



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 04:12 AM UTC

PDB ID : 8QJD / pdb_00008qjd
Title : T6SS-linked Rhs repeat protein - Salmonella bongori Rhs-core domain
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Deposited on : 2023-09-13
Resolution : 2.20 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

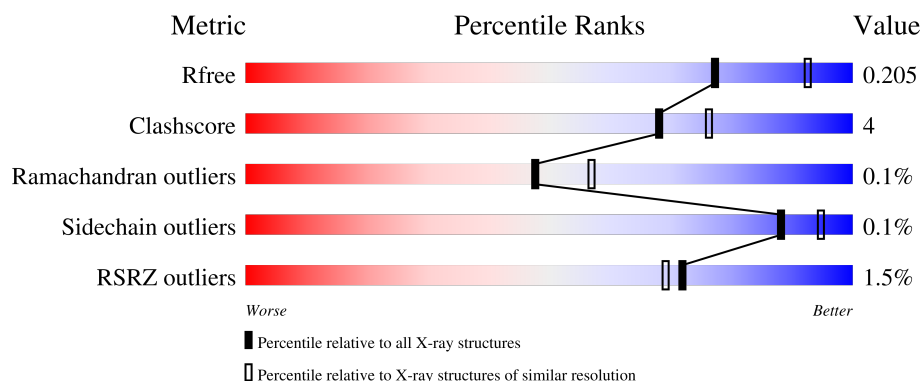
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	1065	% 88% 9% .
1	B	1065	2% 90% 7% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18070 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 Salmonella bongori Rhs core domain (residues 360-1420).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1037	Total	C	N	O	S	0	0	0
			8432	5229	1521	1658	24			
1	B	1036	Total	C	N	O	S	0	0	0
			8427	5226	1522	1655	24			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	GLY	-	expression tag	UNP S5MXP0
A	357	SER	-	expression tag	UNP S5MXP0
A	358	GLY	-	expression tag	UNP S5MXP0
A	359	SER	-	expression tag	UNP S5MXP0
B	356	GLY	-	expression tag	UNP S5MXP0
B	357	SER	-	expression tag	UNP S5MXP0
B	358	GLY	-	expression tag	UNP S5MXP0
B	359	SER	-	expression tag	UNP S5MXP0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

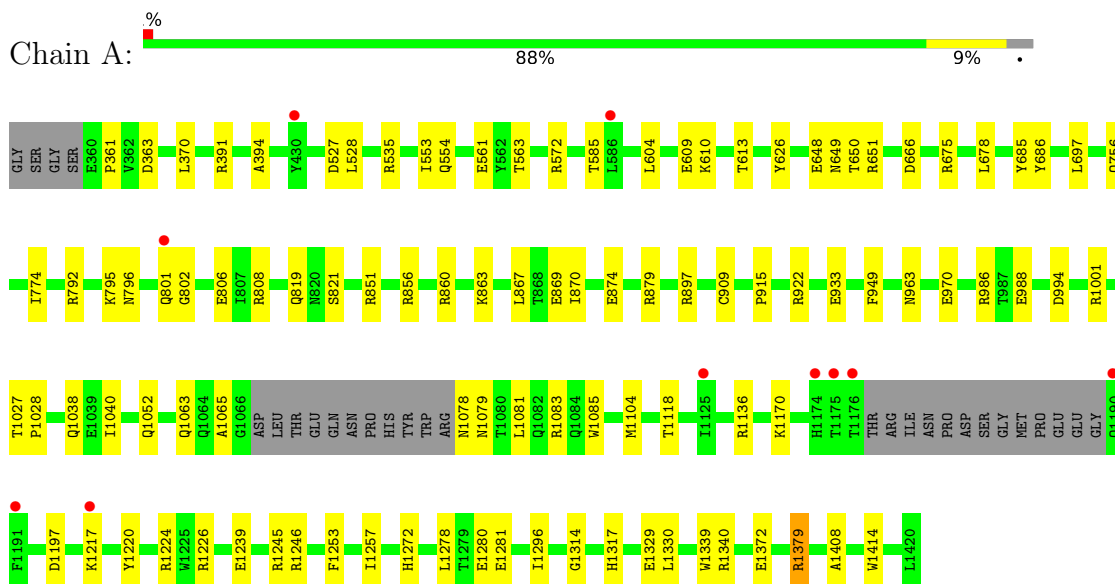
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	613	Total	O	0	0
			613	613		
3	B	596	Total	O	0	0
			596	596		

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: *Salmonella bongori* Rhs core domain (residues 360-1420)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	99.07Å 118.26Å 131.76Å 90.00° 105.52° 90.00°	Depositor
Resolution (Å)	49.17 – 2.20 49.17 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.17-2.20) 99.3 (49.17-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487+SVN, PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.182 , 0.211 (Not available) , 0.205	Depositor DCC
R_{free} test set	7363 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	37.9	Xtriage
Anisotropy	0.733	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18070	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 7.23% 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: ZN

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	0.17	0/8632	0.38	0/11717
1	B	0.17	0/8627	0.39	0/11709
All	All	0.17	0/17259	0.38	0/23426

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

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	8432	0	7934	68	1
1	B	8427	0	7932	49	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	613	0	0	27	1
3	B	596	0	0	11	1
All	All	18070	0	15866	117	2

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 4.

