



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:42 PM UTC

PDB ID : 4P1T / pdb_00004p1t
Title : Crystal structure of the DBL3X-DBL4epsilon double domain from the extra-cellular part of VAR2CSA PfEMP1 from Plasmodium falciparum
Authors : Gangnard, S.; Dechavanne, S.; Srivastava, A.; Amirat, F.; Gamain, B.; Lewit-Bentley, A.; Bentley, G.A.
Deposited on : 2014-02-27
Resolution : 2.90 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
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

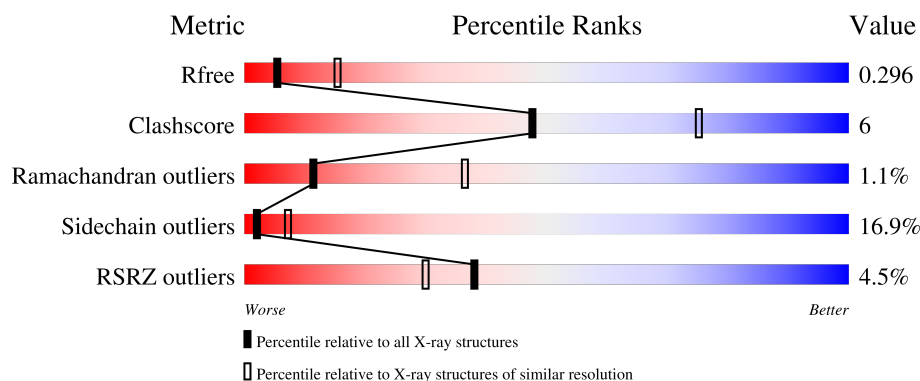
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	746	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5090 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 Erythrocyte membrane protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	649	Total	C	N	O	S	0	1	0
			5076	3203	852	984	37			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1211	MET	-	expression tag	UNP Q6UDW7
A	1212	ALA	-	expression tag	UNP Q6UDW7
A	1213	SER	-	expression tag	UNP Q6UDW7
A	1214	MET	-	expression tag	UNP Q6UDW7
A	1222	GLN	ASN	engineered mutation	UNP Q6UDW7
A	1290	GLN	ASN	engineered mutation	UNP Q6UDW7
A	1430	GLY	SER	engineered mutation	UNP Q6UDW7
A	1594	LEU	SER	engineered mutation	UNP Q6UDW7
A	1746	ALA	THR	engineered mutation	UNP Q6UDW7
A	1751	PRO	THR	engineered mutation	UNP Q6UDW7
A	1846	ALA	THR	engineered mutation	UNP Q6UDW7
A	1916	GLN	ASN	engineered mutation	UNP Q6UDW7
A	1951	HIS	-	expression tag	UNP Q6UDW7
A	1952	HIS	-	expression tag	UNP Q6UDW7
A	1953	HIS	-	expression tag	UNP Q6UDW7
A	1954	HIS	-	expression tag	UNP Q6UDW7
A	1955	HIS	-	expression tag	UNP Q6UDW7
A	1956	HIS	-	expression tag	UNP Q6UDW7

