



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:55 PM UTC

PDB ID : 3R7F / pdb_00003r7f
Title : Crystal Structure of CP-bound Aspartate Transcarbamoylase from *Bacillus subtilis*
Authors : Cockrell, G.M.; Harris, K.M.; Puleo, D.E.; Kantrowitz, E.R.
Deposited on : 2011-03-22
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

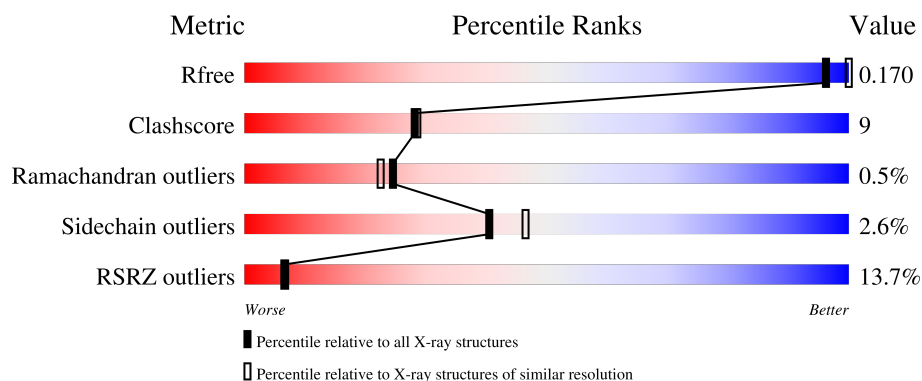
1 Overall quality at a glance

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	304	15% 79% 16% .
1	B	304	12% 81% 14% ..
1	C	304	13% 78% 16% ..

2 Entry composition [i](#)

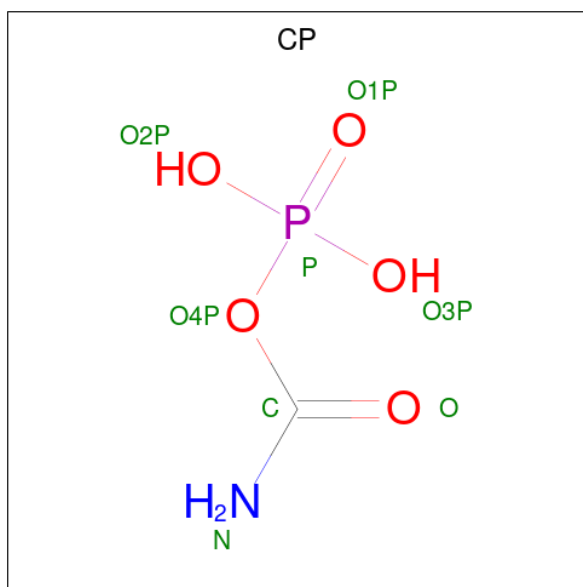
There are 4 unique types of molecules in this entry. The entry contains 7643 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Aspartate carbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	3	1	0
			2302	1433	401	455	13			
1	B	291	Total	C	N	O	S	0	3	0
			2315	1441	404	457	13			
1	C	291	Total	C	N	O	S	0	1	0
			2305	1434	402	456	13			

- Molecule 2 is PHOSPHORIC ACID MONO(FORMAMIDE)ESTER (CCD ID: CP) (formula: $\text{CH}_4\text{NO}_5\text{P}$).