All (117) 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:819:GLN:O	3:A:1602:HOH:O	1.81	0.98
1:A:874:GLU:O	3:A:1601:HOH:O	1.80	0.95
1:A:994:ASP:OD2	3:A:1603:HOH:O	1.83	0.94
1:B:1233:SER:OG	3:B:1601:HOH:O	1.90	0.88
1:A:963:ASN:ND2	3:A:1607:HOH:O	2.09	0.86
1:B:1127:MET:SD	3:B:2113:HOH:O	2.33	0.84
1:B:686:TYR:OH	3:B:1602:HOH:O	2.01	0.78
1:A:863:LYS:NZ	3:A:1604:HOH:O	2.05	0.75
1:A:922:ARG:NE	3:A:1614:HOH:O	2.16	0.75
1:A:1083:ARG:NH2	1:A:1329:GLU:OE2	2.21	0.74
1:A:949:PHE:O	3:A:1606:HOH:O	2.07	0.72
1:A:792:ARG:NH2	1:A:806:GLU:OE2	2.17	0.71
1:B:851:ARG:NH2	1:B:1136:ARG:O	2.21	0.71
1:B:1253:PHE:O	1:B:1379:ARG:NH1	2.19	0.71
1:A:1038:GLN:OE1	3:A:1608:HOH:O	2.09	0.69
1:A:1317:HIS:ND1	3:A:1624:HOH:O	2.26	0.68
1:A:856:ARG:HD3	3:A:1658:HOH:O	1.94	0.67
1:B:1246:ARG:HG3	1:B:1372:GLU:HG3	1.77	0.67
1:A:1253:PHE:O	1:A:1379:ARG:NH1	2.21	0.66
1:A:1197:ASP:OD1	3:A:1610:HOH:O	2.12	0.66
1:A:1340:ARG:NE	3:A:1628:HOH:O	2.29	0.66
1:A:678:LEU:O	3:A:1611:HOH:O	2.13	0.65
1:A:1079:ASN:O	3:A:1613:HOH:O	2.14	0.65
1:B:554:GLN:HG2	3:B:1768:HOH:O	1.97	0.64
1:A:796:ASN:HB2	1:A:802:GLY:H	1.63	0.64
1:B:549:GLU:OE2	3:B:1603:HOH:O	2.16	0.63
1:B:1077:ARG:N	3:B:1621:HOH:O	2.31	0.63
1:A:1246:ARG:HG3	1:A:1372:GLU:HG3	1.79	0.63
1:A:648:GLU:OE2	1:A:651:ARG:NH2	2.32	0.62
1:A:867:LEU:HD21	1:A:870:ILE:HD11	1.82	0.62
1:B:666:ASP:OD2	1:B:675:ARG:NH1	2.33	0.62
1:B:1036:ARG:NH2	1:B:1056:PRO:O	2.33	0.62
1:B:792:ARG:HH22	1:B:808:ARG:HE	1.48	0.61
1:B:1083:ARG:NH2	1:B:1329:GLU:OE2	2.33	0.61
1:B:1009:CYS:SG	3:B:2156:HOH:O	2.56	0.60
1:B:768:THR:O	3:B:1605:HOH:O	2.17	0.59
1:B:732:GLU:OE2	3:B:1606:HOH:O	2.17	0.59
1:A:563:THR:O	3:A:1615:HOH:O	2.17	0.58
1:B:1027:THR:O	3:B:1604:HOH:O	2.16	0.57
1:B:664:ALA:HB3	1:B:677:SER:HB2	1.86	0.57
1:B:937:GLN:HB2	1:B:944:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:795:LYS:NZ	3:A:1648:HOH:O	2.38	0.56
1:A:561:GLU:OE2	3:A:1616:HOH:O	2.18	0.56
1:A:869:GLU:OE2	1:A:879:ARG:NH1	2.39	0.56
1:B:1413:SER:OG	3:B:1607:HOH:O	2.18	0.56
1:B:1260:ARG:HH21	1:B:1284:VAL:HG21	1.72	0.55
1:B:909:CYS:SG	1:B:922:ARG:NH2	2.81	0.54
1:A:528:LEU:HD21	1:A:774:ILE:HD13	1.90	0.54
1:A:756:GLN:OE1	3:A:1617:HOH:O	2.19	0.53
1:A:1052:GLN:HG2	1:A:1063:GLN:HG2	1.90	0.53
1:A:792:ARG:HH22	1:A:808:ARG:CD	2.22	0.53
1:B:391:ARG:HB3	1:B:394:ALA:HB2	1.89	0.53
1:A:1272:HIS:HB3	1:A:1280:GLU:HB2	1.91	0.52
1:A:361:PRO:HD2	3:A:1992:HOH:O	2.08	0.52
1:A:1170:LYS:NZ	3:A:1663:HOH:O	2.43	0.52
1:B:897:ARG:HG3	1:B:915:PRO:HG2	1.92	0.51
1:A:897:ARG:HG3	1:A:915:PRO:HG2	1.92	0.51
1:B:653:ARG:NH1	1:B:666:ASP:HA	2.25	0.51
