46	0
5	ADP	A	504	4	28,29,29	0.45	0	43,45,45	0.55	0
3	DMS	B	502	-	3,3,3	0.35	0	3,3,3	0.30	0
3	DMS	D	502	-	3,3,3	0.24	0	3,3,3	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ADP	B	504	4	-	1/16/32/32	0/3/3/3
5	ADP	D	504	4	-	1/16/32/32	0/3/3/3
5	ADP	C	503	4	-	0/16/32/32	0/3/3/3
5	ADP	A	504	4	-	1/16/32/32	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	504	ADP	PA-O3A-PB-O2B
5	B	504	ADP	PA-O3A-PB-O1B
5	A	504	ADP	C2'-C1'-N9-C8

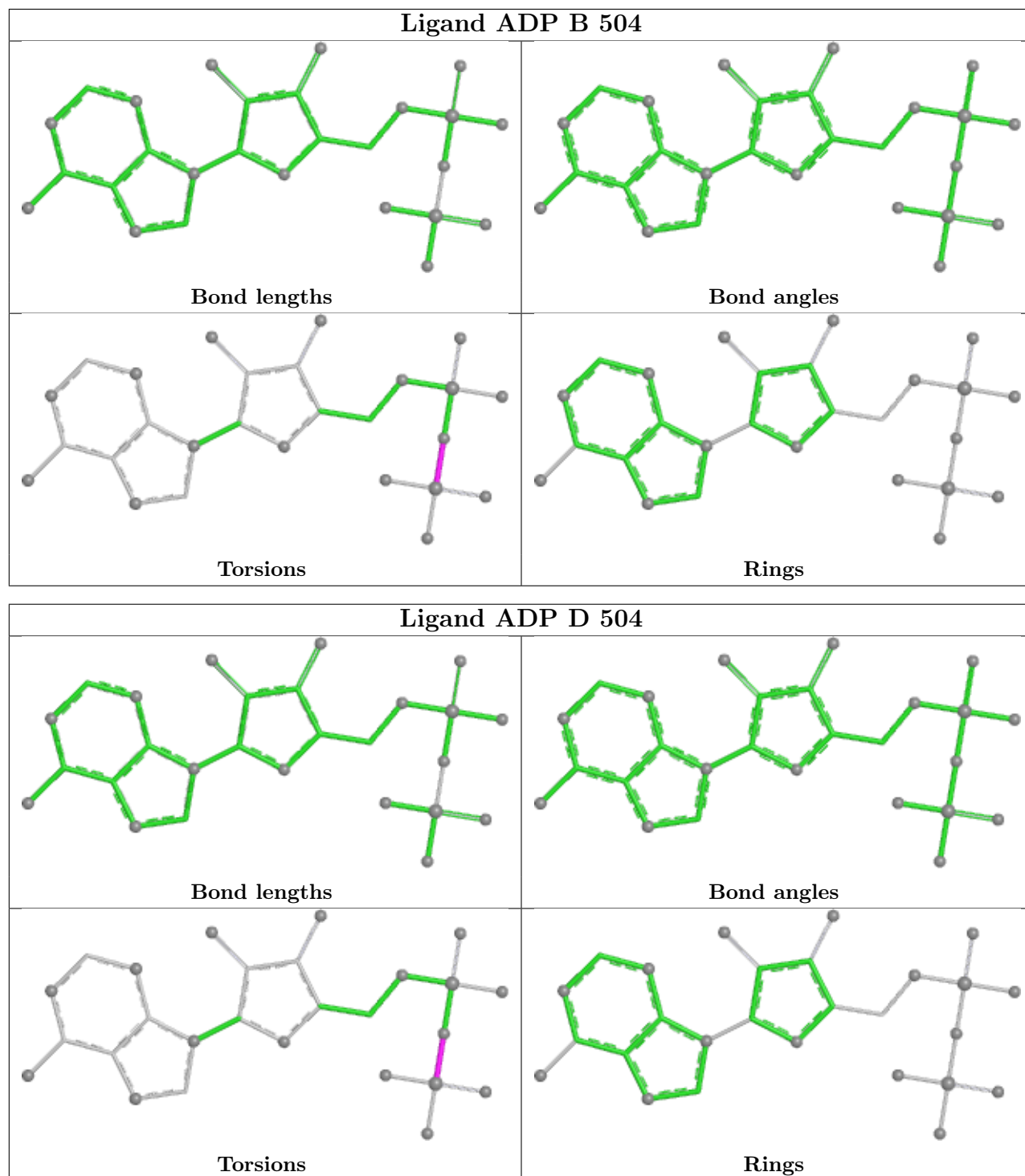
There are no ring outliers.