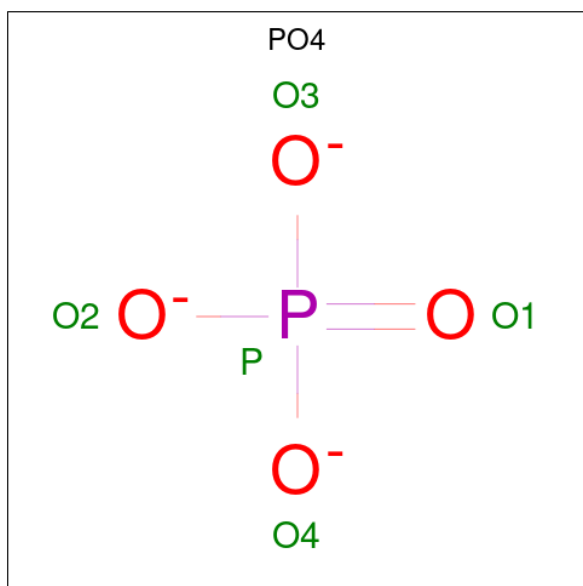
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			8	1	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			8	1	1	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			8	1	1	5	1		

- 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	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		

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

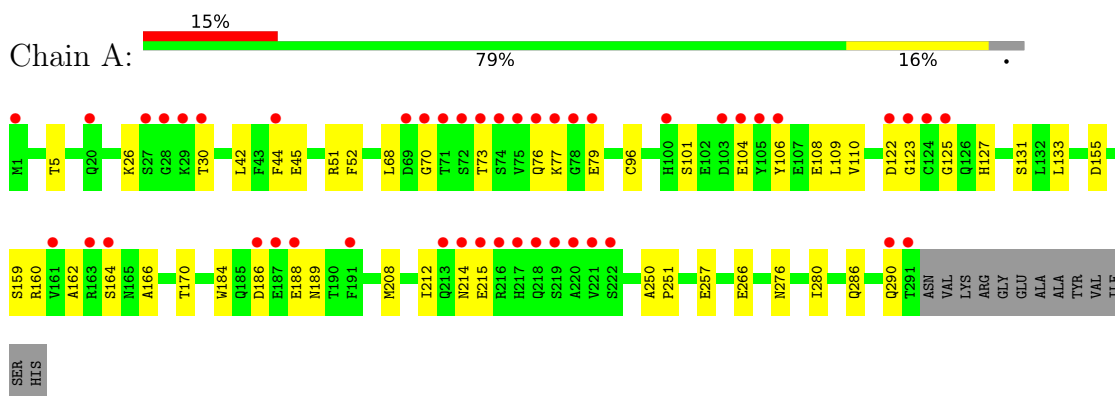
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	220	Total	O	0	0
			220	220		
4	B	232	Total	O	0	0
			232	232		
4	C	172	Total	O	0	0
			172	172		

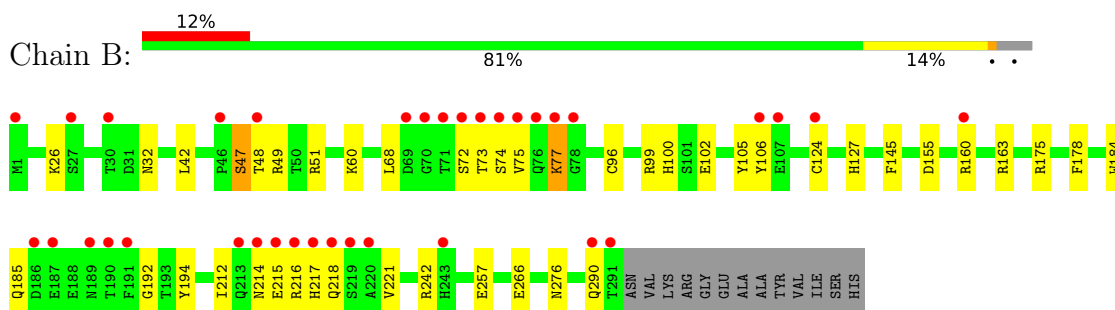
3 Residue-property plots

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.