1:A:391:ARG:HB3	1:A:394:ALA:HB2	1.92	0.51
1:B:554:GLN:HG3	1:B:555:PHE:CE2	2.45	0.51
1:A:363:ASP:HB2	1:A:370:LEU:HD11	1.92	0.51
1:A:851:ARG:NH2	1:A:1136:ARG:O	2.35	0.51
1:A:609:GLU:OE2	3:A:1619:HOH:O	2.19	0.51
1:B:476:THR:HG21	1:B:482:LEU:HD12	1.93	0.50
1:A:801:GLN:O	1:A:821:SER:HA	2.10	0.50
1:A:1040:ILE:O	3:A:1618:HOH:O	2.19	0.50
1:A:1278:LEU:HD22	3:A:2207:HOH:O	2.11	0.50
1:A:909:CYS:SG	1:A:922:ARG:NH2	2.85	0.50
1:B:649:ASN:O	1:B:650:THR:OG1	2.26	0.49
1:A:1083:ARG:HH22	1:A:1329:GLU:CD	2.19	0.49
1:B:1052:GLN:HG2	1:B:1063:GLN:HG2	1.94	0.48
1:B:792:ARG:NH2	1:B:808:ARG:HE	2.10	0.48
1:A:1408:ALA:HB1	1:A:1414:TRP:HB2	1.97	0.47
1:B:801:GLN:HG3	1:B:821:SER:HB3	1.97	0.47
1:A:860:ARG:HD3	1:A:869:GLU:OE1	2.14	0.46
1:B:1272:HIS:HB3	1:B:1280:GLU:HB2	1.98	0.46
1:A:922:ARG:HG2	1:A:933:GLU:HG2	1.97	0.46
1:B:685:TYR:HB2	1:B:698:SER:HB2	1.98	0.46
1:B:1083:ARG:HH22	1:B:1329:GLU:CD	2.24	0.46
1:B:1216:ASP:CG	1:B:1219:GLY:HA3	2.41	0.46
1:B:653:ARG:HH12	1:B:666:ASP:HA	1.81	0.45
1:A:666:ASP:HB2	1:A:675:ARG:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1330:LEU:HB2	1:B:1339:TRP:HB3	1.97	0.45
1:A:1078:ASN:HB2	3:A:1676:HOH:O	2.16	0.45
1:A:1224:ARG:NH1	1:A:1226:ARG:HH21	2.14	0.45
1:B:862:ASP:OD2	1:B:866:ARG:HD2	2.17	0.44
1:A:1239:GLU:OE1	1:A:1245:ARG:NH1	2.50	0.44
1:B:1281:GLU:HG3	1:B:1296:ILE:HB	2.00	0.44
1:A:675:ARG:HD2	1:A:685:TYR:CE1	2.53	0.43
1:B:860:ARG:HB3	1:B:869:GLU:HB3	1.99	0.43
1:A:1065:ALA:HB3	1:A:1081:LEU:HB3	2.01	0.43
1:A:1083:ARG:HD3	1:A:1085:TRP:CZ2	2.53	0.43
1:B:412:LEU:HB2	1:B:481:TYR:HB2	2.00	0.43
1:B:1260:ARG:NH2	1:B:1270:ASP:OD1	2.51	0.43
1:A:604:LEU:HB2	1:A:613:THR:HB	1.99	0.43
1:A:1330:LEU:HB2	1:A:1339:TRP:HB3	2.00	0.43
1:A:553:ILE:HG23	1:A:554:GLN:HG3	2.01	0.43
1:A:527:ASP:OD1	1:A:535:ARG:NE	2.49	0.43
1:B:1261:CYS:SG	1:B:1264:ARG:HB2	2.59	0.42
1:A:970:GLU:OE2	1:A:986:ARG:NH1	2.28	0.42
1:A:686:TYR:CE2	1:A:697:LEU:HD13	2.55	0.42
1:A:1104:MET:HA	1:A:1118:THR:O	2.20	0.42
1:A:1281:GLU:HG3	1:A:1296:ILE:HB	2.00	0.42
1:A:649:ASN:O	1:A:650:THR:OG1	2.30	0.42
1:A:988:GLU:O	1:A:1001:ARG:HA	2.20	0.41
1:A:922:ARG:CZ	3:A:1614:HOH:O	2.64	0.41
1:A:1314:GLY:N	3:A:1650:HOH:O	2.39	0.41
1:B:795:LYS:HE3	1:B:795:LYS:HB3	1.86	0.41
1:B:1209:ARG:HD3	1:B:1233:SER:OG	2.21	0.41
1:B:1172:TRP:HB3	1:B:1192:VAL:HG13	2.01	0.41
1:B:1011:THR:HB	1:B:1020:GLN:HB3	2.03	0.41
1:A:572:ARG:NH1	3:A:1675:HOH:O	2.47	0.40
1:B:1264:ARG:HB2	1:B:1266:ARG:HG3	2.04	0.40
1:B:1332:THR:OG1	1:B:1334:ASP:OD1	2.38	0.40
1:A:610:LYS:HD2	1:A:626:TYR:CE2	2.56	0.40
1:A:1027:THR:HA	1:A:1028:PRO:HD3	1.99	0.40
1:A:1217:LYS:HG3	1:A:1220:TYR:HB2	2.04	0.40

