



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 10:58 pm BST

PDB ID : 3D7K
Title : Crystal structure of benzaldehyde lyase in complex with the inhibitor MBP
Authors : Brandt, G.S.
Deposited on : 2008-05-21
Resolution : 2.49 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	FAILED
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

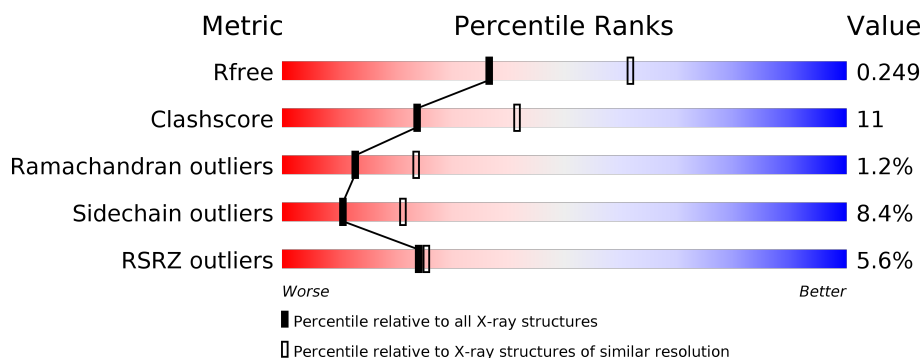
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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	570	<div> <div>8%</div> <div> <div></div> <div>75%</div> <div>20%</div> <div>• •</div> </div> </div>
1	B	570	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>21%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8413 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 Benzaldehyde lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	554	Total	C	N	O	S	0	0	0
			4079	2576	723	764	16			
1	B	554	Total	C	N	O	S	0	0	0
			4079	2576	723	764	16			

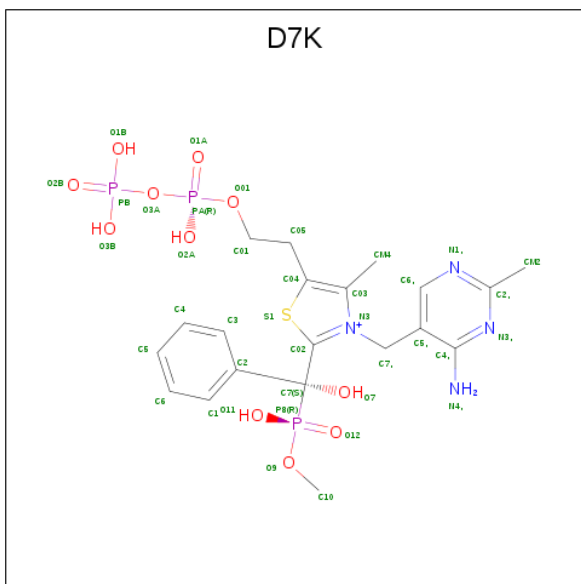
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	563	GLY	-	EXPRESSION TAG	UNP Q9F4L3
A	564	SER	-	EXPRESSION TAG	UNP Q9F4L3
A	565	HIS	-	EXPRESSION TAG	UNP Q9F4L3
A	566	HIS	-	EXPRESSION TAG	UNP Q9F4L3
A	567	HIS	-	EXPRESSION TAG	UNP Q9F4L3
A	568	HIS	-	EXPRESSION TAG	UNP Q9F4L3
A	569	HIS	-	EXPRESSION TAG	UNP Q9F4L3
A	570	HIS	-	EXPRESSION TAG	UNP Q9F4L3
B	563	GLY	-	EXPRESSION TAG	UNP Q9F4L3
B	564	SER	-	EXPRESSION TAG	UNP Q9F4L3
B	565	HIS	-	EXPRESSION TAG	UNP Q9F4L3
B	566	HIS	-	EXPRESSION TAG	UNP Q9F4L3
B	567	HIS	-	EXPRESSION TAG	UNP Q9F4L3
B	568	HIS	-	EXPRESSION TAG	UNP Q9F4L3
B	569	HIS	-	EXPRESSION TAG	UNP Q9F4L3
B	570	HIS	-	EXPRESSION TAG	UNP Q9F4L3