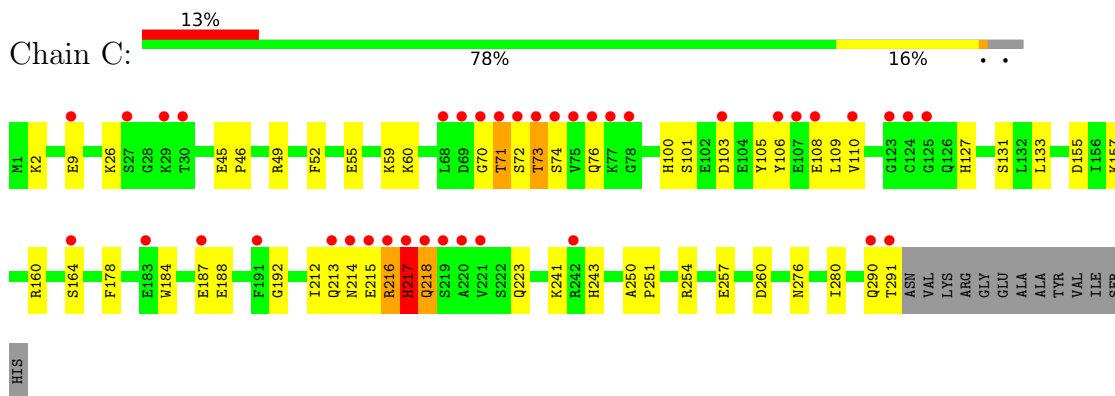
• Molecule 1: Aspartate carbamoyltransferase



• Molecule 1: Aspartate carbamoyltransferase



• Molecule 1: Aspartate carbamoyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	251.92Å 152.96Å 51.24Å 90.00° 96.10° 90.00°	Depositor
Resolution (Å)	34.12 – 2.10 34.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (34.12-2.10) 99.5 (34.12-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.7_650	Depositor
R, R_{free}	0.171 , 0.195 0.168 , 0.170	Depositor DCC
R_{free} test set	5586 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7643	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: CP, PO4

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	0.49	0/2338	0.76	0/3152
1	B	0.50	0/2355	0.75	1/3175 (0.0%)
1	C	0.43	0/2338	0.76	3/3152 (0.1%)
All	All	0.47	0/7031	0.76	4/9479 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	218	GLN	N-CA-C	-5.76	105.59	113.30
1	C	71	THR	N-CA-C	-5.66	106.70	113.21
1	B	214	ASN	N-CA-C	-5.27	105.65	111.71
1	C	217	HIS	N-CA-C	5.20	117.85	107.62

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	2302	0	2290	54	0
1	B	2315	0	2301	29	0
1	C	2305	0	2289	47	0
2	A	8	0	2	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	16	0	4	1	0
2	C	8	0	2	1	0
3	A	30	0	0	0	0
3	B	15	0	0	0	0
3	C	20	0	0	0	0
4	A	220	0	0	4	0
4	B	232	0	0	5	0
4	C	172	0	0	1	0
All	All	7643	0	6888	124	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 9.

