



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 2, 2024 – 05:39 PM EST

PDB ID : 3K0H  
Title : The crystal structure of BRCA1 BRCT in complex with a minimal recognition tetrapeptide with an amidated C-terminus  
Authors : Campbell, S.J.; Edwards, R.A.; Glover, J.N.  
Deposited on : 2009-09-24  
Resolution : 2.70 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

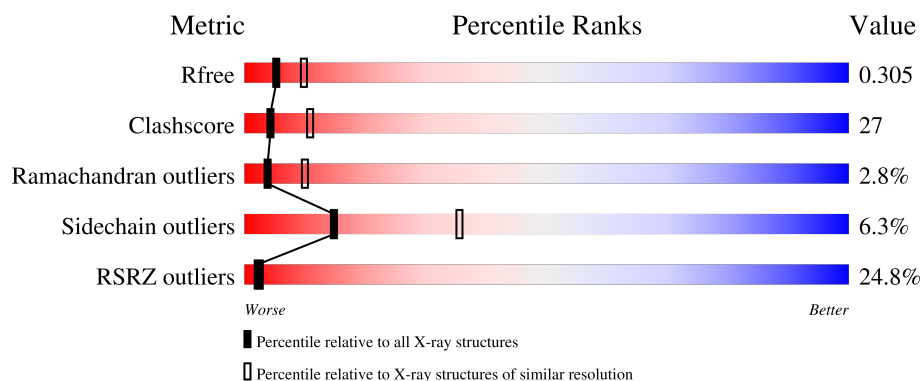
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	215	<div> <div>24%</div> <div>52%</div> <div>42%</div> <div>• •</div> </div>
2	B	5	<div> <div>40%</div> <div>60%</div> <div>20%</div> <div>20%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CL	B	6	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 1751 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 Breast cancer type 1 susceptibility protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	0	0
			1695	1082	289	310	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1645	MET	-	expression tag	UNP P38398

- Molecule 2 is a protein called phospho peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	P	0	0	1
			36	21	5	9	1			

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ni	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	13	Total	O	0	0
			13	13		

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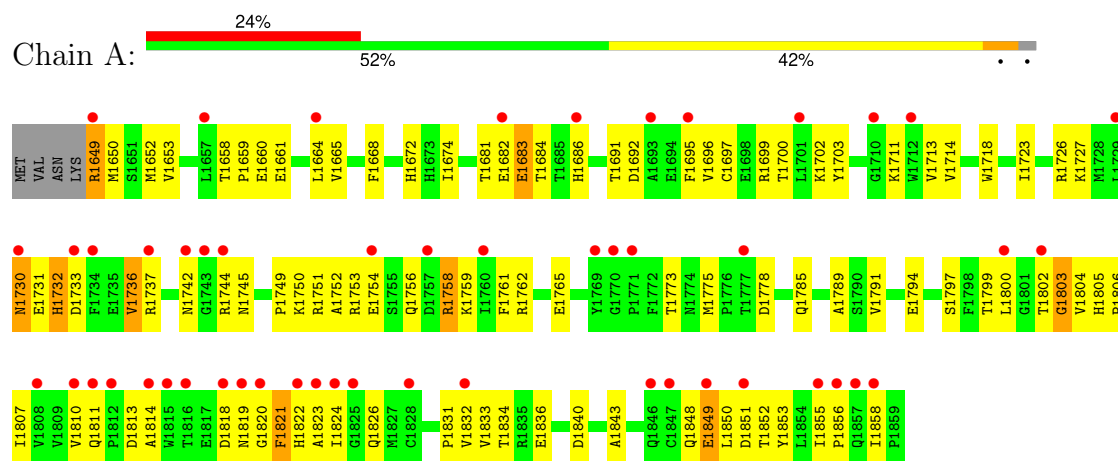
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	5	Total	O	0	0
			5	5		

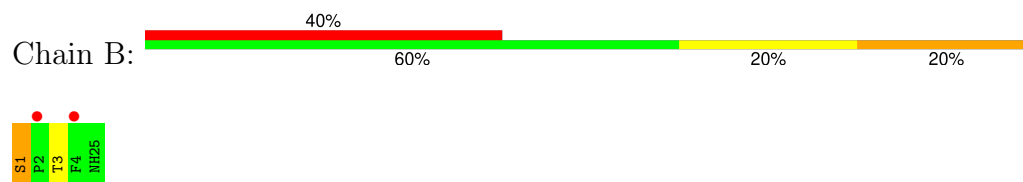
### 3 Residue-property plots [i](#)