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 3 is 3-[(4-amino-2-methylpyrimidin-5-yl)methyl]-2-[(S)-hydroxy[(R)-hydroxy(methoxy)phosphoryl]phenylmethyl]-5-(2-[(R)-hydroxy(phosphonooxy)phosphoryl]oxy)ethyl)-4-methyl-1,3-thiazol-3-ium (three-letter code: D7K) (formula: C₂₀H₂₈N₄O₁₁P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			39	20	4	11	3	1		
3	B	1	Total	C	N	O	P	S	0	0
			39	20	4	11	3	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	79	Total	O	0	0
			79	79		
4	B	96	Total	O	0	0
			96	96		

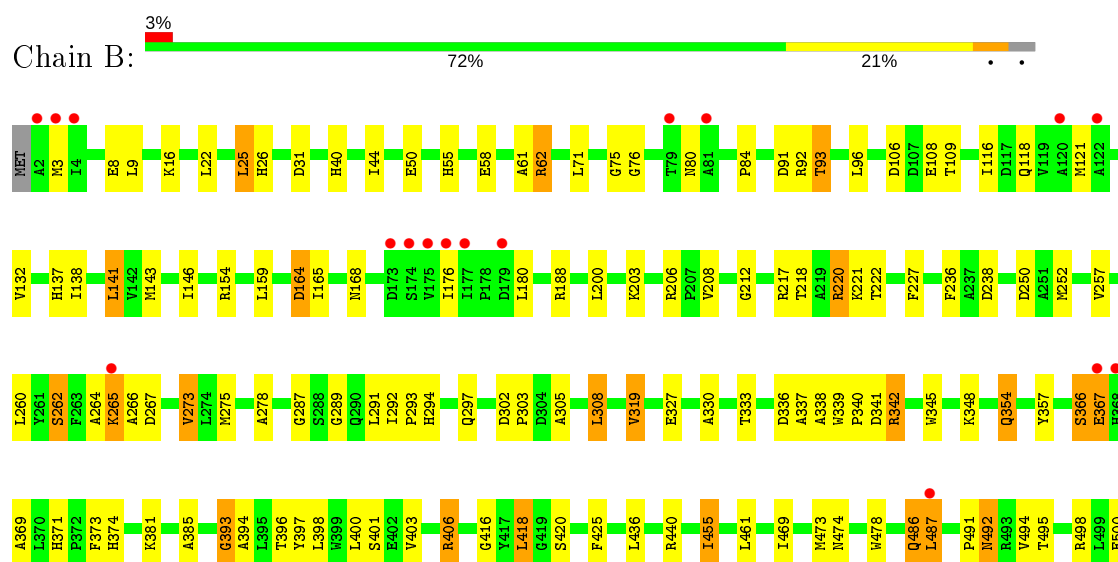
3 Residue-property plots [i](#)

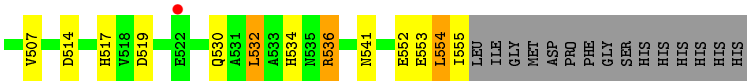
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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