All (124) 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:131:SER:OG	1:A:164:SER:HB3	1.67	0.94
1:C:131:SER:OG	1:C:164:SER:HB3	1.69	0.92
1:A:286:GLN:O	1:A:290:GLN:HG2	1.75	0.85
1:A:290:GLN:HG3	4:A:526:HOH:O	1.77	0.84
1:A:44:PHE:CD1	1:A:70:GLY:HA3	2.16	0.81
1:C:213:GLN:HB3	1:C:215:GLU:O	1.83	0.78
1:C:127:HIS:HB2	1:C:160:ARG:HD3	1.68	0.75
1:B:60:LYS:HE3	4:B:602:HOH:O	1.87	0.75
1:B:127:HIS:HD2	4:B:433:HOH:O	1.72	0.72
1:A:106:TYR:HE1	1:A:122:ASP:CG	1.97	0.71
1:A:186:ASP:HB2	1:A:188:GLU:OE2	1.91	0.71
1:B:124:CYS:O	1:B:160:ARG:HD2	1.93	0.68
1:B:42:LEU:HG	1:B:96[B]:CYS:SG	2.34	0.68
1:C:213:GLN:HG3	1:C:215:GLU:OE2	1.95	0.67
1:B:26:LYS:NZ	1:B:276:ASN:HD21	1.93	0.66
1:A:127:HIS:HD2	4:A:311:HOH:O	1.79	0.66
1:C:26:LYS:NZ	1:C:276:ASN:HD21	1.95	0.65
1:C:217:HIS:H	1:C:217:HIS:CD2	2.13	0.64
1:B:60:LYS:CE	4:B:602:HOH:O	2.45	0.64
1:A:79:GLU:OE2	4:A:525:HOH:O	2.15	0.63
1:A:73:THR:HB	1:C:46:PRO:HB3	1.80	0.63
1:C:216:ARG:HD2	1:C:217:HIS:CG	2.34	0.62
1:A:5:THR:HG23	1:A:106:TYR:CG	2.35	0.62
1:C:127:HIS:HE1	2:C:802:CP:O	1.83	0.62
1:A:26:LYS:NZ	1:A:276:ASN:HD21	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:GLN:O	1:C:76:GLN:HG3	2.00	0.61
1:A:52:PHE:CZ	1:B:68:LEU:HG	2.36	0.61
1:B:100:HIS:CD2	1:B:102:GLU:H	2.19	0.60
1:A:108:GLU:HG2	1:A:109:LEU:N	2.15	0.59
1:B:178:PHE:CE2	1:B:192:GLY:HA3	2.38	0.59
1:A:123:GLY:CA	1:A:160:ARG:HD3	2.33	0.59
1:C:45:GLU:OE1	1:C:101:SER:HB3	2.03	0.58
1:C:49:ARG:HD3	1:C:250:ALA:HB3	1.84	0.58
1:A:186:ASP:HB2	1:A:188:GLU:CD	2.29	0.57
1:A:104:GLU:HA	1:A:106:TYR:CZ	2.40	0.57
1:A:123:GLY:H	1:A:160:ARG:HH21	1.51	0.57
1:C:55:GLU:OE2	1:C:59:LYS:NZ	2.37	0.57
1:A:106:TYR:CE1	1:A:122:ASP:CG	2.83	0.57
1:A:131:SER:OG	1:A:164:SER:CB	2.49	0.57
1:A:108:GLU:HG2	1:A:109:LEU:H	1.71	0.56
1:C:214:ASN:HB3	1:C:223:GLN:OE1	2.06	0.56
1:A:166:ALA:O	1:A:170:THR:HG23	2.06	0.55
1:A:123:GLY:HA3	1:A:160:ARG:HD3	1.88	0.55
1:A:51:ARG:HG2	4:A:471:HOH:O	2.07	0.55
1:B:216:ARG:N	1:B:216:ARG:HD2	2.22	0.55
1:A:123:GLY:HA3	1:A:160:ARG:HH21	1.73	0.54
1:C:127:HIS:HD2	4:C:309:HOH:O	1.90	0.54
1:A:133:LEU:C	1:A:133:LEU:HD12	2.31	0.54
1:A:127:HIS:HE1	2:A:802:CP:O	1.90	0.54
1:C:70:GLY:C	1:C:72:SER:H	2.16	0.54
1:A:44:PHE:CE1	1:A:70:GLY:HA3	2.43	0.53
1:C:26:LYS:HZ2	1:C:276:ASN:HD21	1.57	0.52
1:B:47:SER:HB2	1:B:99:ARG:NH1	2.24	0.52
1:A:42:LEU:HG	1:A:96[B]:CYS:SG	2.50	0.51
1:B:145:PHE:H	2:B:308:CP:HN2	1.59	0.51
1:B:160:ARG:NH2	1:B:163:ARG:HH12	2.09	0.51
1:A:5:THR:HG21	1:A:106:TYR:CD2	2.46	0.51
1:C:212:ILE:HG12	1:C:257:GLU:HB3	1.93	0.51
1:A:5:THR:CG2	1:A:106:TYR:CD2	2.94	0.50
1:A:123:GLY:HA2	1:A:125:GLY:N	2.26	0.50
1:A:186:ASP:C	1:A:188:GLU:H	2.19	0.50
1:B:100:HIS:CD2	1:B:102:GLU:HB3	2.47	0.50
1:A:186:ASP:OD2	1:A:189:ASN:HB2	2.12	0.50
1:B:217:HIS:CE1	1:B:221:VAL:O	2.65	0.49
1:A:26:LYS:HZ2	1:A:276:ASN:HD21	1.58	0.49
