



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 09:53 AM UTC

PDB ID : 2QIZ / pdb_00002qiz
Title : Structure of the yeast U-box-containing ubiquitin ligase Ufd2p
Authors : Tu, D.; Brunger, A.T.
Deposited on : 2007-07-06
Resolution : 2.56 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

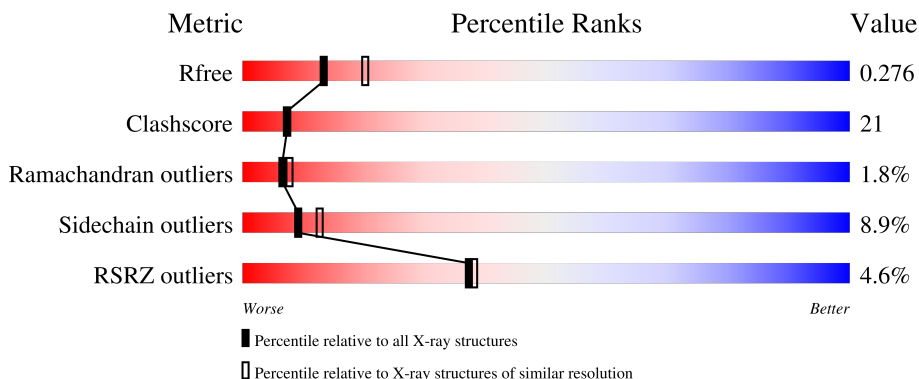
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.56 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	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

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	982	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7767 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 Ubiquitin conjugation factor E4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	943	Total	C	N	O	S	0	0	0
			7621	4896	1255	1442	28			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	GLY	-	expression tag	UNP P54860
A	-19	SER	-	expression tag	UNP P54860
A	-18	HIS	-	expression tag	UNP P54860
A	-17	MET	-	expression tag	UNP P54860
A	-16	ALA	-	expression tag	UNP P54860
A	-15	SER	-	expression tag	UNP P54860
A	-14	MET	-	expression tag	UNP P54860
A	-13	THR	-	expression tag	UNP P54860
A	-12	GLY	-	expression tag	UNP P54860
A	-11	GLY	-	expression tag	UNP P54860
A	-10	GLN	-	expression tag	UNP P54860
A	-9	GLN	-	expression tag	UNP P54860
A	-8	MET	-	expression tag	UNP P54860
A	-7	GLY	-	expression tag	UNP P54860
A	-6	ARG	-	expression tag	UNP P54860
A	-5	GLY	-	expression tag	UNP P54860
A	-4	SER	-	expression tag	UNP P54860
A	-3	GLU	-	expression tag	UNP P54860
A	-2	PHE	-	expression tag	UNP P54860
A	-1	ARG	-	expression tag	UNP P54860
A	0	SER	-	expression tag	UNP P54860
A	102	LEU	SER	engineered mutation	UNP P54860
A	677	VAL	ASP	engineered mutation	UNP P54860

