



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 02:11 PM EDT

PDB ID : 6KZH / pdb_00006kzh
Title : 14-3-3 protein in Complex with CIC S173 phosphorylated peptide
Authors : Wen, Y.; Shao, Y.
Deposited on : 2019-09-24
Resolution : 2.65 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

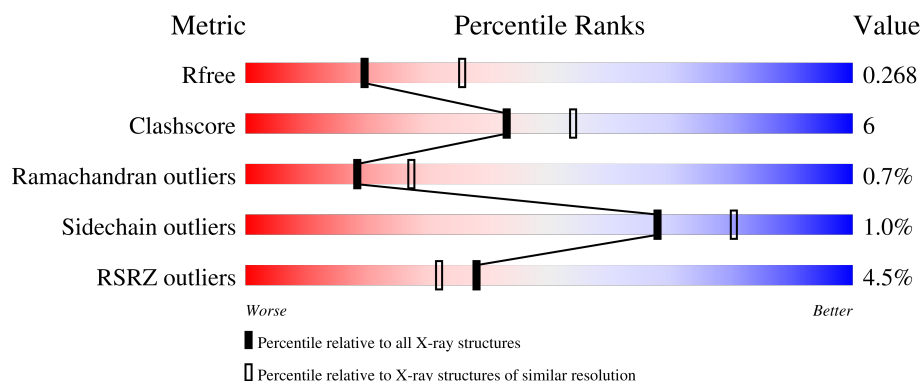
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	2053 (2.66-2.62)
Clashscore	190562	2097 (2.66-2.62)
Ramachandran outliers	187476	2066 (2.66-2.62)
Sidechain outliers	187428	2066 (2.66-2.62)
RSRZ outliers	180081	2052 (2.66-2.62)

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	263	5% 70% 16% 13%
1	B	263	2% 78% 10% 12%
2	C	8	38% 25% 38%
2	Q	8	12% 50% 12% 38%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3723 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 14-3-3 protein theta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1812	1139	305	359	9			
1	B	231	Total	C	N	O	S	0	0	0
			1831	1148	307	367	9			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	expression tag	UNP P27348
A	-27	GLY	-	expression tag	UNP P27348
A	-26	SER	-	expression tag	UNP P27348
A	-25	SER	-	expression tag	UNP P27348
A	-24	HIS	-	expression tag	UNP P27348
A	-23	HIS	-	expression tag	UNP P27348
A	-22	HIS	-	expression tag	UNP P27348
A	-21	HIS	-	expression tag	UNP P27348
A	-20	HIS	-	expression tag	UNP P27348
A	-19	HIS	-	expression tag	UNP P27348
A	-18	SER	-	expression tag	UNP P27348
A	-17	SER	-	expression tag	UNP P27348
A	-16	GLY	-	expression tag	UNP P27348
A	-15	LEU	-	expression tag	UNP P27348
A	-14	VAL	-	expression tag	UNP P27348
A	-13	PRO	-	expression tag	UNP P27348
A	-12	ARG	-	expression tag	UNP P27348
A	-11	GLY	-	expression tag	UNP P27348
A	-10	SER	-	expression tag	UNP P27348
A	-9	HIS	-	expression tag	UNP P27348
A	-8	MET	-	expression tag	UNP P27348
A	-7	ALA	-	expression tag	UNP P27348
A	-6	SER	-	expression tag	UNP P27348
A	-5	GLU	-	expression tag	UNP P27348
A	-4	ASN	-	expression tag	UNP P27348