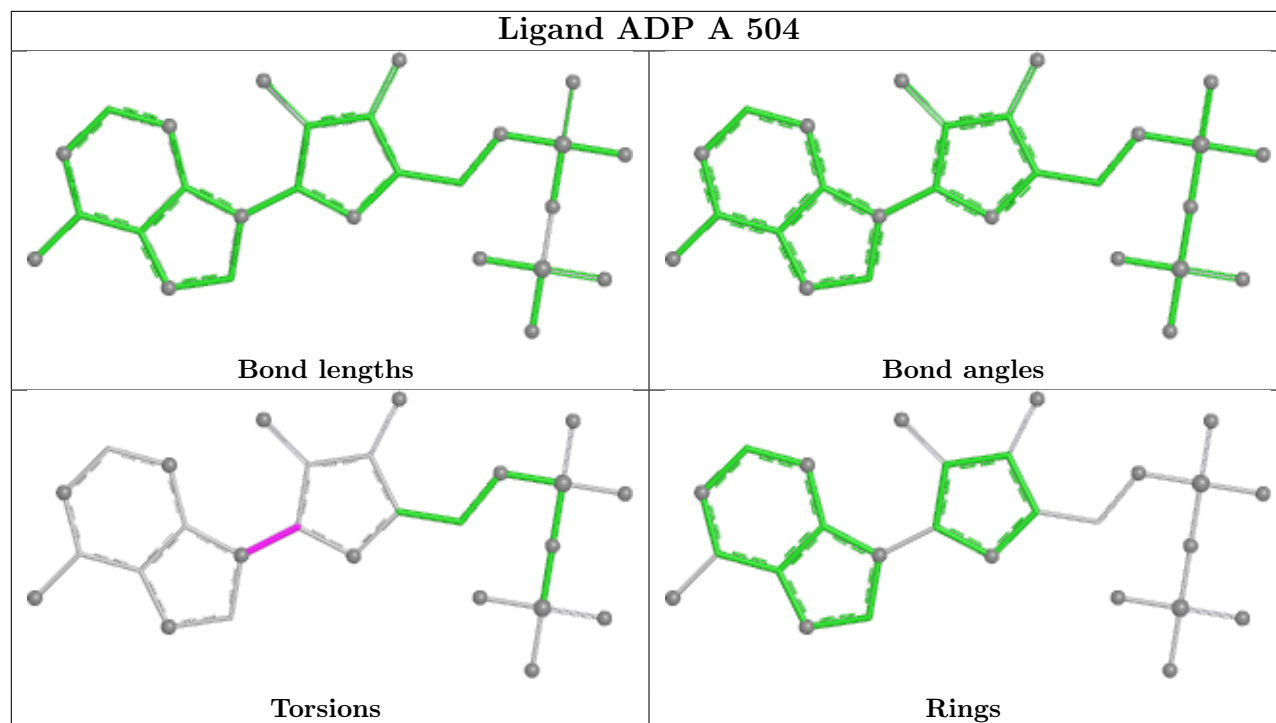
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	502	DMS	1	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	430/445 (96%)	0.89	65 (15%) 5 5	16, 48, 83, 114	3 (0%)
1	B	433/445 (97%)	0.95	76 (17%) 4 3	19, 49, 90, 117	3 (0%)
1	C	426/445 (95%)	1.18	92 (21%) 2 2	27, 57, 96, 123	1 (0%)
1	D	434/445 (97%)	1.17	74 (17%) 4 4	21, 59, 102, 122	2 (0%)
All	All	1723/1780 (96%)	1.05	307 (17%) 4 3	16, 53, 96, 123	9 (0%)

All (307) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	426	ALA	6.7
1	D	320	GLY	6.1
1	A	277	ILE	5.8
1	D	23	VAL	5.8
1	C	23	VAL	5.6
1	C	288	ALA	5.4
1	D	323	VAL	5.3
1	C	324	ASP	4.9
1	D	425	PRO	4.9
1	C	424	LEU	4.9
1	A	284	VAL	4.9
1	B	16	VAL	4.8
1	C	301	VAL	4.5
1	B	104	LEU	4.5
1	A	251	GLY	4.4
1	C	453	TRP	4.4
1	D	100	LEU	4.3
1	B	295	ALA	4.2
1	A	301	VAL	4.2
1	A	310	VAL	4.2
1	D	453	TRP	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	17	ARG	4.1
1	D	16	VAL	4.1
1	C	83	ILE	4.1
1	A	247	LEU	4.1
1	D	22	LYS	4.1
1	D	423	ALA	4.0
1	C	291	ALA	4.0
1	D	82	LEU	4.0
1	B	136	SER	4.0
1	A	235	ILE	4.0
1	B	239	TYR	4.0
1	C	318	SER	3.9
1	D	284	VAL	3.9
1	D	83	ILE	3.9
1	A	238	PRO	3.9
1	A	279	LEU	3.9
1	D	80	ILE	3.8