• Molecule 1: Benzaldehyde lyase





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	151.94Å 151.94Å 98.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.00 – 2.49 46.01 – 2.49	Depositor EDS
% Data completeness (in resolution range)	97.2 (46.00-2.49) 97.2 (46.01-2.49)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.194 , 0.250 0.193 , 0.249	Depositor DCC
R_{free} test set	4485 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8413	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: D7K, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.88	3/4162 (0.1%)	0.90	6/5677 (0.1%)
1	B	0.89	0/4162	0.89	7/5677 (0.1%)
All	All	0.88	3/8324 (0.0%)	0.90	13/11354 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	164	ASP	CB-CG	-6.96	1.37	1.51
1	A	131	ARG	CG-CD	5.60	1.66	1.51
1	A	522	GLU	CG-CD	5.23	1.59	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	ASP	N-CA-CB	-8.19	95.86	110.60
1	A	62	ARG	NE-CZ-NH1	-7.07	116.76	120.30
1	A	392	ASP	CB-CG-OD1	6.60	124.24	118.30
1	A	393	GLY	N-CA-C	6.30	128.85	113.10
1	B	487	LEU	CA-CB-CG	6.11	129.35	115.30
1	B	498	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	A	62	ARG	NE-CZ-NH2	5.66	123.13	120.30
1	B	498	ARG	NE-CZ-NH2	-5.51	117.55	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	62	ARG	NE-CZ-NH1	-5.29	117.66	120.30
1	B	25	LEU	CA-CB-CG	5.17	127.20	115.30
1	B	164	ASP	CB-CA-C	-5.12	100.17	110.40
1	B	393	GLY	N-CA-C	5.10	125.85	113.10
1	A	105	ARG	C-N-CA	-5.09	108.98	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	106	ASP	Peptide

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	4079	0	4069	80	0
1	B	4079	0	4069	99	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	39	0	24	5	0
3	B	39	0	24	5	0
4	A	79	0	0	10	0
4	B	96	0	0	16	0
All	All	8413	0	8186	183	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 11.