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	LEU	-	expression tag	UNP P27348
A	-2	TYR	-	expression tag	UNP P27348
A	-1	PHE	-	expression tag	UNP P27348
A	0	GLN	-	expression tag	UNP P27348
A	1	GLY	-	expression tag	UNP P27348
B	-28	MET	-	expression tag	UNP P27348
B	-27	GLY	-	expression tag	UNP P27348
B	-26	SER	-	expression tag	UNP P27348
B	-25	SER	-	expression tag	UNP P27348
B	-24	HIS	-	expression tag	UNP P27348
B	-23	HIS	-	expression tag	UNP P27348
B	-22	HIS	-	expression tag	UNP P27348
B	-21	HIS	-	expression tag	UNP P27348
B	-20	HIS	-	expression tag	UNP P27348
B	-19	HIS	-	expression tag	UNP P27348
B	-18	SER	-	expression tag	UNP P27348
B	-17	SER	-	expression tag	UNP P27348
B	-16	GLY	-	expression tag	UNP P27348
B	-15	LEU	-	expression tag	UNP P27348
B	-14	VAL	-	expression tag	UNP P27348
B	-13	PRO	-	expression tag	UNP P27348
B	-12	ARG	-	expression tag	UNP P27348
B	-11	GLY	-	expression tag	UNP P27348
B	-10	SER	-	expression tag	UNP P27348
B	-9	HIS	-	expression tag	UNP P27348
B	-8	MET	-	expression tag	UNP P27348
B	-7	ALA	-	expression tag	UNP P27348
B	-6	SER	-	expression tag	UNP P27348
B	-5	GLU	-	expression tag	UNP P27348
B	-4	ASN	-	expression tag	UNP P27348
B	-3	LEU	-	expression tag	UNP P27348
B	-2	TYR	-	expression tag	UNP P27348
B	-1	PHE	-	expression tag	UNP P27348
B	0	GLN	-	expression tag	UNP P27348
B	1	GLY	-	expression tag	UNP P27348

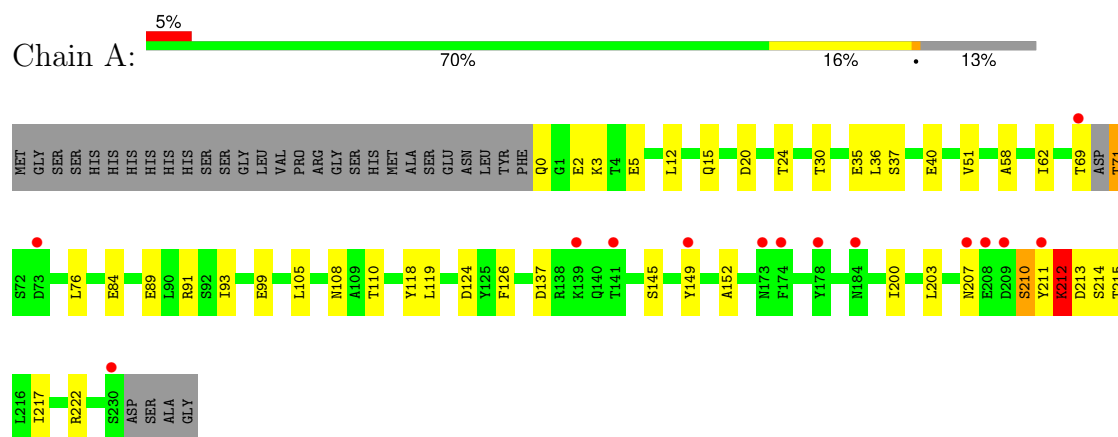
- Molecule 2 is a protein called CIC pS173 peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	5	Total 40	C 21	N 6	O 12	P 1	0	0	0
2	Q	5	Total 40	C 21	N 6	O 12	P 1	0	0	0

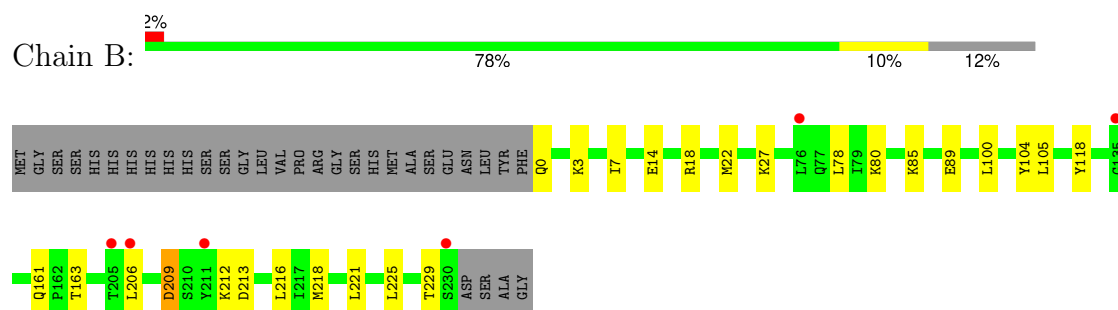
3 Residue-property plots [i](#)

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.