1	B	324	ASP	3.8
1	D	251	GLY	3.8
1	D	95	VAL	3.8
1	C	64	LEU	3.7
1	C	116	LEU	3.7
1	B	319	PHE	3.7
1	C	260	GLY	3.7
1	B	134	ALA	3.7
1	A	452	SER	3.6
1	C	317	ILE	3.6
1	D	72	ILE	3.6
1	B	279	LEU	3.6
1	D	97	VAL	3.6
1	C	26	PHE	3.6
1	C	289	TYR	3.6
1	D	24	PHE	3.5
1	C	29	PHE	3.5
1	D	17	ARG	3.5
1	B	107	GLN	3.5
1	D	288	ALA	3.5
1	D	104	LEU	3.5
1	C	284	VAL	3.5
1	A	305	TRP	3.4
1	B	317	ILE	3.4
1	C	330	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	312	VAL	3.4
1	D	90	LEU	3.4
1	D	91	LEU	3.4
1	C	287	LYS	3.3
1	B	284	VAL	3.3
1	B	286	ALA	3.3
1	C	235	ILE	3.3
1	C	305	TRP	3.3
1	C	239	TYR	3.3
1	A	446	ALA	3.3
1	C	300	LEU	3.2
1	C	24	PHE	3.2
1	C	298	ARG	3.2
1	A	286	ALA	3.2
1	D	239	TYR	3.2
1	B	100	LEU	3.2
1	B	424	LEU	3.2
1	C	299	THR	3.2
1	D	87	VAL	3.2
1	A	179	LEU	3.2
1	B	179	LEU	3.2
1	C	80	ILE	3.2
1	A	288	ALA	3.1
1	B	301	VAL	3.1
1	C	286	ALA	3.1
1	D	79	LEU	3.1
1	D	99	SER	3.1
1	A	276	ALA	3.1
1	B	234	LEU	3.1
1	A	236	SER	3.1
1	C	423	ALA	3.1
1	C	20	LEU	3.1
1	B	235	ILE	3.1
1	A	334	TRP	3.1
1	C	425	PRO	3.1
1	D	310	VAL	3.1
1	B	409	LEU	3.1
1	A	283	GLY	3.0
1	C	89	HIS	3.0
1	D	20	LEU	3.0
1	D	334	TRP	3.0
1	C	279	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	293	LEU	3.0