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. 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. 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: Breast cancer type 1 susceptibility protein



- Molecule 2: phospho peptide



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.08Å 115.08Å 123.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.44 – 2.70 29.44 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.44-2.70) 99.1 (29.44-2.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.56 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, $R_{free}$	0.247 , 0.296 0.249 , 0.305	Depositor DCC
$R_{free}$ test set	682 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	76.6	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 61.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	1751	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.40% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, NI, CL, NH2

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	0.41	0/1736	0.56	0/2355
2	B	0.54	0/26	0.63	0/34
All	All	0.41	0/1762	0.56	0/2389

There are no bond length outliers.

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	1695	0	1671	88	0
2	B	36	0	28	3	0
3	A	1	0	0	0	0
4	B	1	0	0	3	0
5	A	13	0	0	0	0
5	B	5	0	0	0	0
All	All	1751	0	1699	91	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 27.

All (91) 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:1649:ARG:HG3	1:A:1650:MET:H	1.12	1.09
1:A:1726:ARG:O	1:A:1727:LYS:HG2	1.61	1.00
1:A:1855:ILE:HG23	1:A:1856:PRO:HD2	1.47	0.95
1:A:1649:ARG:HG3	1:A:1650:MET:N	1.81	0.94
1:A:1658:THR:OG1	1:A:1661:GLU:HG3	1.69	0.92
1:A:1855:ILE:CG2	1:A:1856:PRO:HD2	1.99	0.92
1:A:1759:LYS:O	1:A:1762:ARG:HG3	1.69	0.92
1:A:1649:ARG:CG	1:A:1650:MET:H	1.82	0.91
2:B:1:SEP:O	4:B:6:CL:CL	2.26	0.91
2:B:1:SEP:N	4:B:6:CL:CL	2.43	0.88
1:A:1819:ASN:HD21	1:A:1858:ILE:HD11	1.44	0.83
1:A:1804:VAL:HG12	1:A:1805:HIS:H	1.45	0.80
1:A:1848:GLN:O	1:A:1849:GLU:C	2.18	0.79
1:A:1819:ASN:ND2	1:A:1858:ILE:HD11	1.98	0.77
1:A:1684:THR:O	1:A:1711:LYS:HD2	1.86	0.75
1:A:1819:ASN:OD1	1:A:1822:HIS:HD2	1.70	0.75
1:A:1726:ARG:O	1:A:1727:LYS:CG	2.35	0.73
1:A:1758:ARG:O	1:A:1758:ARG:HG3	1.90	0.72
1:A:1713:VAL:HG12	1:A:1736:VAL:CG1	2.20	0.71
1:A:1819:ASN:OD1	1:A:1822:HIS:CD2	2.45	0.69
1:A:1804:VAL:HG12	1:A:1805:HIS:N	2.05	0.69
1:A:1744:ARG:HG2	1:A:1744:ARG:HH11	1.57	0.69
1:A:1696:VAL:HG21	1:A:1744:ARG:NH1	2.08	0.68
1:A:1700:THR:O	1:A:1703:TYR:HB3	2.00	0.62
1:A:1713:VAL:HG12	1:A:1736:VAL:HG11	1.82	0.61
1:A:1742:ASN:ND2	1:A:1843:ALA:CB	2.64	0.61
1:A:1821:PHE:C	1:A:1821:PHE:CD1	2.74	0.61
1:A:1810:VAL:O	1:A:1834:THR:HA	2.01	0.60
1:A:1653:VAL:HG21	1:A:1702:LYS:HD3	1.83	0.59
1:A:1802:THR:O	1:A:1803:GLY:C	2.42	0.58
1:A:1823:ALA:HB1	1:A:1826:GLN:NE2	2.19	0.58
1:A:1855:ILE:HG22	1:A:1856:PRO:HD2	1.82	0.58
1:A:1660:GLU:H	1:A:1660:GLU:CD	2.06	0.57