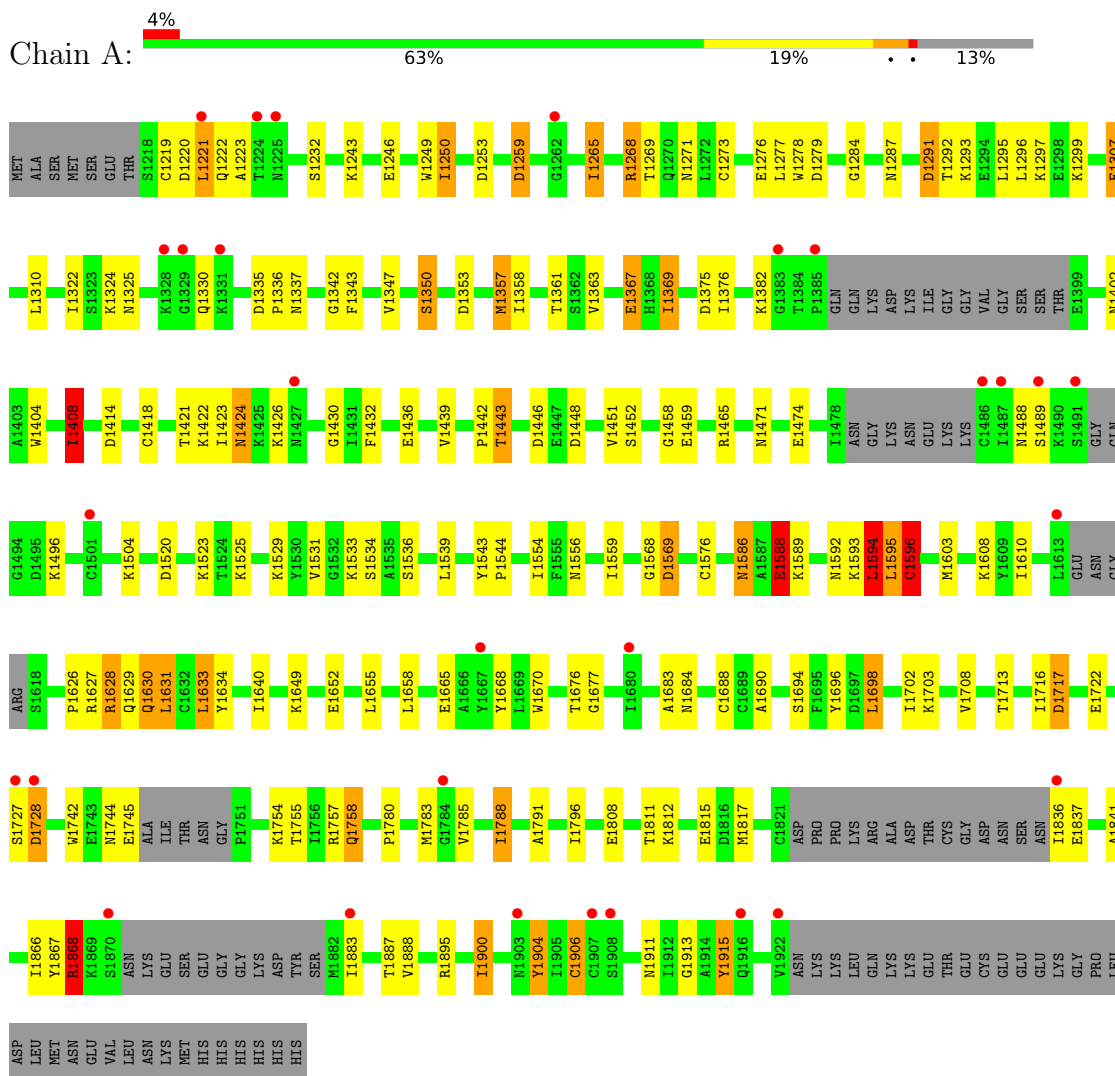
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	14	Total	O	0	0
			14	14		

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: Erythrocyte membrane protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	99.79Å 129.34Å 64.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.16 – 2.90 28.16 – 2.90	Depositor EDS
% Data completeness (in resolution range)	92.2 (28.16-2.90) 92.1 (28.16-2.90)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.90Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.203 , 0.276 0.220 , 0.296	Depositor DCC
R_{free} test set	903 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.631	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 81.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5090	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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 ⓘ

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	0.90	1/5190 (0.0%)	1.53	49/7014 (0.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1250	ILE	CG1-CD1	5.06	1.71	1.51

