



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:26 PM UTC

PDB ID : 1HO5 / pdb_00001ho5
Title : 5'-NUCLEOTIDASE (E. COLI) IN COMPLEX WITH ADENOSINE AND PHOSPHATE
Authors : Knoefel, T.; Straeter, N.
Deposited on : 2000-12-08
Resolution : 2.10 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
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

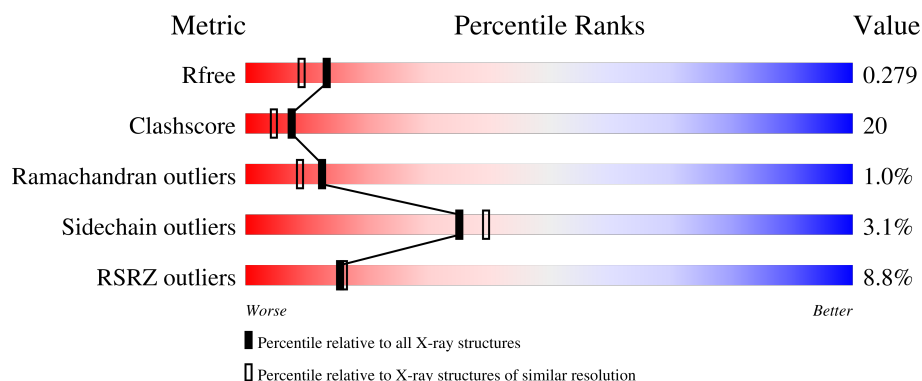
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	525	8% 64% 33% .
1	B	525	10% 59% 37% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8607 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 5'-NUCLEOTIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	525	Total	C	N	O	S	0	0	0
			4100	2590	703	790	17			
1	B	525	Total	C	N	O	S	0	0	0
			4100	2590	703	790	17			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

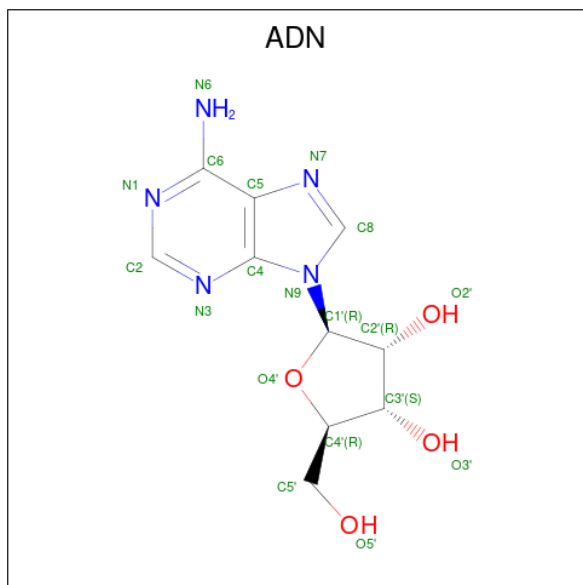
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		
2	B	2	Total	Mn	0	0
			2	2		

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



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

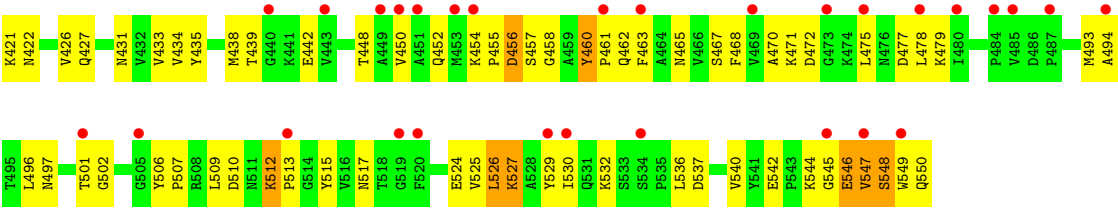
- Molecule 4 is ADENOSINE (CCD ID: ADN) (formula: $C_{10}H_{13}N_5O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			19	10	5	4		
4	B	1	Total	C	N	O	0	0
			19	10	5	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	238	Total	O	0	0
			238	238		
5	B	117	Total	O	0	0
			117	117		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.90Å 75.70Å 221.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.56 – 2.10 29.56 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.56-2.10) 99.5 (29.56-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.98Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.238 , 0.279 0.238 , 0.279	Depositor DCC
R_{free} test set	2116 reflections (2.61%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.4	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	0.93	EDS
Total number of atoms	8607	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.99% 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: ADN, PO4, MN

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	0.83	3/4188 (0.1%)	1.11	21/5666 (0.4%)
1	B	0.66	2/4188 (0.0%)	1.07	28/5666 (0.5%)
All	All	0.75	5/8376 (0.1%)	1.09	49/11332 (0.4%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	218	MET	SD-CE	8.96	2.02	1.79
1	A	345	MET	SD-CE	-8.12	1.59	1.79
1	B	394	MET	SD-CE	-5.72	1.65	1.79
1	B	259	MET	SD-CE	5.31	1.92	1.79
1	A	234	VAL	CA-CB	5.14	1.60	1.54