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	K 1	0	0

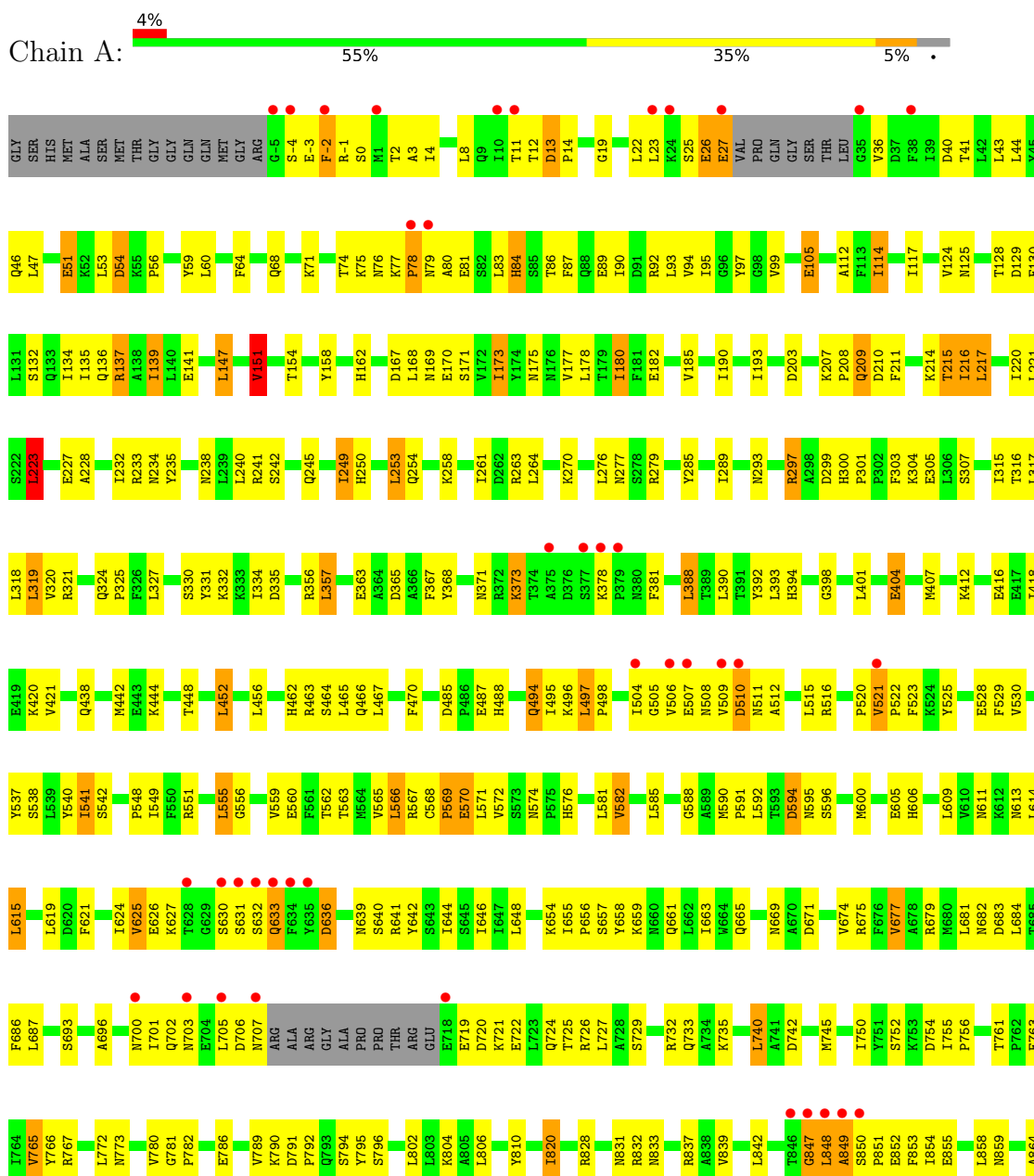
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	145	Total 145	O 145	0	0

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: Ubiquitin conjugation factor E4





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.50Å 122.99Å 176.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.56 50.00 – 2.56	Depositor EDS
% Data completeness (in resolution range)	93.6 (50.00-2.56) 92.9 (50.00-2.56)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.54Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.276 0.221 , 0.276	Depositor DCC
R_{free} test set	4651 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	51.4	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7767	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.93% 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

5.1 Standard geometry

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

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	0.46	0/7781	0.94	24/10515 (0.2%)

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	765	VAL	N-CA-C	9.09	119.90	110.36
1	A	781	GLY	CA-C-N	8.14	127.86	119.56
1	A	781	GLY	C-N-CA	8.14	127.86	119.56
1	A	828	ARG	N-CA-C	7.35	119.99	111.02
1	A	151	VAL	N-CA-C	7.16	117.97	111.81
1	A	568	CYS	CA-C-N	7.14	128.77	119.84
1	A	568	CYS	C-N-CA	7.14	128.77	119.84
1	A	173	ILE	N-CA-C	6.27	117.05	110.72
1	A	606	HIS	N-CA-C	6.17	120.97	113.38
1	A	124	VAL	N-CA-C	6.09	116.75	110.36
1	A	381	PHE	N-CA-C	6.05	117.54	111.07
1	A	300	HIS	CA-C-N	5.96	126.52	120.38
1	A	300	HIS	C-N-CA	5.96	126.52	120.38
1	A	227	GLU	N-CA-C	-5.87	99.67	109.24
1	A	216	ILE	N-CA-C	5.62	116.36	110.62
1	A	540	TYR	N-CA-C	5.55	117.02	110.97
1	A	303	PHE	N-CA-C	5.54	118.04	111.33
1	A	51	GLU	N-CA-C	5.46	119.04	112.38
1	A	924	PHE	N-CA-C	5.40	119.98	112.90
1	A	761	THR	N-CA-C	-5.25	102.84	110.08
1	A	26	GLU	N-CA-C	5.10	116.96	107.99
1	A	654	LYS	N-CA-C	5.08	120.48	113.97
1	A	388	LEU	N-CA-C	-5.06	105.85	112.23
1	A	203	ASP	N-CA-C	-5.02	103.42	110.50

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	7621	0	7597	314	0
2	A	1	0	0	0	0
3	A	145	0	0	5	0
All	All	7767	0	7597	314	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 21.

