



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:04 PM GMT

PDB ID : 4KF7
Title : Nup188(aa1-1160) from Myceliophthora thermophila
Authors : Schwartz, T.U.; Andersen, K.R.
Deposited on : 2013-04-26
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

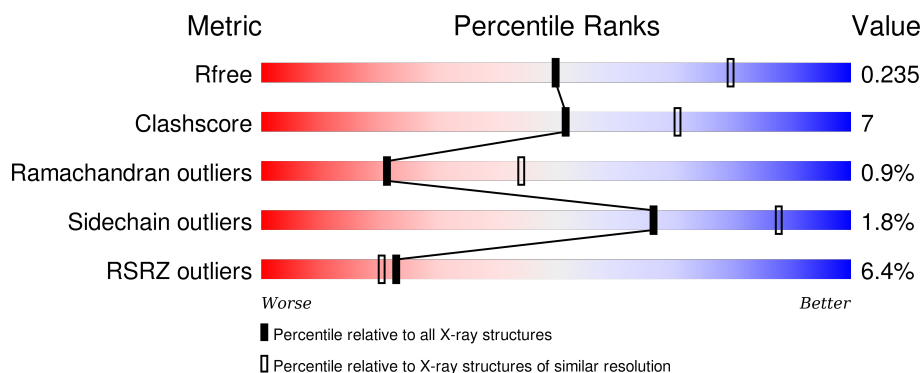
1 Overall quality at a glance

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}	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1160	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8644 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 Nup188.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1096	Total	C	N	O	S	0	0	0
			8516	5387	1467	1625	37			

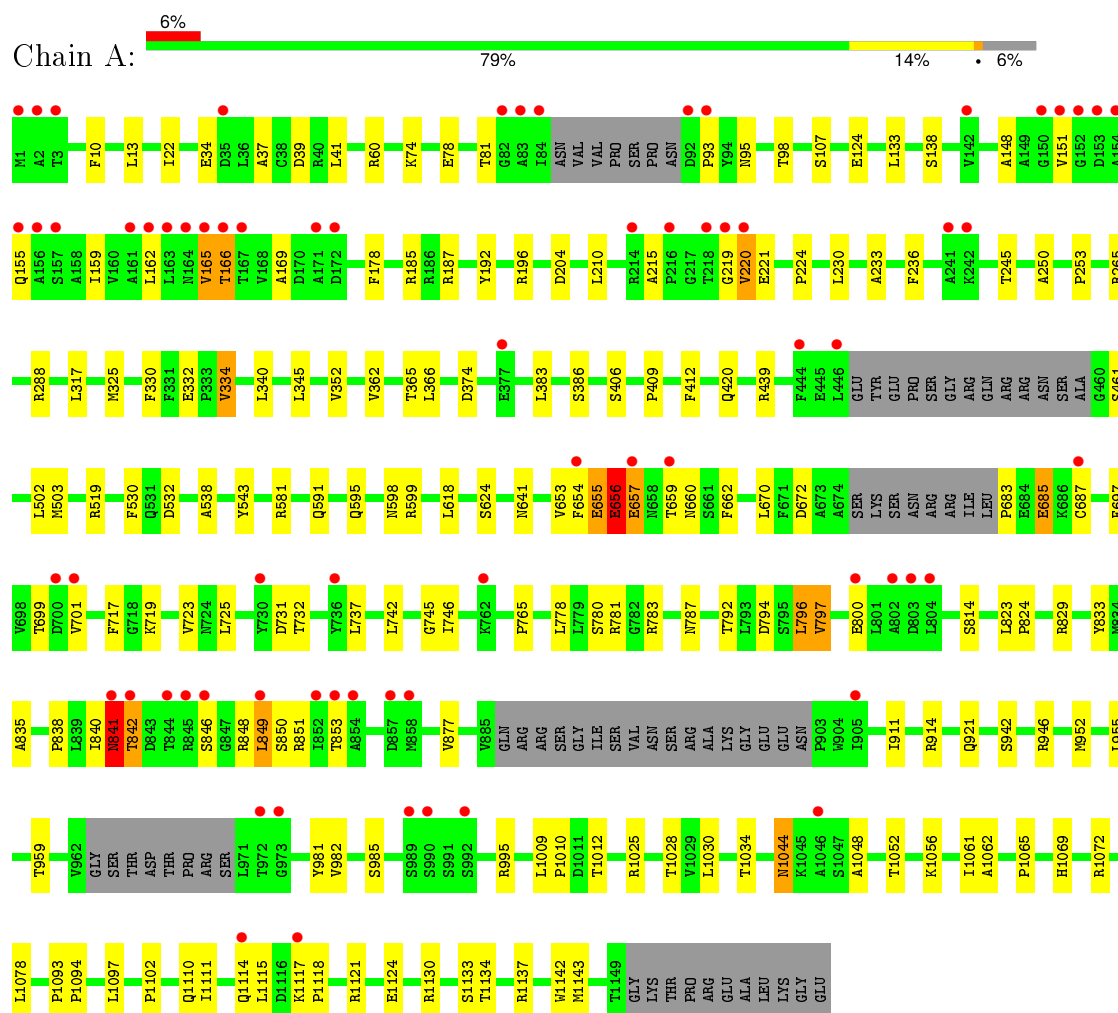
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	128	Total	O	0	0
			128	128		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Nup188