1:A:123:GLY:N	1:A:160:ARG:HH21	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:LYS:HZ2	1:B:276:ASN:HD21	1.60	0.49
1:C:106:TYR:O	1:C:110:VAL:HG13	2.13	0.48
1:C:218:GLN:HG2	1:C:223:GLN:H	1.78	0.48
1:A:76:GLN:CG	1:A:79:GLU:HB2	2.43	0.48
1:C:71:THR:HG22	1:C:76:GLN:OE1	2.13	0.48
1:C:217:HIS:CD2	1:C:217:HIS:N	2.79	0.47
1:A:123:GLY:CA	1:A:160:ARG:HH21	2.26	0.47
1:B:74:SER:O	1:B:77:LYS:HB2	2.15	0.47
1:B:212:ILE:HG12	1:B:257:GLU:HB3	1.97	0.47
1:B:100:HIS:HD2	1:B:102:GLU:H	1.60	0.47
1:C:72:SER:O	1:C:74:SER:N	2.41	0.47
1:C:155:ASP:HA	1:C:184:TRP:HB3	1.97	0.47
1:C:241:LYS:HE2	1:C:243:HIS:CE1	2.50	0.47
1:A:77:LYS:C	1:A:79:GLU:H	2.23	0.46
1:B:155:ASP:HA	1:B:184:TRP:HB3	1.98	0.46
1:A:159:SER:HB3	1:A:162:ALA:HB3	1.98	0.46
1:A:104:GLU:HA	1:A:106:TYR:CE2	2.50	0.46
1:B:175:ARG:HD2	4:B:612:HOH:O	2.16	0.46
1:B:73:THR:C	1:B:75:VAL:H	2.23	0.46
1:C:72:SER:C	1:C:74:SER:H	2.23	0.46
1:B:100:HIS:HD2	1:B:102:GLU:HB3	1.80	0.46
1:C:217:HIS:H	1:C:217:HIS:HD2	1.61	0.46
1:A:212:ILE:HG12	1:A:257:GLU:HB3	1.97	0.45
1:C:133:LEU:C	1:C:133:LEU:HD12	2.41	0.45
1:C:108:GLU:HG3	1:C:109:LEU:H	1.81	0.45
1:A:79:GLU:HG3	1:C:251:PRO:HB2	1.99	0.45
1:A:76:GLN:HG2	1:A:79:GLU:HB2	1.98	0.45
1:C:133:LEU:HA	1:C:280:ILE:HG13	1.99	0.44
1:A:73:THR:HB	1:C:46:PRO:CB	2.48	0.44
1:C:250:ALA:HB1	1:C:251:PRO:HA	1.99	0.44
1:A:5:THR:CG2	1:A:106:TYR:CG	3.00	0.44
1:C:2:LYS:HD3	1:C:2:LYS:HA	1.86	0.43
1:A:186:ASP:OD2	1:A:186:ASP:O	2.35	0.43
1:C:108:GLU:HG3	1:C:109:LEU:N	2.32	0.43
1:C:2:LYS:HG3	1:C:290:GLN:HE21	1.82	0.43
1:B:26:LYS:HZ1	1:B:276:ASN:HD21	1.67	0.43
1:A:250:ALA:HB1	1:A:251:PRO:HA	1.99	0.42
1:A:123:GLY:HA2	1:A:125:GLY:H	1.82	0.42
1:B:185:GLN:HG3	1:B:194:TYR:CE1	2.54	0.42
1:A:68:LEU:HG	1:C:52:PHE:CZ	2.55	0.42
1:A:155:ASP:HA	1:A:184:TRP:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:HIS:HB3	1:C:105:TYR:CD1	2.55	0.42
1:C:178:PHE:CE2	1:C:192:GLY:HA3	2.54	0.42
1:A:133:LEU:HA	1:A:280:ILE:HG13	2.01	0.42
1:A:45:GLU:OE2	1:A:101:SER:HB3	2.18	0.42
1:B:127:HIS:CD2	4:B:433:HOH:O	2.58	0.42
1:B:42:LEU:HD22	1:B:68:LEU:HD22	2.02	0.41
1:A:52:PHE:CE2	1:B:68:LEU:HG	2.55	0.41
1:A:208:MET:HE2	1:A:208:MET:HB2	1.92	0.41
1:C:187:GLU:HG3	1:C:188:GLU:N	2.34	0.41
1:C:290:GLN:O	1:C:291:THR:HB	2.20	0.41
1:C:105:TYR:CD2	1:C:105:TYR:C	2.98	0.41
1:C:254:ARG:HD3	1:C:260:ASP:OD1	2.19	0.41
1:C:73:THR:HA	1:C:76:GLN:HB2	2.04	0.40
1:C:250:ALA:HA	1:C:251:PRO:C	2.46	0.40
1:B:105:TYR:CD2	1:B:106:TYR:N	2.90	0.40
1:C:26:LYS:HZ1	1:C:276:ASN:HD21	1.68	0.40
1:C:73:THR:HA	1:C:76:GLN:CB	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	290/304 (95%)	274 (94%)	16 (6%)	0	100	100
1	B	292/304 (96%)	276 (94%)	14 (5%)	2 (1%)	18	15
1	C	290/304 (95%)	277 (96%)	11 (4%)	2 (1%)	18	15
All	All	872/912 (96%)	827 (95%)	41 (5%)	4 (0%)	24	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	215	GLU
1	C	73	THR
1	C	216	ARG
1	B	218	GLN