1	C	311	PRO	3.0
1	D	86	GLN	3.0
1	C	312	VAL	3.0
1	B	252	GLN	2.9
1	C	114	ALA	2.9
1	B	258	LEU	2.9
1	A	440	VAL	2.9
1	C	275	LEU	2.9
1	D	317	ILE	2.9
1	A	242	LEU	2.9
1	D	126	LEU	2.9
1	A	245	PHE	2.9
1	A	451	SER	2.9
1	B	103	LYS	2.9
1	D	236	SER	2.9
1	A	82	LEU	2.8
1	A	447	LEU	2.8
1	D	15	ARG	2.8
1	A	274	GLN	2.8
1	D	426	ALA	2.8
1	D	424	LEU	2.8
1	B	312	VAL	2.8
1	A	319	PHE	2.8
1	C	266	CYS	2.8
1	B	448	GLU	2.7
1	C	93	LEU	2.7
1	D	68	LEU	2.7
1	A	281	CYS	2.7
1	C	86	GLN	2.7
1	D	305	TRP	2.7
1	D	29	PHE	2.7
1	D	319	PHE	2.7
1	B	311	PRO	2.7
1	C	252	GLN	2.7
1	B	306	MET	2.7
1	D	89	HIS	2.7
1	B	281	CYS	2.7
1	D	98	SER	2.7
1	B	244	ASP	2.7
1	B	112	LEU	2.7
1	C	234	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	285	ASN	2.7
1	A	250	LEU	2.6
1	B	293	LEU	2.6
1	C	112	LEU	2.6
1	B	440	VAL	2.6
1	A	246	CYS	2.6
1	B	326	ALA	2.6
1	B	116	LEU	2.6
1	C	236	SER	2.6
1	C	310	VAL	2.6
1	D	132	MET	2.6
1	B	114	ALA	2.6
1	C	31	THR	2.6
1	A	409	LEU	2.6
1	D	67	LEU	2.6
1	A	282	ARG	2.6
1	C	428	ALA	2.6
1	A	450	SER	2.6
1	B	313	ILE	2.5
1	A	239	TYR	2.5
1	A	260	GLY	2.5
1	B	101	ASN	2.5
1	A	324	ASP	2.5
1	B	452	SER	2.5
1	C	221	PHE	2.5
1	D	259	SER	2.5
1	A	183	LEU	2.5
1	B	142	LEU	2.5
1	C	82	LEU	2.5
1	C	150	LEU	2.5