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.03 Å 94.77 Å 91.64 Å 90.00° 98.94° 90.00°	Depositor
Resolution (Å)	66.76 – 2.65 66.76 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (66.76-2.65) 98.8 (66.76-2.55)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.55 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.181 , 0.225 0.190 , 0.235	Depositor DCC
R_{free} test set	1919 reflections (4.83%)	DCC
Wilson B-factor (Å ²)	50.7	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 59.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 46063 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8644	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0/8670	0.47	1/11781 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	849	LEU	CB-CG-CD2	-5.21	102.14	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	THR	Peptide

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	8516	0	8530	116	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	128	0	0	5	0
All	All	8644	0	8530	116	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 7.

All (116) 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:13:LEU:HD22	1:A:81:THR:HG22	1.61	0.83
1:A:1072:ARG:HE	1:A:1115:LEU:HD12	1.45	0.82
1:A:1097:LEU:HD23	1:A:1142:TRP:HB3	1.69	0.75
1:A:366:LEU:HD22	1:A:420:GLN:HG3	1.71	0.72
1:A:842:THR:HG22	1:A:846:SER:HA	1.73	0.69
1:A:685:GLU:HB2	1:A:719:LYS:HZ1	1.57	0.68
1:A:1009:LEU:HD12	1:A:1010:PRO:HD2	1.76	0.68
1:A:124:GLU:OE2	1:A:187:ARG:NH1	2.28	0.67
1:A:1069:HIS:HA	1:A:1072:ARG:HD2	1.77	0.66
1:A:797:VAL:HA	1:A:800:GLU:HB3	1.79	0.65
1:A:1121:ARG:NH2	1:A:1124:GLU:OE2	2.29	0.65
1:A:787:ASN:OD1	1:A:829:ARG:NH2	2.30	0.64
1:A:265:ARG:NH2	2:A:1267:HOH:O	2.30	0.63
1:A:581:ARG:NH1	2:A:1257:HOH:O	2.27	0.62
1:A:840:ILE:O	1:A:842:THR:N	2.33	0.62
1:A:532:ASP:OD1	1:A:581:ARG:NH2	2.33	0.61
1:A:942:SER:HA	1:A:1025:ARG:HD2	1.83	0.61
1:A:34:GLU:HG2	1:A:37:ALA:HB2	1.83	0.60
1:A:783:ARG:HG2	1:A:787:ASN:HD22	1.67	0.59
1:A:151:VAL:H	1:A:155:GLN:HG3	1.68	0.58
1:A:538:ALA:HB1	1:A:591:GLN:HG2	1.84	0.58
1:A:654:PHE:O	1:A:655:GLU:HB2	2.04	0.57