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	259/268 (97%)	254 (98%)	5 (2%)	50	58
1	B	261/268 (97%)	251 (96%)	10 (4%)	29	32
1	C	259/268 (97%)	254 (98%)	5 (2%)	50	58
All	All	779/804 (97%)	759 (97%)	20 (3%)	40	46

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	THR
1	A	110	VAL
1	A	214	ASN
1	A	215	GLU
1	A	266	GLU
1	B	32	ASN
1	B	47	SER
1	B	48	THR
1	B	49	ARG
1	B	51	ARG
1	B	72	SER
1	B	77	LYS
1	B	242	ARG
1	B	266	GLU
1	B	290	GLN
1	C	9	GLU
1	C	60	LYS
1	C	103	ASP
1	C	157	LYS

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Mol	Chain	Res	Type
1	C	217	HIS

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

Mol	Chain	Res	Type
1	A	23	GLN
1	A	64	ASN
1	A	127	HIS
1	A	213	GLN
1	A	217	HIS
1	A	218	GLN
1	A	276	ASN
1	B	64	ASN
1	B	127	HIS
1	B	217	HIS
1	B	223	GLN
1	B	276	ASN
1	C	23	GLN
1	C	126	GLN
1	C	127	HIS
1	C	217	HIS
1	C	276	ASN
1	C	290	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](#)