All (183) 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:B:164:ASP:HB2	4:B:648:HOH:O	1.18	1.27
1:B:342:ARG:HH11	1:B:342:ARG:HG3	1.08	1.12
1:B:366:SER:HB2	1:B:374:HIS:CD2	2.04	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:SER:HB2	1:B:374:HIS:HD2	1.34	0.92
1:B:342:ARG:CG	1:B:342:ARG:HH11	1.81	0.91
1:B:536:ARG:HB2	1:B:536:ARG:HH11	1.30	0.91
1:B:61:ALA:HB3	4:B:663:HOH:O	1.70	0.91
1:A:116:ILE:CG2	4:A:624:HOH:O	2.21	0.88
1:B:418:LEU:HD13	1:B:420:SER:HB2	1.57	0.86
1:B:371:HIS:HD2	1:B:373:PHE:H	1.26	0.83
1:B:398:LEU:HD22	1:B:552:GLU:HG2	1.59	0.81
1:A:26:HIS:HE1	1:A:31:ASP:OD1	1.64	0.79
1:B:164:ASP:CB	4:B:648:HOH:O	1.93	0.79
1:B:536:ARG:HH11	1:B:536:ARG:CB	1.96	0.79
1:B:342:ARG:NH1	1:B:342:ARG:HG3	1.92	0.78
1:B:474:ASN:HD22	1:B:541:ASN:HD21	1.32	0.78
1:A:131:ARG:HD2	4:A:574:HOH:O	1.86	0.76
1:B:492:ASN:HD22	1:B:492:ASN:H	1.34	0.76
1:A:371:HIS:CD2	1:A:373:PHE:H	2.05	0.74
1:A:3:MET:HE2	4:A:649:HOH:O	1.89	0.72
1:B:218:THR:OG1	4:B:654:HOH:O	2.07	0.71
1:A:342:ARG:NH1	4:A:616:HOH:O	2.24	0.71
1:B:514:ASP:OD1	1:B:536:ARG:NH1	2.16	0.71
1:B:91:ASP:OD1	1:B:416:GLY:HA3	1.90	0.71
1:A:530:GLN:O	1:A:534:HIS:CD2	2.45	0.69
1:B:381:LYS:NZ	4:B:602:HOH:O	2.24	0.68
3:B:572:D7K:H7,	3:B:572:D7K:O7	1.94	0.67
1:A:335:GLN:HG3	4:A:650:HOH:O	1.93	0.67
1:B:367:GLU:HA	4:B:622:HOH:O	1.95	0.66
1:B:455:ILE:HG12	1:B:507:VAL:HG11	1.78	0.65
1:A:371:HIS:HD2	1:A:373:PHE:H	1.44	0.65
1:B:137:HIS:HB3	1:B:141:LEU:HD22	1.78	0.65
1:A:116:ILE:HG23	4:A:624:HOH:O	1.91	0.64
1:A:252:MET:HG2	1:A:346:CYS:SG	2.36	0.64
1:A:393:GLY:O	1:A:394:ALA:HB3	1.98	0.64
1:B:262:SER:HA	1:B:265:LYS:HB3	1.79	0.63
1:B:220:ARG:HD3	1:B:327:GLU:OE2	1.99	0.63
1:A:106:ASP:HA	1:A:109:THR:CG2	2.29	0.63
1:A:26:HIS:CE1	1:A:31:ASP:OD1	2.50	0.62
1:B:289:GLY:HA2	1:B:292:ILE:O	1.98	0.62
1:A:489:VAL:HG12	1:A:493:ARG:HG3	1.82	0.62
1:B:164:ASP:CG	4:B:648:HOH:O	2.22	0.62
1:B:398:LEU:CD2	1:B:552:GLU:HG2	2.28	0.61
1:B:486:GLN:HG3	1:B:491:PRO:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:517:HIS:HD2	1:A:541:ASN:O	1.84	0.61
1:A:106:ASP:HA	1:A:109:THR:HG23	1.83	0.61
1:B:330:ALA:O	1:B:333:THR:HG22	2.00	0.61
1:B:26:HIS:HE1	1:B:31:ASP:OD1	1.82	0.61
1:A:273:VAL:HG21	1:A:292:ILE:HG23	1.83	0.61
1:A:386:GLY:HA2	1:A:440:ARG:HG2	1.83	0.60
1:B:342:ARG:CG	1:B:342:ARG:NH1	2.51	0.60
1:A:8:GLU:OE2	1:A:40:HIS:HE1	1.85	0.60
1:B:357:TYR:CE1	1:B:406:ARG:HD2	2.36	0.60
3:A:572:D7K:HO7	3:A:572:D7K:H7,	1.67	0.59
1:A:357:TYR:CD1	1:A:406:ARG:HD3	2.38	0.59
1:B:536:ARG:NH1	1:B:536:ARG:CB	2.66	0.58
1:A:310:ARG:NH1	1:B:108:GLU:HG3	2.18	0.58
1:B:517:HIS:HD2	4:B:652:HOH:O	1.86	0.58
1:B:492:ASN:ND2	1:B:492:ASN:H	2.00	0.57
3:A:572:D7K:O7	3:A:572:D7K:H7,	2.05	0.57
1:B:220:ARG:NE	4:B:659:HOH:O	2.35	0.57