1:A:796:LEU:O	1:A:800:GLU:N	2.36	0.57
1:A:1111:ILE:HA	1:A:1114:GLN:HB2	1.86	0.56
1:A:215:ALA:O	1:A:220:VAL:HG21	2.06	0.56
1:A:659:THR:O	1:A:697:PHE:HB2	2.05	0.56
1:A:595:GLN:NE2	2:A:1301:HOH:O	2.38	0.56
1:A:717:PHE:CZ	1:A:745:GLY:HA3	2.41	0.55
1:A:838:PRO:HB2	1:A:849:LEU:HD22	1.88	0.55
1:A:618:LEU:HD13	1:A:624:SER:HB3	1.89	0.54
1:A:1097:LEU:HB2	1:A:1143:MET:HG2	1.88	0.54
1:A:687:CYS:SG	1:A:778:LEU:HD21	2.47	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:792:THR:O	1:A:796:LEU:HB2	2.08	0.53
1:A:192:TYR:CZ	1:A:196:ARG:HD2	2.43	0.53
1:A:685:GLU:O	1:A:719:LYS:NZ	2.36	0.53
1:A:985:SER:O	1:A:995:ARG:NH1	2.42	0.53
1:A:178:PHE:O	1:A:187:ARG:NH2	2.42	0.53
1:A:138:SER:HA	1:A:169:ALA:HB3	1.91	0.52
1:A:737:LEU:HD11	1:A:742:LEU:HD13	1.92	0.52
1:A:95:ASN:HB3	1:A:98:THR:HB	1.91	0.52
1:A:719:LYS:NZ	1:A:778:LEU:O	2.43	0.51
1:A:210:LEU:HB3	1:A:230:LEU:HD21	1.93	0.51
1:A:685:GLU:HB2	1:A:719:LYS:NZ	2.26	0.51
1:A:288:ARG:HD3	1:A:340:LEU:HB3	1.92	0.51
1:A:325:MET:HE1	1:A:352:VAL:HG13	1.93	0.50
1:A:60:ARG:HH21	1:A:233:ALA:HA	1.76	0.50
1:A:155:GLN:O	1:A:159:ILE:N	2.41	0.50
1:A:439:ARG:NH1	1:A:461:SER:OG	2.45	0.50
1:A:699:THR:C	1:A:701:VAL:H	2.15	0.50
1:A:851:ARG:NH2	1:A:921:GLN:HB3	2.27	0.49
1:A:219:GLY:O	1:A:221:GLU:N	2.43	0.49
1:A:1030:LEU:HD22	1:A:1078:LEU:HD22	1.93	0.49
1:A:325:MET:HE2	1:A:330:PHE:CD1	2.48	0.48
1:A:723:VAL:HG11	1:A:732:THR:HG23	1.95	0.48
1:A:598:ASN:ND2	2:A:1301:HOH:O	2.45	0.48
1:A:848:ARG:HD2	1:A:851:ARG:CZ	2.44	0.48
1:A:1111:ILE:O	1:A:1115:LEU:N	2.46	0.48
1:A:851:ARG:HH22	1:A:921:GLN:HB3	1.80	0.47
1:A:946:ARG:HA	1:A:1028:THR:HG21	1.96	0.47
1:A:204:ASP:CG	1:A:519:ARG:HH22	2.17	0.47
1:A:672:ASP:HB2	1:A:731:ASP:HB2	1.97	0.46
1:A:835:ALA:HB2	1:A:911:ILE:HG23	1.97	0.46
1:A:22:ILE:HG13	1:A:1117:LYS:HG2	1.97	0.46
1:A:185:ARG:NH1	2:A:1252:HOH:O	2.26	0.46
1:A:365:THR:HG23	1:A:383:LEU:HD21	1.97	0.46
1:A:685:GLU:OE2	1:A:780:SER:HB3	2.15	0.46
1:A:221:GLU:O	1:A:224:PRO:HD2	2.16	0.46
1:A:955:LEU:O	1:A:959:THR:OG1	2.33	0.46
1:A:543:TYR:CD1	1:A:599:ARG:NH2	2.84	0.45
1:A:1030:LEU:O	1:A:1034:THR:HG23	2.17	0.45
1:A:1133:SER:HB3	1:A:1137:ARG:NH1	2.32	0.45