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	256	PRO	N-CA-C	-9.07	95.33	110.21
1	A	233	ASP	N-CA-C	8.34	120.37	111.28
1	A	256	PRO	N-CA-C	-8.17	95.65	112.47
1	B	250	GLY	N-CA-C	7.41	123.19	112.60
1	B	454	LYS	N-CA-C	7.40	120.74	110.01
1	B	295	VAL	N-CA-C	-7.17	95.88	107.28
1	A	512	LYS	CA-C-N	7.17	128.80	119.84
1	A	512	LYS	C-N-CA	7.17	128.80	119.84
1	B	180	ASN	CA-C-N	6.95	128.53	119.84
1	B	180	ASN	C-N-CA	6.95	128.53	119.84
1	A	250	GLY	N-CA-C	6.78	122.16	112.81
1	A	314	LEU	N-CA-C	-6.74	98.22	109.07
1	B	174	ASP	N-CA-C	-6.67	104.37	113.30
1	B	291	TRP	N-CA-C	6.61	120.63	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	267	VAL	N-CA-C	-6.55	98.96	108.71
1	A	107	VAL	N-CA-C	-6.31	104.18	110.62
1	B	233	ASP	N-CA-C	6.27	118.92	111.33
1	B	118	GLU	N-CA-C	-6.16	105.02	112.54
1	A	215	ALA	N-CA-C	-6.04	99.40	109.24
1	B	408	GLY	N-CA-C	-6.03	107.18	114.66
1	B	260	ALA	N-CA-C	-5.99	104.69	112.23
1	A	118	GLU	N-CA-C	-5.92	106.14	113.19
1	B	460	TYR	CA-C-N	5.91	126.80	120.13
1	B	460	TYR	C-N-CA	5.91	126.80	120.13
1	A	184	PHE	N-CA-C	5.86	120.13	112.92
1	A	385	MET	N-CA-C	-5.83	105.01	111.36
1	B	43	HIS	N-CA-C	5.81	119.20	111.30
1	B	58	ALA	N-CA-C	-5.77	105.07	111.36
1	A	406	GLY	N-CA-C	-5.73	105.73	113.24
1	B	215	ALA	N-CA-C	-5.69	99.97	109.24
1	A	323	VAL	N-CA-C	-5.62	100.38	108.48
1	A	260	ALA	N-CA-C	-5.62	105.54	112.90
1	B	314	LEU	N-CA-C	-5.60	99.29	108.41
1	A	267	VAL	N-CA-C	-5.54	100.49	108.53
1	B	102	ARG	N-CA-C	-5.38	105.49	111.36
1	B	336	THR	CA-C-N	5.34	125.35	119.90
1	B	336	THR	C-N-CA	5.34	125.35	119.90
1	B	216	THR	N-CA-C	5.29	117.43	109.23
1	A	39	THR	N-CA-C	-5.22	101.18	108.96
1	A	295	VAL	N-CA-C	-5.22	100.13	107.75
1	A	266	GLN	N-CA-C	-5.14	103.25	110.50
1	B	301	GLU	N-CA-C	-5.13	100.09	108.76
1	A	74	GLY	CA-C-N	-5.10	117.04	122.30
1	A	74	GLY	C-N-CA	-5.10	117.04	122.30
1	B	270	VAL	N-CA-C	5.09	114.06	108.05
1	B	136	PRO	N-CA-C	5.09	118.48	110.80
1	B	138	LEU	N-CA-C	5.09	118.41	110.32
1	B	255	ASP	CB-CA-C	-5.06	100.56	108.91
1	A	86	ASN	N-CA-C	5.05	117.62	110.50

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	4100	0	4019	158	0
1	B	4100	0	4019	172	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	1	0
4	A	19	0	13	1	0
4	B	19	0	13	1	0
5	A	238	0	0	1	0
5	B	117	0	0	1	0
All	All	8607	0	8064	330	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 20.