17 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	A	305	-	4,4,4	0.97	0	6,6,6	0.52	0
2	CP	C	802	-	6,7,7	0.79	0	7,10,10	1.52	2 (28%)
3	PO4	B	305	-	4,4,4	0.89	0	6,6,6	0.67	0
2	CP	A	802	-	6,7,7	0.76	0	7,10,10	1.68	3 (42%)
3	PO4	A	308	-	4,4,4	1.03	0	6,6,6	0.54	0
3	PO4	A	310	-	4,4,4	0.77	0	6,6,6	0.56	0
3	PO4	C	305	-	4,4,4	0.95	0	6,6,6	0.55	0
3	PO4	C	306	-	4,4,4	0.91	0	6,6,6	0.43	0
3	PO4	C	308	-	4,4,4	0.88	0	6,6,6	0.39	0
2	CP	B	802	-	6,7,7	0.78	0	7,10,10	1.40	1 (14%)
2	CP	B	308	-	6,7,7	0.61	0	7,10,10	1.26	0
3	PO4	A	306	-	4,4,4	0.87	0	6,6,6	0.55	0
3	PO4	A	309	-	4,4,4	0.79	0	6,6,6	0.54	0
3	PO4	B	306	-	4,4,4	0.80	0	6,6,6	0.54	0
3	PO4	C	307	-	4,4,4	0.81	0	6,6,6	0.65	0
3	PO4	A	307	-	4,4,4	0.89	0	6,6,6	0.42	0
3	PO4	B	307	-	4,4,4	0.90	0	6,6,6	0.62	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
2	CP	A	802	-	-	0/3/5/5	-
2	CP	B	802	-	-	0/3/5/5	-
2	CP	B	308	-	-	0/3/5/5	-
2	CP	C	802	-	-	0/3/5/5	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	802	CP	O4P-P-O1P	-2.59	101.19	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	802	CP	O4P-P-O1P	-2.36	101.93	109.47
2	B	802	CP	O-C-N	-2.30	121.95	125.58
2	A	802	CP	O3P-P-O4P	-2.21	98.89	105.32
2	C	802	CP	O3P-P-O2P	2.18	115.98	107.80
2	A	802	CP	O3P-P-O1P	2.05	118.82	110.83

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
2	C	802	CP	1	0
2	A	802	CP	1	0
2	B	308	CP	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	291/304 (95%)	0.39	46 (15%) 5 5	25, 38, 85, 116	3 (1%)
1	B	291/304 (95%)	0.33	35 (12%) 9 9	19, 37, 84, 108	3 (1%)
1	C	291/304 (95%)	0.67	39 (13%) 7 7	18, 45, 89, 113	1 (0%)
All	All	873/912 (95%)	0.46	120 (13%) 6 7	18, 41, 86, 116	7 (0%)