1:A:236:PHE:HE2	1:A:245:THR:HG22	1.82	0.45
1:A:670:LEU:HB2	1:A:687:CYS:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:725:LEU:HD21	1:A:792:THR:HA	1.99	0.44
1:A:914:ARG:HA	1:A:914:ARG:HD2	1.78	0.44
1:A:1072:ARG:HB3	1:A:1115:LEU:HD11	1.98	0.44
1:A:823:LEU:HB3	1:A:824:PRO:HD3	1.98	0.44
1:A:921:GLN:HG2	1:A:981:TYR:CE2	2.52	0.44
1:A:332:GLU:OE1	1:A:406:SER:OG	2.33	0.43
1:A:159:ILE:HA	1:A:162:LEU:HG	2.00	0.43
1:A:365:THR:HG23	1:A:383:LEU:HD11	1.98	0.43
1:A:1093:PRO:HA	1:A:1094:PRO:HD3	1.95	0.43
1:A:654:PHE:CG	1:A:655:GLU:N	2.86	0.43
1:A:1114:GLN:O	1:A:1118:PRO:HD3	2.19	0.43
1:A:921:GLN:HG2	1:A:981:TYR:CZ	2.54	0.43
1:A:374:ASP:N	1:A:374:ASP:OD1	2.45	0.43
1:A:1061:ILE:HG21	1:A:1078:LEU:HD23	1.99	0.43
1:A:41:LEU:HA	1:A:41:LEU:HD12	1.91	0.43
1:A:362:VAL:O	1:A:366:LEU:HG	2.19	0.43
1:A:1130:ARG:O	1:A:1134:THR:HG23	2.19	0.42
1:A:39:ASP:OD1	1:A:39:ASP:N	2.52	0.42
1:A:1097:LEU:O	1:A:1097:LEU:HD12	2.19	0.42
1:A:653:VAL:H	1:A:662:PHE:HA	1.84	0.42
1:A:133:LEU:HD12	1:A:1111:ILE:HD12	2.02	0.42
1:A:162:LEU:O	1:A:165:VAL:HG12	2.19	0.42
1:A:503:MET:HE2	1:A:530:PHE:HB3	2.01	0.42
1:A:1097:LEU:HD11	1:A:1102:PRO:HA	2.01	0.42
1:A:683:PRO:HB2	1:A:685:GLU:HG3	2.01	0.42
1:A:409:PRO:HD3	1:A:502:LEU:HD23	2.02	0.42
1:A:656:GLU:HB2	1:A:657:GLU:H	1.65	0.42
1:A:838:PRO:HA	1:A:841:ASN:ND2	2.35	0.41
1:A:250:ALA:O	1:A:253:PRO:HD2	2.20	0.41
1:A:780:SER:HB2	1:A:781:ARG:HG3	2.03	0.41
1:A:797:VAL:CG1	1:A:849:LEU:HD21	2.50	0.41
1:A:151:VAL:O	1:A:155:GLN:NE2	2.53	0.41
1:A:74:LYS:O	1:A:78:GLU:HG2	2.21	0.41
1:A:334:VAL:HG21	1:A:345:LEU:HD21	2.02	0.41
1:A:1062:ALA:O	1:A:1065:PRO:HD2	2.21	0.41
1:A:746:ILE:HB	1:A:814:SER:HB3	2.03	0.41
1:A:148:ALA:HB2	1:A:1056:LYS:HB2	2.03	0.41
1:A:952:MET:HB3	1:A:982:VAL:HG11	2.03	0.41
1:A:93:PRO:C	1:A:95:ASN:H	2.24	0.41
1:A:1052:THR:O	1:A:1056:LYS:HG2	2.21	0.41
1:A:317:LEU:HD12	1:A:317:LEU:HA	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:794:ASP:OD1	1:A:833:TYR:OH	2.22	0.40
1:A:850:SER:HA	1:A:853:THR:HG22	2.03	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	1084/1160 (93%)	1030 (95%)	44 (4%)	10 (1%)	21 44