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1596	CYS	N-CA-C	-9.07	97.84	110.35
1	A	1569	ASP	CA-CB-CG	8.07	120.67	112.60
1	A	1630	GLN	CA-C-N	7.77	132.53	121.42
1	A	1630	GLN	C-N-CA	7.77	132.53	121.42
1	A	1593	LYS	N-CA-C	-6.79	103.97	113.20
1	A	1915	TYR	CA-C-N	6.50	129.28	120.38
1	A	1915	TYR	C-N-CA	6.50	129.28	120.38
1	A	1442	PRO	CA-C-N	6.39	133.75	121.54
1	A	1442	PRO	C-N-CA	6.39	133.75	121.54
1	A	1271	ASN	CA-CB-CG	6.20	118.80	112.60
1	A	1568	GLY	CA-C-N	5.99	130.71	121.19
1	A	1568	GLY	C-N-CA	5.99	130.71	121.19
1	A	1594	LEU	CA-C-N	5.85	132.72	121.54
1	A	1594	LEU	C-N-CA	5.85	132.72	121.54
1	A	1408	ILE	CA-C-N	5.80	128.33	120.38
1	A	1408	ILE	C-N-CA	5.80	128.33	120.38
1	A	1665	GLU	CA-C-N	5.75	127.98	120.28
1	A	1665	GLU	C-N-CA	5.75	127.98	120.28
1	A	1867	TYR	CA-C-N	5.71	132.45	121.54
1	A	1867	TYR	C-N-CA	5.71	132.45	121.54
1	A	1259	ASP	CA-CB-CG	5.64	118.24	112.60
1	A	1287	ASN	N-CA-C	-5.59	106.30	113.23
1	A	1430	GLY	CA-C-N	5.55	128.01	120.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1430	GLY	C-N-CA	5.55	128.01	120.63
1	A	1424	ASN	CA-CB-CG	5.54	118.14	112.60
1	A	1728	ASP	CA-CB-CG	5.50	118.11	112.60
1	A	1376	ILE	CA-C-N	5.49	127.95	120.54
1	A	1376	ILE	C-N-CA	5.49	127.95	120.54
1	A	1727	SER	CA-C-N	5.43	127.82	120.38
1	A	1727	SER	C-N-CA	5.43	127.82	120.38
1	A	1690	ALA	N-CA-C	-5.39	105.48	111.36
1	A	1717	ASP	CA-C-N	5.39	127.44	120.44
1	A	1717	ASP	C-N-CA	5.39	127.44	120.44
1	A	1588	GLU	CA-C-N	5.38	131.82	121.54
1	A	1588	GLU	C-N-CA	5.38	131.82	121.54
1	A	1249	TRP	CA-C-N	-5.38	115.95	123.10
1	A	1249	TRP	C-N-CA	-5.38	115.95	123.10
1	A	1586	ASN	N-CA-C	-5.34	101.94	109.96
1	A	1367	GLU	CB-CG-CD	5.27	121.56	112.60
1	A	1520	ASP	CA-CB-CG	5.25	117.86	112.60
1	A	1459	GLU	CB-CG-CD	5.25	121.52	112.60
1	A	1452	SER	CA-C-N	5.20	127.67	120.29
1	A	1452	SER	C-N-CA	5.20	127.67	120.29
1	A	1330	GLN	CA-C-N	5.16	128.66	121.02
1	A	1330	GLN	C-N-CA	5.16	128.66	121.02
1	A	1307	GLU	CB-CG-CD	5.12	121.31	112.60
1	A	1817	MET	N-CA-C	-5.08	105.92	112.68
1	A	1841	ALA	CA-C-N	5.07	127.07	120.28
1	A	1841	ALA	C-N-CA	5.07	127.07	120.28

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	5076	0	4650	54	0
2	A	14	0	0	0	0
All	All	5090	0	4650	54	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 6.