All (120) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	220	ALA	9.3
1	C	75	VAL	8.5
1	C	217	HIS	8.3
1	C	73	THR	8.1
1	B	75	VAL	8.0
1	A	220	ALA	7.0
1	A	106	TYR	6.8
1	C	77	LYS	6.7
1	B	74	SER	6.5
1	C	219	SER	6.5
1	B	71	THR	6.3
1	A	124	CYS	6.2
1	C	291	THR	6.2
1	B	217	HIS	5.9
1	C	71	THR	5.9
1	C	70	GLY	5.8
1	C	74	SER	5.8
1	C	78	GLY	5.6
1	B	220	ALA	5.4
1	B	48	THR	5.4
1	A	217	HIS	5.3
1	A	219	SER	5.3
1	A	75	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	73	THR	5.0
1	C	124	CYS	5.0
1	B	191	PHE	4.8
1	B	70	GLY	4.7
1	B	218	GLN	4.7
1	A	123	GLY	4.7
1	A	71	THR	4.6
1	A	74	SER	4.6
1	A	291	THR	4.5
1	B	72	SER	4.4
1	B	291	THR	4.4
1	B	219	SER	4.3
1	C	69	ASP	4.3
1	B	73	THR	4.3
1	C	72	SER	4.2
1	A	221	VAL	4.2
1	C	123	GLY	4.1
1	B	77	LYS	4.0
1	B	214	ASN	3.9
1	C	106	TYR	3.8
1	C	76	GLN	3.8
1	A	216	ARG	3.8
1	B	78	GLY	3.8
1	B	216	ARG	3.8
1	A	30	THR	3.7
1	A	187	GLU	3.6
1	C	218	GLN	3.6
1	A	214	ASN	3.6
1	A	218	GLN	3.6
1	B	243[A]	HIS	3.6
1	A	77	LYS	3.5
1	C	214	ASN	3.5
1	A	213	GLN	3.5
1	B	213	GLN	3.4
1	A	72	SER	3.4
1	B	76	GLN	3.4
1	A	105	TYR	3.3
1	C	213	GLN	3.3
1	C	221	VAL	3.3
1	B	189	ASN	3.3
1	A	78	GLY	3.1
1	C	30	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	106	TYR	3.1
1	A	70	GLY	3.1
1	B	30	THR	3.0
1	B	69	ASP	3.0
1	A	79	GLU	2.9
1	A	215	GLU	2.9
1	B	187	GLU	2.9
1	B	215	GLU	2.8
1	B	290	GLN	2.7
1	A	188	GLU	2.7
1	A	103	ASP	2.7
1	A	290	GLN	2.7
1	B	190	THR	2.7
1	C	27	SER	2.7
1	A	161	VAL	2.6
1	C	215	GLU	2.5
1	A	27	SER	2.5
1	C	216	ARG	2.5
1	A	164	SER	2.4
1	C	290	GLN	2.4
1	C	103	ASP	2.4
1	C	68	LEU	2.4
1	A	125	GLY	2.4
1	C	108	GLU	2.4
1	B	186	ASP	2.4
1	C	164	SER	2.4
1	A	28	GLY	2.4
1	B	46	PRO	2.4
1	A	104	GLU	2.3
1	A	20	GLN	2.3
1	A	76	GLN	2.3
1	A	163	ARG	2.3
1	C	183	GLU	2.3
1	A	29	LYS	2.3
1	C	107	GLU	2.3
1	B	27	SER	2.2
1	C	191	PHE	2.2
1	A	186	ASP	2.2
1	B	124	CYS	2.2
1	A	44	PHE	2.2
1	A	69	ASP	2.2
1	B	107	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	110	VAL	2.1
1	C	125	GLY	2.1
1	A	1	MET	2.1
1	A	122	ASP	2.1
1	C	9	GLU	2.1
1	C	29	LYS	2.1
1	A	191	PHE	2.1
1	B	1	MET	2.0
1	C	187	GLU	2.0
1	B	160	ARG	2.0
1	C	242	ARG	2.0
1	A	222	SER	2.0
1	A	100	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PO4	C	308	5/5	0.74	0.15	57,67,78,84	0
3	PO4	C	307	5/5	0.80	0.12	68,75,85,94	0
3	PO4	A	307	5/5	0.84	0.11	60,67,72,78	0
3	PO4	A	310	5/5	0.84	0.13	49,68,78,78	0
3	PO4	B	306	5/5	0.87	0.11	59,67,75,81	0
2	CP	B	308	8/8	0.88	0.10	40,66,75,76	0
3	PO4	A	309	5/5	0.92	0.10	56,59,63,76	0
3	PO4	B	307	5/5	0.93	0.10	60,60,66,76	0
3	PO4	C	305	5/5	0.94	0.09	56,60,68,69	0
3	PO4	B	305	5/5	0.95	0.14	45,49,57,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PO4	A	305	5/5	0.95	0.16	57,59,62,65	0
2	CP	B	802	8/8	0.95	0.09	46,50,55,68	0
3	PO4	C	306	5/5	0.96	0.07	63,64,67,69	0
3	PO4	A	306	5/5	0.96	0.09	45,46,52,53	0
2	CP	C	802	8/8	0.96	0.08	38,42,45,54	0
3	PO4	A	308	5/5	0.97	0.11	48,49,61,66	0
2	CP	A	802	8/8	0.99	0.04	33,35,38,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.