All (330) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:MET:SD	1:A:218:MET:CE	2.02	1.47
1:B:345:MET:HE1	1:B:348:LEU:HD23	1.28	1.09
1:B:345:MET:HE2	1:B:349:LEU:HG	1.39	1.04
1:A:444:ILE:HG12	1:A:478:LEU:HD23	1.46	0.97
1:B:300:PHE:HB3	1:B:307:MET:HE2	1.48	0.95
1:A:368:ASN:HD22	1:A:537:ASP:HA	1.36	0.89
1:A:345:MET:HE2	1:A:349:LEU:CG	2.04	0.86
1:B:298:ALA:HB1	1:B:309:MET:HE1	1.57	0.85
1:A:521:ILE:HB	1:A:524:GLU:HG3	1.58	0.85
1:B:206:THR:HG23	1:B:207:GLU:HG2	1.59	0.83
1:B:114:ILE:HG12	1:B:138:LEU:O	1.80	0.82
1:B:477:ASP:O	1:B:479:LYS:HD2	1.79	0.82
1:B:234:VAL:HG13	1:B:280:GLN:HG3	1.61	0.81
1:A:512:LYS:HB3	1:A:513:PRO:HD2	1.62	0.80
1:A:345:MET:HE2	1:A:349:LEU:HG	1.62	0.80
1:B:363:LYS:NZ	1:B:366:GLU:HB3	1.95	0.80
1:B:345:MET:CE	1:B:348:LEU:HD23	2.09	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:ARG:HD2	1:A:458:GLY:HA2	1.64	0.79
1:A:423:VAL:HG13	1:A:526:LEU:HD23	1.64	0.79
1:B:197:LYS:HG2	1:B:240:LEU:HD23	1.65	0.79
1:B:374:ASP:HB2	1:B:377:LYS:HD3	1.65	0.78
1:B:363:LYS:HZ3	1:B:417:ASP:CG	1.94	0.76
1:B:202:GLU:O	1:B:206:THR:HG22	1.85	0.76
1:B:357:LYS:HE3	1:B:361:GLU:OE2	1.86	0.76
1:B:144:GLN:HB2	1:B:151:LEU:HD21	1.67	0.75
1:A:434:VAL:HG12	1:A:517:ASN:HA	1.70	0.73
1:A:451:ALA:HB1	1:A:549:TRP:HE1	1.53	0.73
1:A:114:ILE:HD11	1:A:137:LEU:HB3	1.70	0.72
1:A:322:LYS:HE2	1:A:332:ARG:NH1	2.05	0.71
1:A:385:MET:HE2	1:A:426:VAL:HG11	1.72	0.71
1:B:401:PHE:CE2	1:B:493:MET:HE3	2.26	0.71
1:B:455:PRO:O	1:B:456:ASP:HB3	1.89	0.71
1:A:401:PHE:CZ	1:A:493:MET:HB2	2.26	0.70
1:B:363:LYS:HZ1	1:B:366:GLU:HB3	1.55	0.70
1:B:303:ARG:O	1:B:306:GLU:HG2	1.92	0.70
1:B:530:ILE:HD12	1:B:536:LEU:HD11	1.73	0.69
1:B:345:MET:HE3	1:B:345:MET:HA	1.75	0.68
1:B:309:MET:HE2	1:B:311:ASN:O	1.93	0.68
1:A:46:PHE:HA	1:A:56:LEU:HD22	1.76	0.68
1:B:31:THR:OG1	1:B:303:ARG:HD2	1.93	0.68
1:A:467:SER:HB3	1:A:546:GLU:HB2	1.76	0.67
1:B:141:ASN:ND2	1:B:192:PRO:HG3	2.10	0.67
1:B:345:MET:HE2	1:B:349:LEU:CG	2.21	0.67
1:A:345:MET:CE	1:A:349:LEU:HG	2.25	0.67
1:A:410:ARG:HG3	1:A:428:PRO:CD	2.25	0.66
1:A:411:ASP:O	1:A:426:VAL:HG22	1.95	0.66
1:B:392:ALA:HA	1:B:529:TYR:CD1	2.30	0.66
1:A:444:ILE:HG12	1:A:478:LEU:CD2	2.22	0.66
1:B:130:GLU:HG2	1:B:137:LEU:HD22	1.77	0.65
1:A:180:ASN:HD21	1:A:182:GLU:CG	2.09	0.65
1:A:507:PRO:O	1:A:509:LEU:HD13	1.97	0.65
1:A:404:MET:SD	1:A:409:ILE:HD11	2.37	0.65
1:A:345:MET:HE2	1:A:349:LEU:CD2	2.27	0.65
1:B:547:VAL:O	1:B:548:SER:HB3	1.97	0.64
1:B:114:ILE:CD1	1:B:137:LEU:HB3	2.28	0.64
1:A:180:ASN:ND2	1:A:182:GLU:HG2	2.12	0.64
1:B:57:ALA:HA	1:B:345:MET:HG2	1.80	0.64
1:B:302:PHE:HB2	1:B:307:MET:HE1	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:GLU:N	1:B:99:PRO:HD2	2.13	0.64
1:A:127:ARG:O	1:A:131:LYS:HG3	1.98	0.63
1:A:367:THR:HA	1:A:536:LEU:HB2	1.80	0.63
1:B:298:ALA:CB	1:B:309:MET:HE1	2.28	0.63
1:A:438:MET:HB2	1:A:442:GLU:HB2	1.81	0.63
1:A:364:ILE:HG12	1:A:418:ILE:O	1.99	0.62
1:A:403:VAL:HG23	1:A:462:GLN:O	1.98	0.62
1:A:379:ARG:HD2	1:A:458:GLY:CA	2.30	0.62
1:A:431:ASN:HB2	1:A:522:ASP:OD2	2.00	0.62
1:A:452:GLN:HA	1:A:452:GLN:OE1	2.00	0.62
1:A:368:ASN:ND2	1:A:537:ASP:HA	2.13	0.61
1:B:370:ARG:HG3	1:B:414:GLU:HA	1.81	0.61
1:A:345:MET:HE2	1:A:349:LEU:HD21	1.83	0.61
1:A:480:ILE:O	1:A:481:LYS:HB2	2.00	0.61
1:A:431:ASN:OD1	4:A:1604:ADN:H2	2.00	0.61
1:A:345:MET:HE1	1:A:348:LEU:HD23	1.81	0.61
1:A:468:PHE:CZ	1:A:547:VAL:HG13	2.36	0.60
1:A:527:LYS:O	1:A:530:ILE:HG12	2.02	0.60
1:B:389:ILE:HG12	1:B:526:LEU:HD21	1.83	0.60
1:A:510:ASP:HA	1:A:515:TYR:CD2	2.35	0.60
1:A:380:PHE:HA	1:A:455:PRO:HB3	1.84	0.59
1:A:403:VAL:HA	1:A:462:GLN:O	2.02	0.59
1:A:257:VAL:HG23	1:A:287:GLN:HB3	1.85	0.59
1:B:114:ILE:HD11	1:B:137:LEU:HB3	1.85	0.59