1:A:4:ILE:HG12	1:A:172:GLU:HB2	1.87	0.56
1:A:136:GLU:CD	1:A:136:GLU:H	2.08	0.56
1:B:530:GLN:O	1:B:534:HIS:HD2	1.88	0.56
1:B:164:ASP:O	1:B:168:ASN:HB2	2.06	0.56
1:A:299:ILE:HG23	1:A:316:LEU:HD23	1.88	0.55
1:B:8:GLU:OE1	1:B:40:HIS:HE1	1.90	0.55
1:A:374:HIS:O	1:A:378:VAL:HG23	2.06	0.55
3:B:572:D7K:O11	3:B:572:D7K:H3	2.05	0.55
1:B:143:MET:HE2	1:B:180:LEU:HD13	1.89	0.55
1:B:264:ALA:C	1:B:266:ALA:H	2.10	0.54
1:A:484:PHE:O	1:A:488:ALA:HB3	2.07	0.54
1:A:118:GLN:HA	1:A:121:MET:HE3	1.90	0.54
1:B:342:ARG:NH1	4:B:653:HOH:O	2.40	0.54
1:A:116:ILE:HG22	4:A:624:HOH:O	1.98	0.53
3:B:572:D7K:HN4,	3:B:572:D7K:C02	2.20	0.53
1:A:202:ARG:HA	1:A:342:ARG:HH22	1.74	0.53
1:B:75:GLY:H	1:B:118:GLN:NE2	2.07	0.53
1:B:132:VAL:HG22	1:B:141:LEU:HD23	1.90	0.52
1:B:366:SER:CB	1:B:374:HIS:HD2	2.14	0.52
1:B:385:ALA:O	1:B:440:ARG:HD3	2.09	0.52
1:A:268:ALA:O	1:A:345:TRP:HH2	1.94	0.51
1:B:367:GLU:HG2	4:B:622:HOH:O	2.09	0.51
1:A:390:VAL:HG21	1:A:428:ALA:HA	1.92	0.51
1:A:451:VAL:HG11	1:A:472:ILE:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ASP:CG	1:B:303:PRO:HD2	2.32	0.50
3:B:572:D7K:H7,	3:B:572:D7K:HO7	1.76	0.50
1:B:302:ASP:O	1:B:319:VAL:HA	2.11	0.50
1:A:357:TYR:CG	1:A:406:ARG:HD3	2.46	0.50
1:A:354:GLN:OE1	1:A:358:ALA:HB2	2.12	0.50
1:B:227:PHE:HD2	1:B:333:THR:HG21	1.77	0.49
1:B:305:ALA:HA	1:B:308:LEU:HD22	1.93	0.49
1:B:264:ALA:O	1:B:266:ALA:N	2.44	0.49
1:A:143:MET:HE2	1:A:180:LEU:HD13	1.94	0.49
1:A:478:TRP:HB3	3:A:572:D7K:H05A	1.95	0.49
1:A:75:GLY:H	1:A:118:GLN:NE2	2.10	0.48
1:B:58:GLU:O	4:B:663:HOH:O	2.20	0.48
1:A:371:HIS:CD2	1:A:373:PHE:HB3	2.49	0.48
1:B:354:GLN:HB2	1:B:354:GLN:HE21	1.34	0.48
1:A:8:GLU:OE2	1:A:40:HIS:CE1	2.65	0.48
1:B:206:ARG:HD2	1:B:345:TRP:CZ3	2.49	0.48
1:B:553:GLU:O	1:B:555:ILE:N	2.47	0.48
1:B:474:ASN:HB2	1:B:541:ASN:ND2	2.29	0.48
1:A:547:ASP:N	1:A:548:PRO:CD	2.77	0.48
1:A:257:VAL:O	1:A:260:LEU:HB2	2.13	0.47
1:A:429:LEU:HD23	1:A:429:LEU:O	2.14	0.47
1:A:429:LEU:HD23	1:A:429:LEU:C	2.35	0.47
1:A:310:ARG:HH11	1:B:108:GLU:HG3	1.78	0.47
1:B:393:GLY:O	1:B:394:ALA:HB3	2.15	0.47
1:B:478:TRP:HB3	3:B:572:D7K:H05A	1.96	0.47
1:B:91:ASP:HB2	1:B:93:THR:CG2	2.45	0.47
1:A:526:ALA:O	1:A:530:GLN:HB2	2.14	0.47
1:B:208:VAL:HG12	1:B:273:VAL:HB	1.96	0.47
1:A:241:GLY:O	1:A:244:MET:HB2	2.15	0.47
1:A:498:ARG:NE	4:A:630:HOH:O	2.05	0.47
1:B:371:HIS:CD2	1:B:373:PHE:H	2.18	0.47
1:A:268:ALA:O	1:A:345:TRP:CH2	2.68	0.46
3:A:572:D7K:HN4,	3:A:572:D7K:C02	2.29	0.46
1:B:62:ARG:HG3	4:B:663:HOH:O	2.15	0.46
1:A:224:LEU:O	1:A:228:VAL:HG23	2.16	0.46
1:B:552:GLU:O	1:B:555:ILE:HG12	2.15	0.46
1:B:287:GLY:O	1:B:294:HIS:HE1	1.99	0.45
1:B:396:THR:HG23	1:B:473:MET:HG3	1.97	0.45
1:B:474:ASN:HB2	1:B:541:ASN:HD21	1.81	0.45
1:B:146:ILE:HB	4:B:662:HOH:O	2.17	0.45