1	A	287	LYS	2.5
1	B	310	VAL	2.5
1	A	270	GLU	2.5
1	A	137	SER	2.5
1	A	64	LEU	2.5
1	B	300	LEU	2.5
1	D	93	LEU	2.5
1	C	245	PHE	2.5
1	C	87	VAL	2.4
1	B	296	SER	2.4
1	B	299	THR	2.4
1	C	105	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	79	LEU	2.4
1	C	113	LEU	2.4
1	C	95	VAL	2.4
1	C	165	TRP	2.4
1	A	102	SER	2.4
1	D	127	TYR	2.4
1	D	137	SER	2.4
1	A	291	ALA	2.4
1	B	175	ARG	2.4
1	B	441	ARG	2.4
1	D	81	ALA	2.4
1	A	68	LEU	2.4
1	C	104	LEU	2.4
1	D	279	LEU	2.4
1	D	300	LEU	2.4
1	B	283	GLY	2.4
1	C	220	CYS	2.4
1	D	326	ALA	2.4
1	C	240	GLY	2.4
1	C	27	ASP	2.4
1	A	231	PHE	2.4
1	D	26	PHE	2.4
1	D	138	PHE	2.4
1	C	313	ILE	2.4
1	B	167	HIS	2.4
1	C	427	CYS	2.4
1	D	281	CYS	2.4
1	D	289	TYR	2.3
1	A	145	LEU	2.3
1	B	113	LEU	2.3
1	B	444	LEU	2.3
1	D	247	LEU	2.3
1	D	287	LYS	2.3
1	A	174	LEU	2.3
1	C	247	LEU	2.3
1	D	150	LEU	2.3
1	C	22	LYS	2.3
1	A	138	PHE	2.3
1	B	238	PRO	2.3
1	D	106	ALA	2.3
1	C	90	LEU	2.3
1	D	96	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	248	LYS	2.3
1	C	290	HIS	2.3
1	B	277	ILE	2.3
1	C	97	VAL	2.3
1	D	14	ARG	2.3
1	B	106	ALA	2.3
1	B	93	LEU	2.3
1	C	67	LEU	2.3
1	A	24	PHE	2.2
1	B	231	PHE	2.2
1	C	125	ILE	2.2
1	A	95	VAL	2.2
1	C	440	VAL	2.2
1	B	247	LEU	2.2
1	C	250	LEU	2.2