1:A:103:GLY:HA2	1:A:345:MET:HE1	1.85	0.59
1:B:402:ALA:HB2	1:B:494:ALA:HB3	1.85	0.58
1:A:364:ILE:CD1	1:A:530:ILE:HD11	2.33	0.58
1:B:114:ILE:CG1	1:B:139:SER:HB2	2.34	0.58
1:B:467:SER:OG	1:B:479:LYS:HG2	2.04	0.58
1:B:379:ARG:HD2	1:B:458:GLY:HA2	1.85	0.58
1:B:545:GLY:O	1:B:547:VAL:O	2.21	0.57
1:B:388:LEU:HD21	1:B:530:ILE:HD11	1.86	0.57
1:B:60:LYS:HE2	1:B:106:LEU:HG	1.87	0.57
1:B:388:LEU:O	1:B:388:LEU:HD23	2.04	0.57
1:B:371:LEU:HA	1:B:384:ASN:HD21	1.69	0.57
1:B:28:GLN:HG3	5:B:2712:HOH:O	2.04	0.56
1:B:200:ILE:HD12	1:B:240:LEU:HD22	1.87	0.56
1:B:450:VAL:O	1:B:461:PRO:HG2	2.04	0.56
1:B:526:LEU:O	1:B:530:ILE:HG12	2.04	0.56
1:B:363:LYS:NZ	1:B:417:ASP:HA	2.20	0.56
1:B:371:LEU:HA	1:B:384:ASN:ND2	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:439:THR:OG1	1:B:442:GLU:HG3	2.05	0.56
1:B:173:ASP:OD2	1:B:191:LYS:HD3	2.05	0.56
1:B:385:MET:O	1:B:389:ILE:HG13	2.05	0.56
1:A:382:GLN:HA	1:A:462:GLN:HE22	1.70	0.56
1:B:345:MET:HE3	1:B:348:LEU:HB3	1.86	0.56
1:B:433:VAL:HG21	1:B:525:VAL:HG21	1.86	0.56
1:A:495:THR:HG23	1:A:496:LEU:N	2.21	0.56
1:B:496:LEU:HD22	1:B:496:LEU:N	2.21	0.56
1:A:376:ASP:OD1	1:A:377:LYS:HG2	2.06	0.55
1:A:379:ARG:CD	1:A:458:GLY:HA2	2.35	0.55
1:B:140:ALA:C	1:B:195:GLU:HG2	2.32	0.55
1:A:98:GLU:HG3	1:A:132:TRP:CE2	2.42	0.55
1:A:546:GLU:CD	1:A:546:GLU:H	2.14	0.55
1:A:454:LYS:HB3	1:A:455:PRO:CD	2.37	0.55
1:A:345:MET:CE	1:A:348:LEU:HD23	2.36	0.55
1:A:471:LYS:HE2	1:A:550:GLN:HE21	1.70	0.54
1:A:477:ASP:CG	1:A:477:ASP:O	2.50	0.54
1:B:373:GLY:HA3	1:B:411:ASP:O	2.08	0.54
1:A:372:GLU:CD	1:A:377:LYS:HG3	2.33	0.54
1:B:363:LYS:HZ2	1:B:366:GLU:HB3	1.71	0.54
1:A:180:ASN:ND2	1:A:182:GLU:CG	2.70	0.54
1:B:388:LEU:HD23	1:B:388:LEU:C	2.33	0.54
1:A:201:GLN:HG2	1:A:205:GLN:NE2	2.23	0.53
1:A:379:ARG:HD2	1:A:457:SER:C	2.32	0.53
1:B:394:MET:HE2	1:B:401:PHE:C	2.32	0.53
1:B:388:LEU:HD22	1:B:526:LEU:HD11	1.90	0.53
1:A:410:ARG:HD2	1:A:429:PHE:CE2	2.44	0.53
1:B:427:GLN:NE2	1:B:526:LEU:HD23	2.24	0.53
1:B:468:PHE:CD1	1:B:468:PHE:C	2.86	0.53
1:A:364:ILE:HD12	1:A:530:ILE:HD11	1.91	0.53
1:A:459:ALA:CB	1:A:504:ASP:HB3	2.38	0.53
1:B:390:LEU:O	1:B:394:MET:HB2	2.07	0.53
1:A:548:SER:O	1:A:549:TRP:HB2	2.09	0.53
1:B:51:TYR:HB3	1:B:332:ARG:HD2	1.90	0.53
1:B:115:GLY:O	1:B:118:GLU:HB2	2.09	0.52
1:B:502:GLY:HA2	1:B:506:TYR:O	2.08	0.52
1:B:98:GLU:HG3	1:B:132:TRP:CE2	2.45	0.52
1:A:410:ARG:HE	1:A:410:ARG:HA	1.74	0.52
1:B:76:SER:HB3	1:B:160:ARG:HD2	1.92	0.52
1:B:329:LYS:HG2	1:B:330:SER:N	2.25	0.52
1:A:98:GLU:N	1:A:99:PRO:HD2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:ALA:HB3	1:A:549:TRP:HA	1.92	0.52
1:A:486:ASP:OD2	1:A:489:LYS:HG2	2.10	0.51
1:B:84:ASP:CG	1:B:217:HIS:CE1	2.87	0.51
1:B:371:LEU:HD12	1:B:413:ILE:HB	1.92	0.51
1:B:461:PRO:HB2	1:B:463:PHE:CE1	2.45	0.51
1:B:290:GLU:HG3	1:B:291:TRP:CG	2.44	0.51
1:A:549:TRP:O	1:A:550:GLN:HB3	2.09	0.51
1:A:368:ASN:HB2	1:A:538:VAL:H	1.75	0.51
1:B:325:TRP:O	1:B:328:GLY:N	2.41	0.51
1:B:393:GLN:HE22	1:B:496:LEU:HD21	1.76	0.51
1:A:401:PHE:CE1	1:A:493:MET:HB2	2.46	0.51
1:A:439:THR:OG1	1:A:442:GLU:HG3	2.11	0.51
1:B:379:ARG:CD	1:B:458:GLY:HA2	2.40	0.51
1:A:174:ASP:O	1:A:178:ILE:HG12	2.11	0.51
1:B:413:ILE:HG21	1:B:418:ILE:HG12	1.93	0.51
1:B:542:GLU:O	1:B:544:LYS:HG3	2.11	0.51
1:A:438:MET:HG3	1:A:443:VAL:CG2	2.42	0.50
1:B:141:ASN:CG	1:B:192:PRO:HG3	2.37	0.50
1:B:332:ARG:HG2	1:B:332:ARG:HH11	1.76	0.50
1:A:394:MET:HG3	1:A:402:ALA:HB2	1.93	0.50
1:B:115:GLY:N	1:B:118:GLU:OE1	2.45	0.50
1:B:529:TYR:HA	1:B:532:LYS:HE2	1.92	0.50
1:B:256:PRO:HD3	1:B:289:HIS:CG	2.45	0.50
1:B:390:LEU:HD21	1:B:462:GLN:O	2.12	0.50
1:A:345:MET:HE2	1:A:349:LEU:CD1	2.41	0.50
1:B:251:GLY:HA2	1:B:287:GLN:CD	2.37	0.50