1:B:55:HIS:O	1:B:58:GLU:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:GLU:HB2	1:B:80:ASN:HB2	1.98	0.45
1:A:105:ARG:O	1:A:106:ASP:CG	2.54	0.45
1:A:448:ASP:N	1:A:448:ASP:OD1	2.39	0.45
1:A:23:PHE:O	1:A:70:ALA:HA	2.18	0.44
1:A:2:ALA:HB1	4:A:649:HOH:O	2.17	0.44
1:B:398:LEU:HD22	1:B:552:GLU:CG	2.37	0.44
1:B:116:ILE:HB	1:B:121:MET:HE1	1.98	0.44
1:B:341:ASP:O	1:B:342:ARG:HB2	2.17	0.44
1:B:212:GLY:HA2	1:B:238:ASP:OD1	2.17	0.44
1:B:400:LEU:O	1:B:403:VAL:HG22	2.17	0.44
1:B:339:TRP:HA	1:B:340:PRO:HD2	1.88	0.44
1:B:236:PHE:CD2	1:B:236:PHE:N	2.87	0.43
1:A:372:PRO:HB2	1:A:399:TRP:CD1	2.53	0.43
1:A:420:SER:OG	1:B:76:GLY:HA3	2.18	0.43
1:A:56:ALA:HA	1:A:426:GLY:O	2.18	0.43
1:B:397:TYR:O	1:B:401:SER:HB3	2.18	0.43
1:A:106:ASP:HA	1:A:109:THR:HG21	1.98	0.43
1:A:369:ALA:HB1	1:A:545:ALA:HB2	1.99	0.43
1:A:490:GLY:HA2	1:A:491:PRO:HD2	1.82	0.42
1:B:275:MET:HB3	1:B:278:ALA:HB3	2.01	0.42
1:A:304:ASP:OD1	1:A:306:CYS:HB2	2.19	0.42
1:A:311:LEU:HD21	1:B:109:THR:HA	2.01	0.42
1:B:93:THR:HG22	1:B:217:ARG:HH21	1.84	0.42
1:B:22:LEU:HB2	1:B:44:ILE:HG12	2.01	0.42
1:B:9:LEU:HD23	1:B:9:LEU:HA	1.71	0.42
1:A:416:GLY:HA3	4:A:593:HOH:O	2.19	0.42
1:A:188:ARG:HB3	1:A:188:ARG:HE	1.71	0.42
1:A:75:GLY:H	1:A:118:GLN:HE22	1.67	0.42
1:B:116:ILE:HG12	4:B:664:HOH:O	2.18	0.41
1:B:154:ARG:N	1:B:154:ARG:HD2	2.35	0.41
1:A:371:HIS:HD2	1:A:373:PHE:N	2.14	0.41
1:A:514:ASP:OD2	1:A:536:ARG:HD2	2.20	0.41
1:B:336:ASP:O	1:B:338:ALA:N	2.53	0.41
1:B:357:TYR:CZ	1:B:406:ARG:HD2	2.54	0.41
1:A:432:GLN:HE21	1:A:436:LEU:HD13	1.86	0.41
1:B:469:ILE:CD1	1:B:532:LEU:HD13	2.49	0.41
1:A:141:LEU:HD23	1:A:141:LEU:HA	1.83	0.41
1:A:112:LEU:HG	1:A:113:GLN:HE21	1.85	0.41
1:A:249:PRO:HG2	1:A:252:MET:CE	2.50	0.41
1:B:291:LEU:O	1:B:293:PRO:HD3	2.20	0.41
1:B:474:ASN:ND2	1:B:541:ASN:HD21	2.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:ILE:HG12	1:A:274:LEU:HD23	2.03	0.41
1:A:41:ASP:CG	1:A:41:ASP:O	2.59	0.41
1:B:200:LEU:HD22	1:B:297:GLN:NE2	2.36	0.41
1:B:92:ARG:HA	1:B:154:ARG:O	2.20	0.41
1:A:432:GLN:NE2	1:A:436:LEU:HD13	2.36	0.41
1:B:138:ILE:HD11	1:B:165:ILE:HG22	2.02	0.41
1:A:206:ARG:HB3	1:A:345:TRP:CZ2	2.56	0.40
1:A:99:THR:CG2	1:A:158:LEU:HD11	2.51	0.40
1:A:358:ALA:HA	1:A:361:ALA:HB3	2.03	0.40
1:B:138:ILE:HD11	1:B:165:ILE:CG2	2.51	0.40
1:A:225:SER:O	1:A:226:ALA:C	2.59	0.40
1:B:180:LEU:HD13	4:B:662:HOH:O	2.21	0.40
1:B:221:LYS:HG3	1:B:221:LYS:H	1.69	0.40
1:A:265:LYS:C	1:A:267:ASP:H	2.25	0.40
1:A:436:LEU:HD12	1:A:436:LEU:HA	1.92	0.40
3:A:572:D7K:H10A	3:A:572:D7K:C1	2.52	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	552/570 (97%)	506 (92%)	38 (7%)	8 (1%)	11	20
1	B	552/570 (97%)	513 (93%)	34 (6%)	5 (1%)	17	31
All	All	1104/1140 (97%)	1019 (92%)	72 (6%)	13 (1%)	13	24