All (54) 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:1335:ASP:HB2	1:A:1336:PRO:HD2	1.64	0.80
1:A:1424:ASN:HB2	1:A:1432:PHE:HB2	1.72	0.71
1:A:1278:TRP:HH2	1:A:1367:GLU:HG2	1.59	0.68
1:A:1592:ASN:C	1:A:1594:LEU:H	2.03	0.66
1:A:1232:SER:HA	1:A:1310:LEU:HD22	1.78	0.65
1:A:1357:MET:HE1	1:A:1369:ILE:HG12	1.78	0.65
1:A:1322:ILE:HG22	1:A:1342:GLY:HA3	1.84	0.59
1:A:1279:ASP:O	1:A:1284:GLY:HA2	2.07	0.55
1:A:1658:LEU:HD21	1:A:1702:ILE:HD11	1.89	0.55
1:A:1900:ILE:HG12	1:A:1906:CYS:HA	1.87	0.54
1:A:1677:GLY:HA3	1:A:1683:ALA:HA	1.90	0.54
1:A:1361:THR:HG22	1:A:1363:VAL:H	1.73	0.53
1:A:1423:ILE:HA	1:A:1426:LYS:HD3	1.90	0.53
1:A:1291:ASP:OD1	1:A:1295:LEU:HB3	2.09	0.52
1:A:1250:ILE:HG23	1:A:1265:ILE:HD12	1.93	0.51
1:A:1696:TYR:CD1	1:A:1791:ALA:HB2	2.45	0.51
1:A:1628:ARG:HH22	1:A:1713:THR:HG21	1.74	0.50
1:A:1596:CYS:HB3	1:A:1634:TYR:HE2	1.76	0.50
1:A:1868:ARG:HE	1:A:1887:THR:HG22	1.77	0.49
1:A:1788:ILE:HD12	1:A:1788:ILE:H	1.76	0.49
1:A:1268:ARG:HH21	1:A:1350:SER:HA	1.78	0.48
1:A:1458:GLY:HA3	1:A:1539:LEU:HD22	1.96	0.47
1:A:1629:GLN:O	1:A:1631:LEU:HD22	2.14	0.47
1:A:1811:THR:O	1:A:1815:GLU:HB3	2.14	0.47
1:A:1276:GLU:HG3	1:A:1299:LYS:HG2	1.96	0.46
1:A:1631:LEU:HG	1:A:1633:LEU:HG	1.98	0.46
1:A:1268:ARG:HH11	1:A:1268:ARG:HB3	1.81	0.45
1:A:1471:ASN:HB3	1:A:1504:LYS:HD2	1.98	0.45
1:A:1596:CYS:HB3	1:A:1634:TYR:CE2	2.52	0.45
1:A:1223:ALA:HB1	1:A:1422:LYS:HE3	1.99	0.44
1:A:1559:ILE:H	1:A:1559:ILE:HD12	1.82	0.44
1:A:1595:LEU:HA	1:A:1668:TYR:CE2	2.52	0.44
1:A:1543:TYR:HA	1:A:1544:PRO:HD2	1.85	0.44
1:A:1292:THR:HG23	1:A:1295:LEU:HD22	2.00	0.43
1:A:1465:ARG:HD2	1:A:1569:ASP:OD2	2.18	0.43
1:A:1273:CYS:HB3	1:A:1307:GLU:HB2	2.01	0.43
1:A:1694:SER:O	1:A:1698:LEU:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1755:THR:OG1	1:A:1758:GLN:HB2	2.19	0.43
1:A:1343:PHE:O	1:A:1347:VAL:HG23	2.19	0.43
1:A:1603:MET:HB3	1:A:1626:PRO:HB3	2.01	0.43
1:A:1649:LYS:HA	1:A:1652:GLU:HB2	2.00	0.43
1:A:1357:MET:HE3	1:A:1357:MET:HB2	1.90	0.43
1:A:1448:ASP:HB3	1:A:1451:VAL:HG22	2.01	0.43
1:A:1269:THR:HG23	1:A:1353:ASP:OD2	2.19	0.42
1:A:1688:CYS:SG	1:A:1783:MET:HG2	2.59	0.42
1:A:1322:ILE:CG2	1:A:1342:GLY:HA3	2.49	0.42
1:A:1780:PRO:HG2	1:A:1783:MET:HB2	2.02	0.42
1:A:1219[A]:CYS:HB2	1:A:1221:LEU:HG	2.02	0.42
1:A:1757:ARG:HE	1:A:1788:ILE:HD13	1.84	0.42
1:A:1588:GLU:HB2	1:A:1589:LYS:H	1.68	0.41
1:A:1404:TRP:NE1	1:A:1408:ILE:HD13	2.35	0.41
1:A:1554:ILE:HG12	1:A:1569:ASP:HB2	2.03	0.41
1:A:1742:TRP:HE1	1:A:1757:ARG:HG3	1.85	0.41
1:A:1335:ASP:CB	1:A:1336:PRO:HD2	2.44	0.41

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	634/746 (85%)	566 (89%)	61 (10%)	7 (1%)	11	36

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1443	THR
1	A	1595	LEU
1	A	1868	ARG
1	A	1904	TYR