1:A:392:ALA:HA	1:A:529:TYR:CD1	2.47	0.50
1:B:456:ASP:OD1	1:B:456:ASP:C	2.54	0.49
1:B:61:THR:OG1	1:B:340:ALA:O	2.24	0.49
1:A:432:VAL:HG11	1:A:517:ASN:OD1	2.12	0.49
1:B:323:VAL:O	1:B:330:SER:HA	2.12	0.49
1:A:65:GLY:O	1:A:69:GLU:HG3	2.12	0.49
1:A:371:LEU:HD13	1:A:388:LEU:CD2	2.43	0.49
1:A:539:SER:HA	1:A:542:GLU:OE2	2.12	0.49
1:B:298:ALA:CA	1:B:309:MET:HE1	2.43	0.49
1:A:502:GLY:HA2	1:A:506:TYR:O	2.12	0.49
1:A:221:TYR:O	1:A:222:ASP:C	2.56	0.48
1:A:434:VAL:HB	1:A:516:VAL:O	2.13	0.48
1:A:495:THR:HG23	1:A:496:LEU:O	2.14	0.48
1:A:419:SER:O	1:A:422:ASN:HB2	2.14	0.48
1:A:439:THR:OG1	1:A:441:LYS:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:ALA:HA	1:A:345:MET:HG2	1.94	0.48
1:A:389:ILE:CD1	1:A:409:ILE:HD12	2.42	0.48
1:A:470:ALA:O	1:A:549:TRP:O	2.32	0.48
1:B:452:GLN:O	1:B:452:GLN:HG2	2.14	0.48
1:A:466:VAL:HG12	1:A:467:SER:N	2.29	0.48
1:A:321:LYS:HB3	1:A:335:TYR:CZ	2.49	0.48
1:A:114:ILE:CD1	1:A:137:LEU:HB3	2.42	0.47
1:A:358:ALA:O	1:A:362:VAL:HG23	2.14	0.47
1:A:378:VAL:HG11	1:A:409:ILE:HG21	1.96	0.47
1:A:218:MET:CE	1:A:218:MET:CG	2.91	0.47
1:B:312:TYR:CD1	1:B:313:GLN:N	2.83	0.47
1:A:371:LEU:HD23	1:A:384:ASN:ND2	2.29	0.47
1:B:141:ASN:N	1:B:195:GLU:HG2	2.29	0.47
1:B:170:LEU:HB3	1:B:192:PRO:HB3	1.97	0.47
1:B:510:ASP:HA	1:B:515:TYR:CD2	2.49	0.47
1:A:521:ILE:N	1:A:521:ILE:HD13	2.30	0.47
1:B:322:LYS:HG2	1:B:332:ARG:NH1	2.30	0.47
1:B:545:GLY:O	1:B:546:GLU:C	2.57	0.47
1:A:403:VAL:HG12	1:A:493:MET:HE2	1.96	0.47
1:B:357:LYS:C	1:B:359:GLN:H	2.22	0.47
1:A:53:GLU:HG2	1:A:318:ASN:O	2.15	0.47
1:A:471:LYS:HE2	1:A:550:GLN:NE2	2.29	0.47
1:B:117:HIS:NE2	3:B:2603:PO4:O1	2.48	0.47
1:A:375:ARG:NE	1:A:379:ARG:NH2	2.63	0.46
1:B:470:ALA:HB3	1:B:549:TRP:CD1	2.50	0.46
1:A:459:ALA:HB2	1:A:504:ASP:HB3	1.97	0.46
1:B:312:TYR:CD1	1:B:312:TYR:C	2.93	0.46
1:A:420:TYR:CD1	1:A:527:LYS:HD3	2.49	0.46
1:A:446:TYR:CE1	1:A:509:LEU:HD11	2.51	0.46
1:B:394:MET:SD	1:B:465:ASN:ND2	2.88	0.46
1:B:448:THR:HA	1:B:475:LEU:HD11	1.96	0.46
1:B:524:GLU:O	1:B:527:LYS:HG3	2.15	0.46
1:B:368:ASN:ND2	1:B:537:ASP:HA	2.30	0.46
1:B:545:GLY:O	1:B:547:VAL:N	2.49	0.46
1:B:168:ILE:HG22	1:B:169:GLY:N	2.29	0.46
1:B:204:GLN:OE1	1:B:204:GLN:HA	2.15	0.46
1:B:56:LEU:HD23	1:B:103:GLY:HA3	1.97	0.46
1:B:170:LEU:HD11	1:B:196:ALA:HB2	1.98	0.46
1:B:379:ARG:HD2	1:B:457:SER:C	2.41	0.46
1:A:467:SER:CB	1:A:546:GLU:HB2	2.45	0.46
1:A:84:ASP:CG	1:A:217:HIS:CE1	2.94	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:ILE:HG12	1:B:139:SER:HB2	1.97	0.45
1:B:368:ASN:OD1	1:B:369:GLY:N	2.49	0.45
1:A:345:MET:CE	1:A:349:LEU:HD21	2.47	0.45
1:B:130:GLU:CG	1:B:137:LEU:HD22	2.42	0.45
1:A:125:VAL:O	1:A:129:GLN:HG3	2.16	0.45
1:B:363:LYS:HZ2	1:B:417:ASP:HA	1.80	0.45
1:A:475:LEU:HD13	1:A:478:LEU:HD13	1.97	0.45
1:B:380:PHE:CE2	1:B:456:ASP:HA	2.51	0.45
1:A:401:PHE:CE2	1:A:493:MET:HE3	2.52	0.45
1:B:84:ASP:CG	1:B:217:HIS:NE2	2.74	0.45
1:A:364:ILE:HD11	1:A:530:ILE:HD11	1.97	0.45
1:A:401:PHE:HB2	1:A:466:VAL:CG2	2.46	0.45
1:B:302:PHE:HB2	1:B:307:MET:CE	2.46	0.45
1:B:155:TRP:CD1	1:B:155:TRP:C	2.95	0.45
1:A:508:ARG:HD2	1:A:510:ASP:OD1	2.17	0.45
1:B:150:ARG:NH2	1:B:195:GLU:OE2	2.47	0.45
1:A:367:THR:HG23	1:A:415:ALA:HA	1.99	0.45
1:A:438:MET:HG3	1:A:443:VAL:HG22	1.98	0.45
1:B:167:VAL:HA	1:B:213:ILE:O	2.16	0.45
1:B:301:GLU:O	1:B:307:MET:HE3	2.16	0.45
1:B:326:GLU:C	1:B:328:GLY:H	2.22	0.45
1:A:90:PRO:O	1:A:94:LEU:HG	2.17	0.44
1:A:112:MET:HE2	1:A:137:LEU:HG	1.99	0.44
1:A:486:ASP:HB3	1:A:489:LYS:HB2	1.98	0.44
1:B:114:ILE:HD11	1:B:137:LEU:C	2.43	0.44
1:A:375:ARG:HA	1:A:378:VAL:HG22	1.99	0.44
1:B:377:LYS:HD2	1:B:377:LYS:N	2.32	0.44
1:B:517:ASN:OD1	1:B:517:ASN:C	2.60	0.44