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	265	LYS
1	B	337	ALA

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Mol	Chain	Res	Type
1	A	364	SER
1	A	369	ALA
1	B	554	LEU
1	A	394	ALA
1	B	519	ASP
1	A	16	LYS
1	A	337	ALA
1	A	467	PRO
1	B	369	ALA
1	A	164	ASP
1	A	257	VAL

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	412/426 (97%)	387 (94%)	25 (6%)	18	36
1	B	412/426 (97%)	368 (89%)	44 (11%)	6	13
All	All	824/852 (97%)	755 (92%)	69 (8%)	11	21

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	38	LEU
1	A	71	LEU
1	A	96	LEU
1	A	106	ASP
1	A	164	ASP
1	A	172	GLU
1	A	188	ARG
1	A	203	LYS
1	A	308	LEU
1	A	344	ASP
1	A	354	GLN

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Mol	Chain	Res	Type
1	A	359	SER
1	A	363	LYS
1	A	366	SER
1	A	397	TYR
1	A	425	PHE
1	A	436	LEU
1	A	454	SER
1	A	461	LEU
1	A	486	GLN
1	A	492	ASN
1	A	495	THR
1	A	525	SER
1	A	547	ASP
1	B	3	MET
1	B	16	LYS
1	B	25	LEU
1	B	71	LEU
1	B	84	PRO
1	B	93	THR
1	B	96	LEU
1	B	106	ASP
1	B	141	LEU
1	B	159	LEU
1	B	176	ILE
1	B	188	ARG
1	B	203	LYS
1	B	220	ARG
1	B	222	THR
1	B	250	ASP
1	B	252	MET
1	B	257	VAL
1	B	260	LEU
1	B	262	SER
1	B	267	ASP
1	B	273	VAL
1	B	308	LEU
1	B	319	VAL
1	B	342	ARG
1	B	348	LYS
1	B	354	GLN
1	B	366	SER
1	B	367	GLU