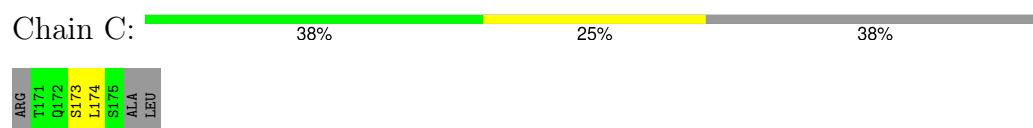
- Molecule 1: 14-3-3 protein theta



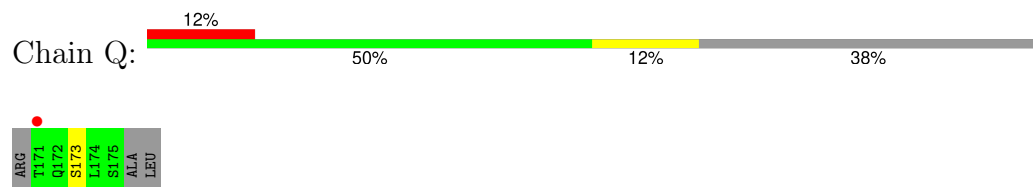
- Molecule 1: 14-3-3 protein theta



- Molecule 2: CIC pS173 peptide



- Molecule 2: CIC pS173 peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.17Å 80.81Å 107.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.63 – 2.65 44.63 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.63-2.65) 99.8 (44.63-2.65)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.215 , 0.274 0.221 , 0.268	Depositor DCC
R_{free} test set	1837 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	72.9	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3723	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0.26	1/1835 (0.1%)	0.35	0/2476
1	B	0.13	0/1855	0.30	0/2503
2	C	0.10	0/28	0.25	0/35
2	Q	0.17	0/28	0.34	0/35
All	All	0.21	1/3746 (0.0%)	0.33	0/5049

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	222	ARG	C-O	-5.10	1.18	1.24

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1812	0	1796	30	1
1	B	1831	0	1819	18	1
2	C	40	0	33	1	0
2	Q	40	0	33	0	0
All	All	3723	0	3681	46	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (46) 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:212:LYS:HG3	1:B:213:ASP:N	1.99	0.76
1:A:37:SER:HG	1:A:40:GLU:H	1.37	0.69
1:A:207:ASN:N	1:A:210:SER:OG	2.28	0.67
1:A:3:LYS:NZ	1:A:40:GLU:OE1	2.33	0.61
1:B:225:LEU:O	1:B:229:THR:HG22	2.00	0.61
1:B:0:GLN:HB3	1:B:3:LYS:HB2	1.83	0.60
1:B:209:ASP:OD1	1:B:209:ASP:N	2.28	0.58
1:A:58:ALA:O	1:A:62:ILE:HG13	2.04	0.57
1:B:212:LYS:CG	1:B:213:ASP:N	2.68	0.56
1:A:30:THR:HG22	1:A:36:LEU:HD21	1.88	0.56
1:A:212:LYS:HD2	1:A:213:ASP:N	2.21	0.55
1:A:35:GLU:HG3	1:A:108:ASN:O	2.09	0.53
1:A:200:ILE:HD12	1:A:203:LEU:HD11	1.91	0.52
1:A:217:ILE:HG12	2:C:174:LEU:HD11	1.91	0.52
1:B:27:LYS:HG3	1:B:100:LEU:HD21	1.92	0.52
1:A:0:GLN:HG3	1:A:2:GLU:H	1.76	0.51
1:A:119:LEU:HB3	1:A:152:ALA:HB2	1.94	0.50
1:A:126:PHE:HB3	1:A:145:SER:HB3	1.94	0.50
1:A:69:THR:OG1	1:A:76:LEU:HD12	2.13	0.49
1:A:200:ILE:HD12	1:A:203:LEU:CD1	2.42	0.49
1:A:212:LYS:O	1:A:215:THR:HG22	2.12	0.48
1:B:161:GLN:CD	1:B:161:GLN:H	2.24	0.46
1:A:37:SER:HG	1:A:40:GLU:N	2.09	0.46
1:A:71:THR:O	1:A:71:THR:OG1	2.27	0.46
1:A:51:VAL:HG12	1:A:93:ILE:HD13	1.98	0.45
1:B:212:LYS:HG3	1:B:213:ASP:H	1.81	0.45
1:B:163:THR:HB	1:B:206:LEU:HG	1.99	0.45
1:A:84:GLU:OE1	1:A:91:ARG:NH2	2.50	0.44
1:B:105:LEU:HD22	1:B:118:TYR:CZ	2.53	0.43
1:A:212:LYS:HD2	1:A:213:ASP:H	1.83	0.43
1:A:212:LYS:C	1:A:214:SER:N	2.76	0.43
1:B:3:LYS:O	1:B:7:ILE:HG12	2.17	0.43
1:A:15:GLN:H	1:A:15:GLN:HG2	1.58	0.43
1:A:89:GLU:OE1	1:B:18:ARG:NH2	2.52	0.43
1:A:124:ASP:OD1	1:A:149:TYR:OH	2.35	0.43
1:A:20:ASP:O	1:A:24:THR:HG22	2.19	0.42
1:A:137:ASP:OD2	1:A:137:ASP:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:MET:HA	1:B:221:LEU:HD12	2.01	0.42
1:A:105:LEU:HD22	1:A:118:TYR:CZ	2.55	0.41
1:A:126:PHE:CB	1:A:145:SER:HB3	2.49	0.41
1:B:85:LYS:O	1:B:89:GLU:HG3	2.20	0.41
1:A:12:LEU:HD12	1:A:15:GLN:HE21	1.85	0.41
1:B:80:LYS:HE2	1:B:80:LYS:HB2	1.69	0.41
1:B:212:LYS:O	1:B:216:LEU:HG	2.21	0.41
1:A:5:GLU:HG2	1:B:78:LEU:HD22	2.02	0.41
1:B:14:GLU:HB2	1:B:22:MET:SD	2.61	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:GLU:OE1	1:B:104:TYR:OH[4_545]	2.13	0.07