1:A:155:TRP:CE3	1:A:199:VAL:HG13	2.52	0.44
1:A:390:LEU:HD11	1:A:404:MET:HG2	2.00	0.44
1:A:469:VAL:HG23	1:A:477:ASP:HB3	1.99	0.44
1:B:86:ASN:CG	1:B:129:GLN:HE22	2.24	0.44
1:A:26:TYR:N	5:A:1809:HOH:O	2.49	0.44
1:A:394:MET:CG	1:A:402:ALA:HB2	2.48	0.44
1:B:99:PRO:HB3	1:B:352:PHE:CD2	2.53	0.44
1:B:394:MET:CE	1:B:401:PHE:C	2.91	0.44
1:B:394:MET:HA	1:B:399:ALA:HB3	2.00	0.44
1:A:213:ILE:HG12	1:A:247:MET:HG2	1.99	0.43
1:A:345:MET:HE2	1:A:349:LEU:HD11	2.00	0.43
1:A:528:ALA:HA	1:A:531:GLN:OE1	2.17	0.43
1:B:49:ASN:HB3	1:B:54:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:476:ASN:O	1:A:477:ASP:HB3	2.18	0.43
1:A:375:ARG:O	1:A:379:ARG:HB2	2.19	0.43
1:B:98:GLU:N	1:B:99:PRO:CD	2.79	0.43
1:B:512:LYS:HG3	1:B:513:PRO:HD2	2.00	0.43
1:B:300:PHE:HB3	1:B:307:MET:CE	2.34	0.43
1:A:439:THR:O	1:A:443:VAL:HG23	2.18	0.43
1:B:321:LYS:HB3	1:B:335:TYR:CZ	2.53	0.43
1:B:380:PHE:CZ	1:B:456:ASP:HA	2.53	0.43
1:A:170:LEU:HD11	1:A:196:ALA:HB2	2.00	0.43
1:A:369:GLY:HA2	1:A:415:ALA:HB2	2.01	0.43
1:A:378:VAL:O	1:A:460:TYR:HD2	2.02	0.43
1:B:438:MET:HB2	1:B:442:GLU:HB2	2.01	0.43
1:A:379:ARG:HD2	1:A:458:GLY:N	2.34	0.43
1:A:511:ASN:OD1	1:A:512:LYS:HG3	2.19	0.43
1:B:301:GLU:HG3	1:B:310:VAL:HG11	2.01	0.43
1:A:267:VAL:O	1:A:268:ASP:HB2	2.20	0.42
1:A:454:LYS:HB3	1:A:455:PRO:HD2	2.00	0.42
1:A:405:SER:HB3	1:A:458:GLY:O	2.19	0.42
1:A:406:GLY:C	1:A:408:GLY:H	2.28	0.42
1:B:348:LEU:O	1:B:348:LEU:HG	2.20	0.42
1:A:180:ASN:CG	1:A:182:GLU:HG2	2.44	0.42
1:A:493:MET:HG2	1:A:494:ALA:N	2.35	0.42
1:B:115:GLY:CA	1:B:118:GLU:OE1	2.68	0.42
1:B:255:ASP:O	1:B:287:GLN:HG2	2.19	0.42
1:B:106:LEU:HD21	1:B:344:GLN:HG2	2.02	0.42
1:B:345:MET:CE	1:B:348:LEU:HB3	2.50	0.42
1:B:359:GLN:HA	1:B:359:GLN:NE2	2.35	0.42
1:A:401:PHE:HB2	1:A:466:VAL:HG23	2.02	0.42
1:B:434:VAL:HG12	1:B:517:ASN:HA	2.01	0.42
1:A:384:ASN:HD22	1:A:538:VAL:HG13	1.83	0.41
1:B:260:ALA:HB2	1:B:266:GLN:HA	2.02	0.41
1:B:431:ASN:OD1	4:B:2604:ADN:H2	2.19	0.41
1:B:379:ARG:HD2	1:B:458:GLY:CA	2.49	0.41
1:B:460:TYR:HA	1:B:461:PRO:HD3	1.69	0.41
1:B:86:ASN:HD21	1:B:129:GLN:HE22	1.69	0.41
1:B:96:ASP:O	1:B:97:ALA:HB3	2.20	0.41
1:B:507:PRO:O	1:B:509:LEU:HD13	2.20	0.41
1:A:474:LYS:HE3	1:A:474:LYS:HB2	1.91	0.41
1:B:86:ASN:ND2	1:B:129:GLN:HE22	2.18	0.41
1:B:155:TRP:CE3	1:B:199:VAL:HG13	2.56	0.41
1:A:389:ILE:O	1:A:393:GLN:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:LEU:HD12	1:A:421:LYS:HB2	2.01	0.41
1:A:401:PHE:N	1:A:401:PHE:CD1	2.89	0.41
1:A:521:ILE:HB	1:A:524:GLU:CG	2.41	0.41
1:A:360:LEU:HD11	1:A:424:LEU:HD12	2.03	0.41
1:A:389:ILE:HD12	1:A:409:ILE:HD12	2.03	0.41
1:A:401:PHE:CG	1:A:480:ILE:HD12	2.55	0.41
1:B:371:LEU:O	1:B:412:SER:HB3	2.21	0.41
1:B:435:TYR:HA	1:B:493:MET:O	2.20	0.41
1:A:57:ALA:CA	1:A:345:MET:HG2	2.51	0.41
1:A:167:VAL:HA	1:A:213:ILE:O	2.21	0.41
1:B:91:GLU:OE2	1:B:421:LYS:HD2	2.20	0.41
1:B:401:PHE:CD2	1:B:493:MET:HE3	2.54	0.41
1:B:123:LEU:HD12	1:B:123:LEU:HA	1.89	0.41
1:B:151:LEU:HD23	1:B:151:LEU:HA	1.90	0.41
1:B:422:ASN:O	1:B:426:VAL:HG23	2.21	0.41
1:B:497:ASN:O	1:B:501:THR:HG23	2.21	0.41
1:B:86:ASN:HD21	1:B:129:GLN:NE2	2.19	0.40
1:B:471:LYS:HE2	1:B:550:GLN:HG3	2.03	0.40
1:B:475:LEU:HD13	1:B:478:LEU:HD13	2.04	0.40
1:A:468:PHE:CE1	1:A:547:VAL:HG13	2.55	0.40
1:B:540:VAL:O	1:B:540:VAL:HG12	2.21	0.40
1:A:326:GLU:C	1:A:328:GLY:H	2.29	0.40
1:B:141:ASN:CA	1:B:195:GLU:HG2	2.52	0.40
1:B:173:ASP:OD1	1:B:173:ASP:N	2.53	0.40
1:A:26:TYR:CE1	1:A:304:ASN:HA	2.57	0.40
1:B:44:GLY:HA2	1:B:100:ASP:OD2	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	523/525 (100%)	490 (94%)	29 (6%)	4 (1%)	16	12
1	B	523/525 (100%)	481 (92%)	36 (7%)	6 (1%)	11	8
All	All	1046/1050 (100%)	971 (93%)	65 (6%)	10 (1%)	12	9