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	655	GLU
1	A	657	GLU
1	A	841	ASN
1	A	220	VAL
1	A	166	THR
1	A	1044	ASN
1	A	656	GLU
1	A	660	ASN
1	A	1048	ALA
1	A	765	PRO

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	924/979 (94%)	907 (98%)	17 (2%)	66 88

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	PHE
1	A	107	SER
1	A	165	VAL
1	A	334	VAL
1	A	386	SER
1	A	412	PHE
1	A	641	ASN
1	A	656	GLU
1	A	685	GLU
1	A	796	LEU
1	A	797	VAL
1	A	841	ASN
1	A	842	THR
1	A	877	VAL
1	A	1012	THR
1	A	1044	ASN
1	A	1110	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	1096/1160 (94%)	0.17	70 (6%)	23 20	17, 58, 132, 182	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	7.7
1	A	164	ASN	7.5
1	A	218	THR	7.5
1	A	151	VAL	7.2
1	A	154	ALA	6.8
1	A	162	LEU	6.6
1	A	1	MET	6.5
1	A	167	THR	6.4
1	A	163	LEU	6.3
1	A	846	SER	6.2
1	A	972	THR	6.2
1	A	845	ARG	6.2
1	A	153	ASP	6.1
1	A	165	VAL	5.9
1	A	853	THR	5.4
1	A	687	CYS	5.3
1	A	803	ASP	5.0
1	A	93	PRO	5.0
1	A	150	GLY	4.8
1	A	152	GLY	4.7
1	A	166	THR	4.6
1	A	905	ILE	4.6
1	A	92	ASP	4.5
1	A	142	VAL	4.3
1	A	804	LEU	4.3
1	A	156	ALA	4.1
1	A	155	GLN	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	762	LYS	3.9
1	A	157	SER	3.6
1	A	852	ILE	3.4
1	A	857	ASP	3.4
1	A	84	ILE	3.3
1	A	83	ALA	3.3
1	A	842	THR	3.2
1	A	736	TYR	3.1
1	A	990	SER	3.1
1	A	3	THR	3.0
1	A	989	SER	3.0
1	A	172	ASP	3.0
1	A	216	PRO	2.9
1	A	446	LEU	2.9
1	A	844	THR	2.9
1	A	800	GLU	2.8
1	A	219	GLY	2.8
1	A	1114	GLN	2.7
1	A	659	THR	2.7
1	A	858	MET	2.6
1	A	241	ALA	2.6
1	A	802	ALA	2.5
1	A	1117	LYS	2.5
1	A	992	SER	2.5
1	A	242	LYS	2.5
1	A	701	VAL	2.4
1	A	444	PHE	2.3
1	A	730	TYR	2.3
1	A	220	VAL	2.3
1	A	841	ASN	2.3
1	A	35	ASP	2.3
1	A	1046	ALA	2.3
1	A	657	GLU	2.3
1	A	82	GLY	2.3
1	A	377	GLU	2.2
1	A	654	PHE	2.2
1	A	700	ASP	2.1
1	A	214	ARG	2.1
1	A	171	ALA	2.1
1	A	973	GLY	2.0
1	A	161	ALA	2.0
1	A	854	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	849	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 carbohydrates 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.