1	B	109	ARG	2.2
1	A	311	PRO	2.2
1	A	314	VAL	2.2
1	B	110	LYS	2.2
1	C	285	ASN	2.2
1	D	12	PRO	2.2
1	B	111	GLU	2.2
1	C	259	SER	2.2
1	B	29	PHE	2.2
1	B	146	VAL	2.2
1	B	328	VAL	2.2
1	D	428	ALA	2.2
1	C	60	LEU	2.2
1	D	64	LEU	2.2
1	A	449	ARG	2.2
1	B	42	VAL	2.1
1	D	286	ALA	2.1
1	B	447	LEU	2.1
1	C	100	LEU	2.1
1	C	325	LYS	2.1
1	B	92	THR	2.1
1	A	165	TRP	2.1
1	B	138	PHE	2.1
1	A	175	ARG	2.1
1	B	288	ALA	2.1
1	A	136	SER	2.1
1	A	374	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	236	SER	2.1
1	D	237	ASP	2.1
1	A	122	GLN	2.1
1	D	438	THR	2.1
1	C	185	HIS	2.1
1	C	277	ILE	2.1
1	C	354	GLY	2.1
1	D	175	ARG	2.1
1	C	231	PHE	2.1
1	C	328	VAL	2.1
1	A	178	ALA	2.1
1	C	56	ALA	2.1
1	C	151	LEU	2.1
1	D	275	LEU	2.1
1	C	132	MET	2.1
1	A	80	ILE	2.1
1	C	30	LYS	2.1
1	B	97	VAL	2.1
1	B	408	GLU	2.0
1	C	269	ARG	2.0
1	A	243	LYS	2.0
1	B	355	LYS	2.0
1	A	16	VAL	2.0
1	B	233	GLU	2.0
1	D	233	GLU	2.0
1	D	245	PHE	2.0
1	A	249	ALA	2.0
1	C	334	TRP	2.0
1	C	91	LEU	2.0
1	C	302	GLN	2.0
1	B	433	HIS	2.0
1	B	12	PRO	2.0
1	C	283	GLY	2.0
1	B	289	TYR	2.0

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

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](#)

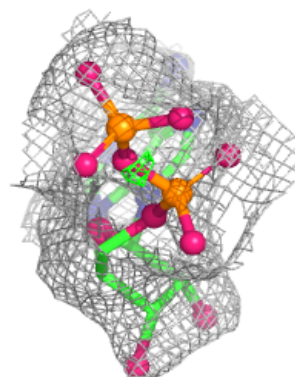