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	513	PRO
1	B	546	GLU
1	A	87	THR
1	B	548	SER
1	B	289	HIS
1	B	87	THR
1	B	378	VAL
1	B	472	ASP
1	A	378	VAL
1	A	484	PRO

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	433/433 (100%)	417 (96%)	16 (4%)	30	33
1	B	433/433 (100%)	422 (98%)	11 (2%)	42	48
All	All	866/866 (100%)	839 (97%)	27 (3%)	35	39

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	LEU
1	A	153	LYS
1	A	235	GLU
1	A	307	MET
1	A	327	ASP
1	A	375	ARG

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Mol	Chain	Res	Type
1	A	401	PHE
1	A	410	ARG
1	A	428	PRO
1	A	508	ARG
1	A	513	PRO
1	A	521	ILE
1	A	522	ASP
1	A	524	GLU
1	A	546	GLU
1	A	550	GLN
1	B	56	LEU
1	B	73	GLU
1	B	202	GLU
1	B	228	SER
1	B	323	VAL
1	B	390	LEU
1	B	456	ASP
1	B	512	LYS
1	B	526	LEU
1	B	527	LYS
1	B	547	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	86	ASN
1	A	129	GLN
1	A	144	GLN
1	A	180	ASN
1	A	204	GLN
1	A	368	ASN
1	A	462	GLN
1	A	476	ASN
1	A	550	GLN
1	B	45	HIS
1	B	86	ASN
1	B	129	GLN
1	B	144	GLN
1	B	266	GLN
1	B	279	GLN
1	B	313	GLN