All (314) 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:114:ILE:H	1:A:114:ILE:HD12	1.12	1.14
1:A:850:SER:HB2	1:A:851:PRO:HA	1.45	0.99
1:A:207:LYS:HB3	1:A:209:GLN:NE2	1.79	0.95
1:A:926:ARG:HB2	1:A:926:ARG:HH11	1.28	0.94
1:A:293:ASN:HD21	1:A:307:SER:H	0.98	0.93
1:A:576:HIS:HB2	1:A:633:GLN:NE2	1.84	0.92
1:A:207:LYS:HB3	1:A:209:GLN:HE22	1.35	0.92
1:A:842:LEU:HB3	1:A:848:LEU:HD13	1.52	0.91
1:A:125:ASN:O	1:A:128:THR:HG22	1.70	0.90
1:A:630:SER:HB2	1:A:633:GLN:HB3	1.54	0.87
1:A:494:GLN:HE21	1:A:495:ILE:H	1.19	0.86
1:A:209:GLN:HG2	1:A:304:LYS:O	1.80	0.82
1:A:567:ARG:HG3	1:A:613:ASN:HB3	1.65	0.78
1:A:293:ASN:HD21	1:A:307:SER:N	1.81	0.78
1:A:566:LEU:HD21	1:A:582:VAL:HG23	1.65	0.76
1:A:876:LEU:O	1:A:876:LEU:HD12	1.86	0.76
1:A:494:GLN:HE21	1:A:495:ILE:N	1.84	0.76
1:A:64:PHE:O	1:A:68:GLN:HG2	1.85	0.76
1:A:68:GLN:HE22	1:A:71:LYS:NZ	1.84	0.75
1:A:68:GLN:HE22	1:A:71:LYS:HZ2	1.31	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:SER:O	1:A:661:GLN:HG3	1.87	0.75
1:A:215:THR:HG21	1:A:285:TYR:OH	1.85	0.75
1:A:804:LYS:HZ1	1:A:849:ALA:H	1.35	0.74
1:A:99:VAL:HG22	1:A:134:ILE:HG23	1.70	0.73
1:A:276:LEU:HA	1:A:279:ARG:NH1	2.03	0.73
1:A:852:GLU:O	1:A:855:GLU:HB3	1.88	0.73
1:A:894:MET:HE3	1:A:908:ASP:N	2.02	0.73
1:A:114:ILE:H	1:A:114:ILE:CD1	1.89	0.73
1:A:234:ASN:HB3	1:A:249:ILE:HD12	1.71	0.71
1:A:926:ARG:HB2	1:A:926:ARG:NH1	2.04	0.71
1:A:494:GLN:NE2	1:A:495:ILE:H	1.89	0.71
1:A:147:LEU:O	1:A:151:VAL:HG12	1.90	0.70
1:A:789:VAL:HG23	1:A:792:PRO:HG3	1.71	0.70
1:A:335:ASP:HB2	3:A:1107:HOH:O	1.89	0.70
1:A:26:GLU:O	1:A:27:GLU:HB2	1.91	0.70
1:A:848:LEU:HG	1:A:850:SER:OG	1.92	0.70
1:A:95:ILE:HD11	1:A:137:ARG:NH1	2.07	0.70
1:A:421:VAL:HG21	1:A:442:MET:HE1	1.73	0.69
1:A:497:LEU:HD22	1:A:609:LEU:HD11	1.72	0.69
1:A:185:VAL:HG22	1:A:270:LYS:HB3	1.73	0.68
1:A:114:ILE:HD12	1:A:114:ILE:N	1.98	0.68
1:A:404:GLU:HA	1:A:407:MET:HG3	1.76	0.68
1:A:894:MET:HE3	1:A:907:ILE:C	2.18	0.68
1:A:234:ASN:HB3	1:A:249:ILE:CD1	2.24	0.67
1:A:23:LEU:HD23	1:A:23:LEU:H	1.59	0.67
1:A:289:ILE:HB	1:A:392:TYR:OH	1.95	0.67
1:A:898:VAL:HG21	1:A:912:ILE:HD11	1.78	0.66
1:A:373:LYS:HA	1:A:373:LYS:HZ3	1.59	0.66
1:A:848:LEU:C	1:A:850:SER:H	2.03	0.66
1:A:721:LYS:HG3	1:A:722:GLU:H	1.60	0.66
1:A:684:LEU:HD21	1:A:745:MET:HE2	1.76	0.66
1:A:721:LYS:HG3	1:A:722:GLU:N	2.12	0.65
1:A:850:SER:HA	1:A:853:PHE:H	1.62	0.65