1:A:1855:ILE:CG2	1:A:1856:PRO:CD	2.78	0.56
1:A:1821:PHE:CE1	1:A:1822:HIS:CE1	2.94	0.55
1:A:1744:ARG:HG2	1:A:1744:ARG:NH1	2.22	0.55
1:A:1773:THR:C	1:A:1775:MET:H	2.10	0.55
1:A:1649:ARG:HA	1:A:1649:ARG:HE	1.71	0.54
1:A:1730:ASN:HD22	1:A:1732:HIS:HB2	1.72	0.54
1:A:1821:PHE:C	1:A:1821:PHE:HD1	2.11	0.54
1:A:1681:THR:OG1	1:A:1683:GLU:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1804:VAL:CG1	1:A:1805:HIS:H	2.17	0.54
1:A:1682:GLU:HB2	1:A:1683:GLU:OE2	2.09	0.53
1:A:1699:ARG:HH11	1:A:1742:ASN:HD21	1.56	0.53
1:A:1752:ALA:O	1:A:1756:GLN:NE2	2.35	0.53
1:A:1665:VAL:O	1:A:1668:PHE:HB3	2.09	0.53
1:A:1713:VAL:HG12	1:A:1736:VAL:HG13	1.90	0.52
1:A:1836:GLU:O	1:A:1840:ASP:HB2	2.11	0.51
1:A:1658:THR:HB	1:A:1660:GLU:OE1	2.11	0.51
1:A:1672:HIS:HB2	1:A:1674:ILE:HD12	1.93	0.50
1:A:1750:LYS:O	1:A:1751:ARG:C	2.48	0.50
1:A:1799:THR:HG22	1:A:1799:THR:O	2.10	0.50
1:A:1696:VAL:HG21	1:A:1744:ARG:CZ	2.42	0.50
1:A:1749:PRO:O	1:A:1753:ARG:HG3	2.12	0.49
1:A:1761:PHE:HB3	1:A:1789:ALA:HB2	1.93	0.49
1:A:1773:THR:HG23	1:A:1814:ALA:HB2	1.94	0.49
1:A:1692:ASP:OD1	1:A:1692:ASP:C	2.51	0.49
1:A:1765:GLU:OE2	1:A:1799:THR:HB	2.13	0.48
1:A:1806:PRO:C	1:A:1807:ILE:HG13	2.34	0.48
1:A:1855:ILE:HG23	1:A:1856:PRO:CD	2.32	0.48
1:A:1824:ILE:C	1:A:1826:GLN:H	2.18	0.47
1:A:1737:ARG:HD3	1:A:1745:ASN:OD1	2.15	0.47
1:A:1691:THR:CB	1:A:1695:PHE:HA	2.45	0.46
1:A:1649:ARG:CG	1:A:1650:MET:N	2.53	0.46
1:A:1819:ASN:ND2	1:A:1858:ILE:CD1	2.75	0.46
1:A:1773:THR:O	1:A:1775:MET:N	2.50	0.45
1:A:1727:LYS:HD3	1:A:1727:LYS:HA	1.80	0.45
1:A:1811:GLN:HE21	1:A:1813:ASP:HB2	1.81	0.45
1:A:1848:GLN:O	1:A:1849:GLU:O	2.35	0.45
1:A:1691:THR:HB	1:A:1695:PHE:HA	1.99	0.44
1:A:1773:THR:C	1:A:1775:MET:N	2.70	0.44
1:A:1691:THR:HG22	1:A:1697:CYS:HB3	1.99	0.44
1:A:1848:GLN:HB3	1:A:1853:TYR:HE1	1.82	0.43
2:B:1:SEP:C	4:B:6:CL:CL	3.02	0.43
1:A:1658:THR:HB	1:A:1659:PRO:HD2	2.01	0.43
1:A:1731:GLU:O	1:A:1732:HIS:C	2.57	0.42
1:A:1832:VAL:O	1:A:1833:VAL:HG13	2.18	0.42
1:A:1684:THR:O	1:A:1711:LYS:CD	2.62	0.42
1:A:1731:GLU:OE1	1:A:1731:GLU:N	2.35	0.42
1:A:1752:ALA:O	1:A:1754:GLU:N	2.53	0.42
1:A:1731:GLU:O	1:A:1733:ASP:N	2.53	0.42
1:A:1742:ASN:HD22	1:A:1843:ALA:CB	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1650:MET:HE3	1:A:1718:TRP:HH2	1.85	0.41
1:A:1850:LEU:O	1:A:1851:ASP:C	2.59	0.41
1:A:1806:PRO:O	1:A:1831:PRO:HD2	2.21	0.41
1:A:1824:ILE:C	1:A:1826:GLN:N	2.75	0.41
1:A:1785:GLN:CG	1:A:1791:VAL:HG23	2.51	0.41
1:A:1664:LEU:HD22	1:A:1723:ILE:HD13	2.03	0.40
1:A:1650:MET:HB3	1:A:1650:MET:HE2	1.82	0.40
1:A:1652:MET:HG2	1:A:1686:HIS:HB2	2.03	0.40
1:A:1664:LEU:HD23	1:A:1664:LEU:HA	1.91	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	209/215 (97%)	183 (88%)	20 (10%)	6 (3%)	3	9
2	B	3/5 (60%)	3 (100%)	0	0	100	100
All	All	212/220 (96%)	186 (88%)	20 (9%)	6 (3%)	4	10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1818	ASP
1	A	1849	GLU
1	A	1732	HIS
1	A	1800	LEU
1	A	1803	GLY
1	A	1820	GLY