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Mol	Chain	Res	Type
1	A	1222	GLN
1	A	1594	LEU
1	A	1913	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	515/661 (78%)	428 (83%)	87 (17%)	2 7

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1220	ASP
1	A	1221	LEU
1	A	1243	LYS
1	A	1246	GLU
1	A	1253	ASP
1	A	1259	ASP
1	A	1265	ILE
1	A	1268	ARG
1	A	1277	LEU
1	A	1291	ASP
1	A	1293	LYS
1	A	1296	LEU
1	A	1297	LYS
1	A	1324	LYS
1	A	1325	ASN
1	A	1337	ASN
1	A	1350	SER
1	A	1357	MET
1	A	1358	ILE
1	A	1369	ILE
1	A	1375	ASP
1	A	1382	LYS
1	A	1402	ASN

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Mol	Chain	Res	Type
1	A	1408	ILE
1	A	1414	ASP
1	A	1418	CYS
1	A	1421	THR
1	A	1436	GLU
1	A	1439	VAL
1	A	1443	THR
1	A	1446	ASP
1	A	1474	GLU
1	A	1488	ASN
1	A	1489	SER
1	A	1496	LYS
1	A	1523	LYS
1	A	1525	LYS
1	A	1529	LYS
1	A	1531	VAL
1	A	1533	LYS
1	A	1534	SER
1	A	1536	SER
1	A	1556	ASN
1	A	1576	CYS
1	A	1586	ASN
1	A	1588	GLU
1	A	1596	CYS
1	A	1608	LYS
1	A	1610	ILE
1	A	1627	ARG
1	A	1628	ARG
1	A	1630	GLN
1	A	1631	LEU
1	A	1633	LEU
1	A	1640	ILE
1	A	1655	LEU
1	A	1670	TRP
1	A	1676	THR
1	A	1684	ASN
1	A	1698	LEU
1	A	1703	LYS
1	A	1708	VAL
1	A	1716	ILE
1	A	1717	ASP
1	A	1722	GLU

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Mol	Chain	Res	Type
1	A	1728	ASP
1	A	1744	ASN
1	A	1745	GLU
1	A	1754	LYS
1	A	1758	GLN
1	A	1785	VAL
1	A	1788	ILE
1	A	1796	ILE
1	A	1808	GLU
1	A	1812	LYS
1	A	1836	ILE
1	A	1837	GLU
1	A	1866	ILE
1	A	1868	ARG
1	A	1883	ILE
1	A	1888	VAL
1	A	1895	ARG
1	A	1900	ILE
1	A	1904	TYR
1	A	1906	CYS
1	A	1911	ASN
1	A	1915	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1334	ASN
1	A	1356	ASN
1	A	1368	HIS
1	A	1498	GLN
1	A	1522	GLN
1	A	1550	ASN
1	A	1585	ASN
1	A	1744	ASN
1	A	1758	GLN
1	A	1787	HIS
1	A	1850	ASN
1	A	1857	ASN
1	A	1864	ASN
1	A	1893	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](#)

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](#)

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	649/746 (86%)	0.34	29 (4%) 38 30	29, 58, 99, 126	1 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1501	CYS	4.7
1	A	1491	SER	3.6
1	A	1331	LYS	3.3
1	A	1908	SER	3.3
1	A	1486	CYS	3.2
1	A	1224	THR	3.1
1	A	1221	LEU	3.1
1	A	1328	LYS	3.0
1	A	1225	ASN	3.0
1	A	1262	GLY	2.9
1	A	1922	VAL	2.9
1	A	1784	GLY	2.8
1	A	1907	CYS	2.8
1	A	1883	ILE	2.6
1	A	1916	GLN	2.6
1	A	1489	SER	2.5
1	A	1487	ILE	2.5
1	A	1836	ILE	2.5
1	A	1383	GLY	2.5
1	A	1427	ASN	2.3
1	A	1385	PRO	2.3
1	A	1680	ILE	2.2
1	A	1728	ASP	2.2
1	A	1727	SER	2.2
1	A	1903	ASN	2.1
1	A	1329	GLY	2.1
1	A	1667	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1870	SER	2.1
1	A	1613	LEU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.