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	226/263 (86%)	217 (96%)	6 (3%)	3 (1%)	9	14
1	B	229/263 (87%)	221 (96%)	8 (4%)	0	100	100
2	C	2/8 (25%)	2 (100%)	0	0	100	100
2	Q	2/8 (25%)	2 (100%)	0	0	100	100
All	All	459/542 (85%)	442 (96%)	14 (3%)	3 (1%)	18	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	211	TYR

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Mol	Chain	Res	Type
1	A	212	LYS
1	A	110	THR

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	194/229 (85%)	191 (98%)	3 (2%)	57	74
1	B	199/229 (87%)	198 (100%)	1 (0%)	81	89
2	C	4/6 (67%)	4 (100%)	0	100	100
2	Q	4/6 (67%)	4 (100%)	0	100	100
All	All	401/470 (85%)	397 (99%)	4 (1%)	68	80

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	THR
1	A	210	SER
1	A	212	LYS
1	B	209	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	A	184	ASN
1	B	8	GLN
1	B	42	ASN
1	B	111	ASN
1	B	183	ASN
1	B	184	ASN
1	B	219	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SEP	C	173	2	8,9,10	1.60	1 (12%)	7,12,14	1.44	1 (14%)
2	SEP	Q	173	2	8,9,10	1.60	1 (12%)	7,12,14	1.37	1 (14%)

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	SEP	C	173	2	-	0/6/8/10	-
2	SEP	Q	173	2	-	1/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	173	SEP	P-O1P	3.49	1.61	1.50
2	Q	173	SEP	P-O1P	3.47	1.61	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	173	SEP	OG-CB-CA	3.11	111.17	108.14
2	Q	173	SEP	OG-CB-CA	2.94	111.00	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Q	173	SEP	C-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	230/263 (87%)	0.35	14 (6%) 27 22	54, 79, 136, 168	0
1	B	231/263 (87%)	0.21	6 (2%) 57 52	51, 73, 120, 168	0
2	C	4/8 (50%)	0.34	0 100 100	80, 84, 85, 120	0
2	Q	4/8 (50%)	1.02	1 (25%) 2 1	73, 76, 88, 120	0
All	All	469/542 (86%)	0.29	21 (4%) 38 32	51, 76, 131, 168	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	211	TYR	5.2
1	B	211	TYR	4.8
1	A	174	PHE	3.2
1	A	209	ASP	3.2
1	A	149	TYR	3.2
1	B	230	SER	2.9
1	B	135	GLY	2.9
1	A	230	SER	2.7
1	B	205	THR	2.5
1	A	178	TYR	2.4
1	A	207	ASN	2.4
1	A	184	ASN	2.3
2	Q	171	THR	2.3
1	A	139	LYS	2.3
1	A	173	ASN	2.3
1	A	141	THR	2.2
1	A	73	ASP	2.2
1	B	76	LEU	2.2
1	A	208	GLU	2.2
1	B	206	LEU	2.1
1	A	69	THR	2.1

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SEP	Q	173	10/11	0.94	0.10	58,66,71,74	0
2	SEP	C	173	10/11	0.97	0.07	62,68,76,79	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.