### 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	188/192 (98%)	177 (94%)	11 (6%)	16	38
2	B	3/3 (100%)	2 (67%)	1 (33%)	0	0
All	All	191/195 (98%)	179 (94%)	12 (6%)	15	35

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1649	ARG
1	A	1683	GLU
1	A	1714	VAL
1	A	1730	ASN
1	A	1736	VAL
1	A	1758	ARG
1	A	1778	ASP
1	A	1794	GLU
1	A	1797	SER
1	A	1821	PHE
1	A	1852	THR
2	B	3	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1678	ASN
1	A	1730	ASN
1	A	1742	ASN
1	A	1774	ASN
1	A	1822	HIS
1	A	1826	GLN
1	A	1846	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	B	1	2	8,9,10	1.49	1 (12%)	7,12,14	1.45	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	SEP	B	1	2	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	SEP	P-O1P	3.27	1.60	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	SEP	3	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 ⓘ

**Warning:** The R factor obtained from EDS is 0.313, which does not match the depositor's R factor of 0.247. Please interpret the results in this section carefully.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	211/215 (98%)	1.39	51 (24%) 2 3	33, 49, 59, 68	1 (0%)
2	B	3/5 (60%)	2.18	2 (66%) 0 0	41, 41, 41, 42	3 (100%)
All	All	214/220 (97%)	1.40	53 (24%) 2 2	33, 49, 59, 68	4 (1%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1743	GLY	7.0
1	A	1730	ASN	4.7
1	A	1815	TRP	4.5
1	A	1820	GLY	4.4
1	A	1825	GLY	4.1
1	A	1811	GLN	4.0
1	A	1849	GLU	3.9
1	A	1800	LEU	3.6
1	A	1812	PRO	3.5
1	A	1742	ASN	3.4
1	A	1770	GLY	3.4
1	A	1686	HIS	3.4
1	A	1819	ASN	3.4
1	A	1733	ASP	3.3
1	A	1754	GLU	3.3
1	A	1760	ILE	3.3
1	A	1824	ILE	3.3
1	A	1818	ASP	3.1
1	A	1769	TYR	2.9
1	A	1682	GLU	2.8
1	A	1856	PRO	2.8
1	A	1858	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	1777	THR	2.8
1	A	1737	ARG	2.7
1	A	1823	ALA	2.7
1	A	1729	LEU	2.6
1	A	1855	ILE	2.6
2	B	2	PRO	2.6
1	A	1734	PHE	2.6
1	A	1802	THR	2.6
1	A	1808	VAL	2.5
1	A	1822	HIS	2.5
2	B	4	PHE	2.4
1	A	1814	ALA	2.4
1	A	1710	GLY	2.4
1	A	1701	LEU	2.3
1	A	1846	GLN	2.3
1	A	1851	ASP	2.3
1	A	1744	ARG	2.3
1	A	1847	CYS	2.3
1	A	1664	LEU	2.3
1	A	1712	TRP	2.3
1	A	1649	ARG	2.2
1	A	1810	VAL	2.1
1	A	1857	GLN	2.1
1	A	1816	THR	2.1
1	A	1757	ASP	2.1
1	A	1693	ALA	2.1
1	A	1695	PHE	2.1
1	A	1657	LEU	2.1
1	A	1771	PRO	2.0
1	A	1832	VAL	2.0
1	A	1828	CYS	2.0

## 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, 95<sup>th</sup> 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	B	1	10/11	0.88	0.21	50,54,58,58	10



### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 95<sup>th</sup> 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
3	NI	A	1	1/1	0.63	0.41	82,82,82,82	1
4	CL	B	6	1/1	0.85	0.33	55,55,55,55	1

### 6.5 Other polymers [i](#)

There are no such residues in this entry.