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Mol	Chain	Res	Type
1	B	406	ARG
1	B	418	LEU
1	B	425	PHE
1	B	436	LEU
1	B	455	ILE
1	B	461	LEU
1	B	486	GLN
1	B	487	LEU
1	B	492	ASN
1	B	494	VAL
1	B	495	THR
1	B	500	GLU
1	B	532	LEU
1	B	536	ARG
1	B	554	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	40	HIS
1	A	87	ASN
1	A	113	GLN
1	A	118	GLN
1	A	144	GLN
1	A	283	ASN
1	A	335	GLN
1	A	371	HIS
1	A	517	HIS
1	A	530	GLN
1	A	534	HIS
1	B	26	HIS
1	B	40	HIS
1	B	87	ASN
1	B	113	GLN
1	B	118	GLN
1	B	290	GLN
1	B	294	HIS
1	B	297	GLN
1	B	331	GLN
1	B	354	GLN
1	B	371	HIS

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Mol	Chain	Res	Type
1	B	415	HIS
1	B	492	ASN
1	B	530	GLN
1	B	534	HIS
1	B	541	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

Mogul failed to run properly - this section is therefore empty.

5.5 Carbohydrates [i](#)

Mogul failed to run properly - this section is therefore empty.

5.6 Ligand geometry [i](#)

Mogul failed to run properly - this section is therefore empty.

5.7 Other polymers [i](#)

Mogul failed to run properly - this section is therefore empty.

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	554/570 (97%)	0.34	44 (7%) 12 12	26, 48, 89, 96	0
1	B	554/570 (97%)	0.12	18 (3%) 47 51	28, 47, 70, 80	0
All	All	1108/1140 (97%)	0.23	62 (5%) 24 25	26, 47, 80, 96	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	HIS	7.7
1	A	337	ALA	6.7
1	A	269	ALA	5.8
1	A	264	ALA	5.1
1	A	297	GLN	5.0
1	A	265	LYS	4.9
1	A	367	GLU	4.7
1	B	174	SER	4.6
1	A	295	SER	4.5
1	A	268	ALA	4.3
1	A	335	GLN	4.3
1	A	555	ILE	4.2
1	B	175	VAL	4.1
1	A	266	ALA	3.8
1	B	3	MET	3.5
1	A	294	HIS	3.4
1	A	336	ASP	3.4
1	B	79	THR	3.4
1	A	203	LYS	3.3
1	B	368	HIS	3.2
1	A	334	ALA	3.1
1	A	339	TRP	3.1
1	A	263	PHE	3.0
1	A	338	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	2	ALA	2.9
1	A	369	ALA	2.9
1	A	554	LEU	2.8
1	A	267	ASP	2.7
1	B	173	ASP	2.7
1	A	82	VAL	2.6
1	A	288	SER	2.6
1	B	265	LYS	2.6
1	B	177	ILE	2.6
1	A	201	LEU	2.5
1	A	360	ILE	2.5
1	A	83	THR	2.5
1	A	86	ALA	2.5
1	B	81	ALA	2.5
1	B	367	GLU	2.4
1	A	362	ALA	2.4
1	A	85	ILE	2.4
1	A	489	VAL	2.4
1	B	4	ILE	2.4
1	A	195	ASP	2.4
1	A	202	ARG	2.3
1	A	296	ALA	2.3
1	A	393	GLY	2.3
1	B	487	LEU	2.3
1	B	522	GLU	2.3
1	A	122	ALA	2.3
1	A	487	LEU	2.3
1	B	120	ALA	2.2
1	A	491	PRO	2.1
1	A	124	PRO	2.1
1	A	342	ARG	2.1
1	B	176	ILE	2.1
1	A	418	LEU	2.1
1	A	125	ILE	2.1
1	A	272	LEU	2.1
1	B	122	ALA	2.0
1	A	79	THR	2.0
1	B	179	ASP	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 carbohydrates 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(\AA^2)	Q<0.9
2	CA	A	571	1/1	0.97	0.07	56,56,56,56	0
3	D7K	A	572	39/39	0.98	0.13	31,43,53,54	1
3	D7K	B	572	39/39	0.98	0.10	23,36,40,41	1
2	CA	B	571	1/1	0.99	0.05	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.