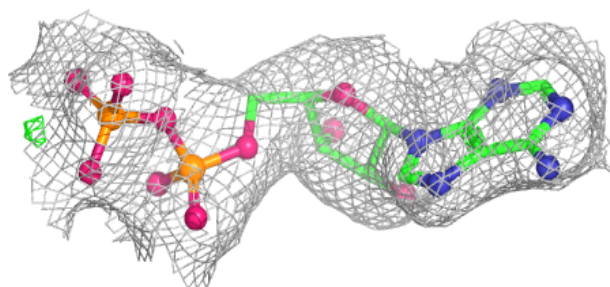
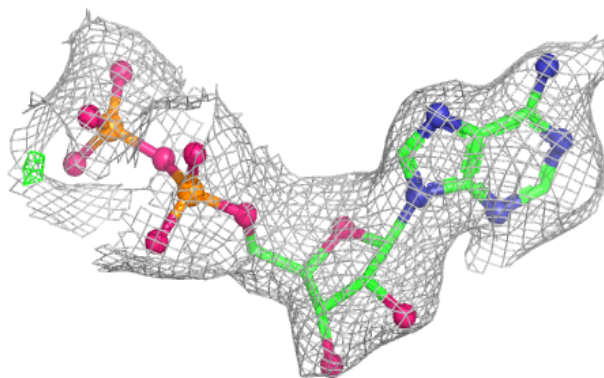
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
4	MG	C	502	1/1	0.80	0.11	71,71,71,71	0
4	MG	D	503	1/1	0.86	0.08	68,68,68,68	0
3	DMS	A	502	4/4	0.90	0.14	30,37,40,43	0
5	ADP	C	503	27/27	0.90	0.10	60,68,73,73	0
5	ADP	D	504	27/27	0.90	0.10	65,81,87,87	0
3	DMS	B	502	4/4	0.91	0.20	86,87,87,87	0
3	DMS	D	502	4/4	0.94	0.12	71,71,71,71	0
5	ADP	A	504	27/27	0.94	0.08	39,46,51,53	0
4	MG	A	503	1/1	0.96	0.06	53,53,53,53	0
5	ADP	B	504	27/27	0.96	0.06	31,40,44,47	0
2	ZN	C	501	1/1	0.97	0.04	46,46,46,46	0
2	ZN	D	501	1/1	0.97	0.04	45,45,45,45	0
4	MG	B	503	1/1	0.97	0.03	50,50,50,50	0
2	ZN	B	501	1/1	0.98	0.05	45,45,45,45	0
2	ZN	A	501	1/1	0.98	0.03	39,39,39,39	0

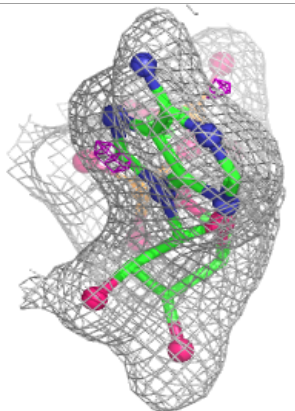
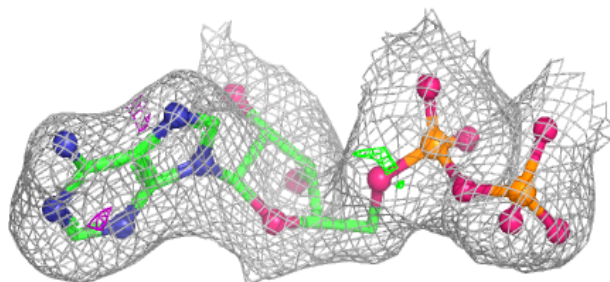
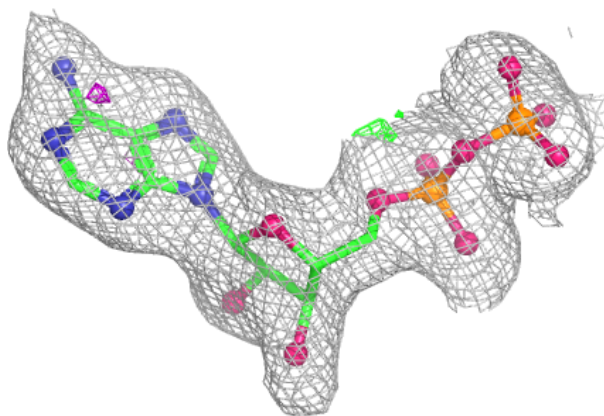
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

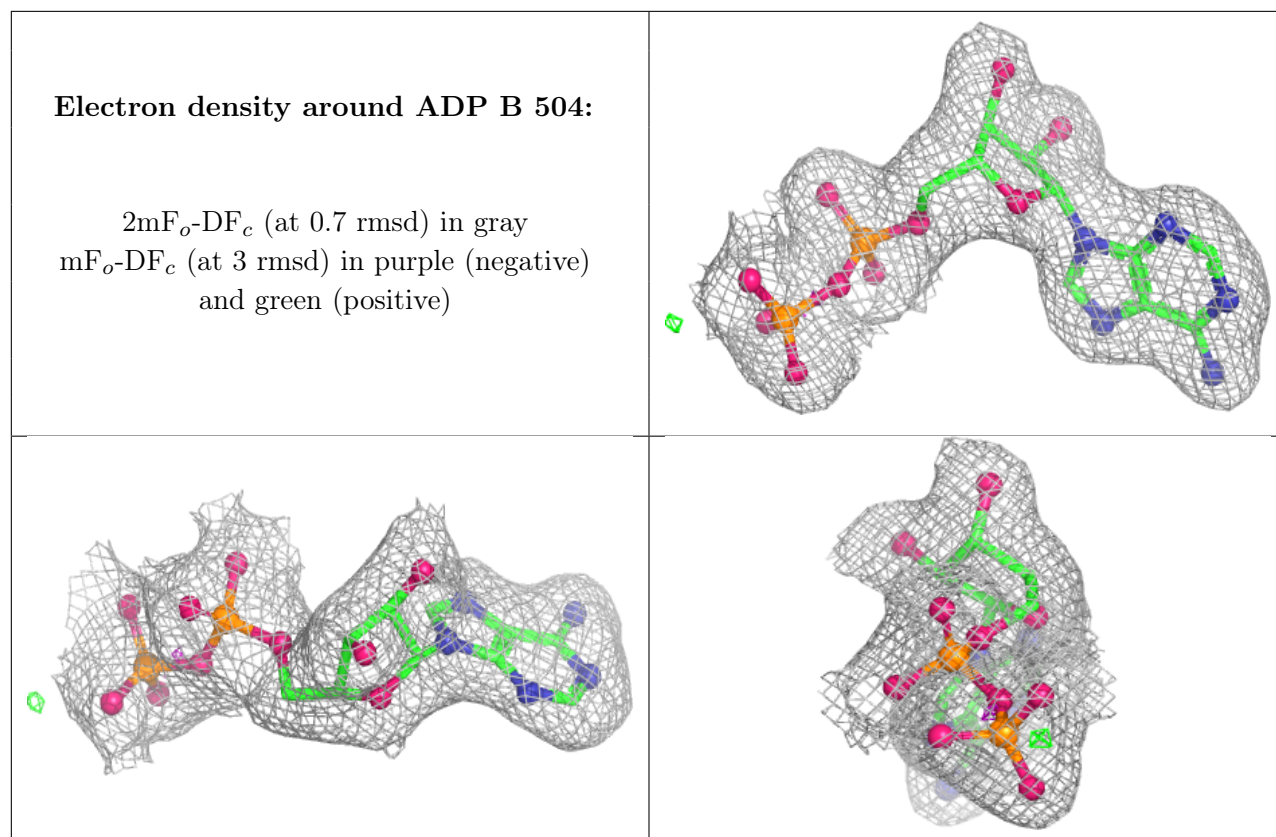
Electron density around ADP D 504:

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

**Electron density around ADP A 504:**

$2mF_o-DF_c$ (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.