All (2) 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)
3:A:2059:HOH:O	3:B:1914:HOH:O[2_647]	1.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:585:THR:O	1:B:1122:SER:OG[2_646]	2.16	0.04

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	1031/1065 (97%)	1008 (98%)	22 (2%)	1 (0%)	48	57
1	B	1030/1065 (97%)	1007 (98%)	22 (2%)	1 (0%)	48	57
All	All	2061/2130 (97%)	2015 (98%)	44 (2%)	2 (0%)	48	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1379	ARG
1	B	1379	ARG

5.3.2 Protein sidechains [i](#)

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	898/922 (97%)	897 (100%)	1 (0%)	88	95
1	B	897/922 (97%)	897 (100%)	0	100	100
All	All	1795/1844 (97%)	1794 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1257	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	540	HIS
1	A	703	GLN
1	A	722	GLN
1	A	1020	GLN
1	A	1111	ASN
1	A	1190	GLN
1	A	1274	ASN
1	A	1344	HIS
1	A	1367	GLN
1	A	1378	ASN
1	B	424	HIS
1	B	520	GLN
1	B	691	HIS
1	B	722	GLN
1	B	801	GLN
1	B	1078	ASN
1	B	1111	ASN
1	B	1113	GLN
1	B	1137	ASN
1	B	1148	ASN
1	B	1174	HIS
1	B	1274	ASN
1	B	1328	GLN
1	B	1343	GLN
1	B	1403	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

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

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	1037/1065 (97%)	-0.08	10 (0%) 79 77	33, 46, 70, 116	0
1	B	1036/1065 (97%)	-0.08	22 (2%) 63 60	31, 45, 71, 109	0
All	All	2073/2130 (97%)	-0.08	32 (1%) 72 69	31, 45, 71, 116	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1191	PHE	5.2
1	B	796	ASN	5.1
1	B	1220	TYR	5.1
1	A	1176	THR	4.6
1	B	1079	ASN	4.3
1	A	1191	PHE	4.2
1	B	801	GLN	4.0
1	B	798	ALA	3.9
1	B	1175	THR	3.6
1	B	1221	ARG	3.6
1	B	800	PRO	3.5
1	B	795	LYS	3.4
1	B	1077	ARG	3.1
1	B	774	ILE	3.1
1	B	799	GLY	3.0
1	B	1078	ASN	3.0
1	B	797	HIS	2.8
1	A	586	LEU	2.7
1	A	1125	ILE	2.6
1	A	430	TYR	2.6
1	A	1190	GLN	2.5
1	A	1174	HIS	2.5
1	B	1125	ILE	2.4
1	B	817	MET	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	1174	HIS	2.3
1	A	1175	THR	2.3
1	A	801	GLN	2.3
1	B	1228	ARG	2.2
1	A	1217	LYS	2.2
1	B	937	GLN	2.1
1	B	1066	GLY	2.1
1	B	1080	THR	2.1

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($\text{\AA}^2$)	Q<0.9
2	ZN	A	1501	1/1	0.98	0.06	102,102,102,102	0
2	ZN	B	1501	1/1	0.98	0.04	86,86,86,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.