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Mol	Chain	Res	Type
1	B	353	GLN
1	B	359	GLN
1	B	393	GLN
1	B	452	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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ADN	B	2604	-	21,21,21	0.20	0	31,31,31	0.32	0
4	ADN	A	1604	-	21,21,21	0.21	0	31,31,31	0.33	0
3	PO4	A	1603	2	4,4,4	1.45	1 (25%)	6,6,6	0.57	0
3	PO4	B	2603	2	4,4,4	1.57	0	6,6,6	0.46	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
4	ADN	B	2604	-	-	0/6/22/22	0/3/3/3
4	ADN	A	1604	-	-	0/6/22/22	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1603	PO4	P-O3	-2.12	1.48	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2604	ADN	1	0
4	A	1604	ADN	1	0
3	B	2603	PO4	1	0

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	525/525 (100%)	0.43	41 (7%)	19 20	16, 34, 76, 91	0
1	B	525/525 (100%)	0.88	51 (9%)	13 14	24, 48, 74, 86	0
All	All	1050/1050 (100%)	0.66	92 (8%)	15 16	16, 44, 75, 91	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	475	LEU	5.7
1	A	530	ILE	5.5
1	A	549	TRP	5.4
1	A	444	ILE	4.5
1	A	469	VAL	4.1
1	B	358	ALA	4.1
1	A	464	ALA	3.9
1	B	478	LEU	3.8
1	B	450	VAL	3.8
1	A	480	ILE	3.6
1	B	505	GLY	3.4
1	B	545	GLY	3.3
1	A	449	ALA	3.3
1	A	443	VAL	3.1
1	A	470	ALA	3.1
1	A	446	TYR	3.1
1	B	485	VAL	3.1
1	B	440	GLY	3.0
1	A	547	VAL	3.0
1	B	378	VAL	3.0
1	A	453	MET	3.0
1	A	466	VAL	2.9
1	B	547	VAL	2.9
1	A	447	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	478	LEU	2.9
1	A	381	VAL	2.9
1	A	485	VAL	2.8
1	B	549	TRP	2.8
1	B	463	PHE	2.8
1	B	469	VAL	2.7
1	A	463	PHE	2.7
1	B	475	LEU	2.7
1	B	201	GLN	2.7
1	B	530	ILE	2.7
1	B	519	GLY	2.7
1	B	501	THR	2.6
1	A	373	GLY	2.6
1	B	403	VAL	2.6
1	B	487	PRO	2.6
1	B	148	GLY	2.6
1	B	443	VAL	2.5
1	A	380	PHE	2.5
1	A	514	GLY	2.5
1	B	200	ILE	2.5
1	A	461	PRO	2.4
1	B	473	GLY	2.4
1	A	468	PHE	2.4
1	B	204	GLN	2.4
1	B	364	ILE	2.4
1	B	449	ALA	2.4
1	B	494	ALA	2.4
1	A	360	LEU	2.4
1	B	381	VAL	2.4
1	A	459	ALA	2.3
1	A	401	PHE	2.3
1	B	451	ALA	2.3
1	B	388	LEU	2.3
1	B	390	LEU	2.3
1	A	383	THR	2.3
1	B	453	MET	2.3
1	B	185	THR	2.2
1	B	178	ILE	2.2
1	B	360	LEU	2.2
1	B	155	TRP	2.2
1	B	152	PHE	2.2
1	B	534	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	367	THR	2.2
1	B	184	PHE	2.1
1	A	540	VAL	2.1
1	B	362	VAL	2.1
1	A	458	GLY	2.1
1	A	462	GLN	2.1
1	A	523	ALA	2.1
1	B	380	PHE	2.1
1	B	137	LEU	2.1
1	A	435	TYR	2.1
1	B	529	TYR	2.1
1	B	461	PRO	2.1
1	B	484	PRO	2.1
1	B	389	ILE	2.1
1	A	465	ASN	2.1
1	B	513	PRO	2.1
1	B	480	ILE	2.1
1	A	496	LEU	2.0
1	A	495	THR	2.0
1	A	409	ILE	2.0
1	B	520	PHE	2.0
1	A	500	ALA	2.0
1	A	550	GLN	2.0
1	B	191	LYS	2.0
1	B	454	LYS	2.0
1	A	515	TYR	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
4	ADN	A	1604	19/19	0.86	0.14	46,52,56,57	0
4	ADN	B	2604	19/19	0.87	0.13	59,62,62,63	0
3	PO4	B	2603	5/5	0.92	0.10	60,61,62,62	0
3	PO4	A	1603	5/5	0.94	0.08	23,31,37,39	0
2	MN	B	2601	1/1	0.99	0.02	38,38,38,38	0
2	MN	B	2602	1/1	0.99	0.03	41,41,41,41	0
2	MN	A	1602	1/1	0.99	0.02	23,23,23,23	0
2	MN	A	1601	1/1	1.00	0.04	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.