1:A:132:SER:O	1:A:136:GLN:HG3	1.96	0.65
1:A:238:ASN:O	1:A:241:ARG:HG2	1.96	0.64
1:A:235:TYR:OH	1:A:250:HIS:HD2	1.79	0.64
1:A:722:GLU:O	1:A:726:ARG:HB2	1.98	0.64
1:A:592:LEU:HD12	1:A:592:LEU:N	2.13	0.64
1:A:117:ILE:HG12	1:A:154:THR:HG22	1.80	0.63
1:A:356:ARG:HG3	1:A:525:TYR:O	1.99	0.63
1:A:848:LEU:HD11	1:A:854:ILE:HD11	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:GLY:O	1:A:560:GLU:HG3	1.98	0.62
1:A:128:THR:HG23	1:A:129:ASP:H	1.64	0.62
1:A:925:ASN:C	1:A:925:ASN:HD22	2.07	0.62
1:A:591:PRO:C	1:A:592:LEU:HD12	2.25	0.61
1:A:850:SER:HB2	1:A:851:PRO:CA	2.26	0.61
1:A:837:ARG:HB3	1:A:837:ARG:NH1	2.15	0.61
1:A:833:ASN:O	1:A:837:ARG:HG2	2.01	0.61
1:A:506:VAL:HG11	1:A:675:ARG:HH21	1.65	0.60
1:A:727:LEU:HD23	1:A:727:LEU:C	2.26	0.60
1:A:839:VAL:HG22	1:A:854:ILE:HG23	1.84	0.60
1:A:605:GLU:HB2	1:A:655:ILE:HD13	1.84	0.60
1:A:250:HIS:O	1:A:254:GLN:HG3	2.01	0.59
1:A:249:ILE:HG13	1:A:253:LEU:HD22	1.84	0.59
1:A:498:PRO:HG3	1:A:567:ARG:NH1	2.17	0.59
1:A:404:GLU:HB3	1:A:456:LEU:HD13	1.85	0.59
1:A:922:ASP:HB3	1:A:925:ASN:ND2	2.18	0.59
1:A:735:LYS:HA	1:A:795:TYR:O	2.02	0.58
1:A:732:ARG:HB2	1:A:732:ARG:NH1	2.17	0.58
1:A:820:ILE:CD1	1:A:864:ALA:HA	2.33	0.58
1:A:752:SER:O	1:A:756:PRO:HG3	2.03	0.58
1:A:848:LEU:O	1:A:850:SER:N	2.36	0.58
1:A:701:ILE:O	1:A:705:LEU:HG	2.04	0.58
1:A:56:PRO:O	1:A:59:TYR:HB3	2.03	0.58
1:A:509:VAL:O	1:A:510:ASP:C	2.47	0.58
1:A:789:VAL:CG2	1:A:792:PRO:HG3	2.34	0.57
1:A:915:HIS:CD2	1:A:923:PRO:HG3	2.39	0.57
1:A:77:LYS:HB3	1:A:78:PRO:HD2	1.85	0.57
1:A:505:GLY:C	1:A:507:GLU:H	2.13	0.57
1:A:117:ILE:HD12	1:A:117:ILE:C	2.28	0.57
1:A:261:ILE:HD11	1:A:321:ARG:NH2	2.19	0.57
1:A:494:GLN:HE21	1:A:494:GLN:CA	2.17	0.57
1:A:520:PRO:HG3	1:A:571:LEU:CD2	2.35	0.57
1:A:897:PRO:HD2	1:A:941:ARG:HG3	1.87	0.57
1:A:659:LYS:O	1:A:663:ILE:HG13	2.05	0.57
1:A:83:LEU:HB3	1:A:87:PHE:CE2	2.40	0.57
1:A:36:VAL:HG22	1:A:86:THR:HG22	1.87	0.56
1:A:180:ILE:HD12	1:A:180:ILE:O	2.05	0.56
1:A:631:SER:O	1:A:632:SER:HB2	2.06	0.56
1:A:14:PRO:HA	1:A:22:LEU:HD11	1.88	0.56
1:A:68:GLN:NE2	1:A:71:LYS:NZ	2.54	0.55
1:A:521:VAL:HB	1:A:522:PRO:CD	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:PHE:O	1:A:625:VAL:HG22	2.06	0.55
1:A:208:PRO:HG2	1:A:305:GLU:O	2.06	0.55
1:A:521:VAL:HB	1:A:522:PRO:HD3	1.88	0.55
1:A:848:LEU:HD23	1:A:848:LEU:N	2.21	0.55
1:A:724:GLN:HA	1:A:724:GLN:NE2	2.21	0.55
1:A:820:ILE:HD12	1:A:820:ILE:O	2.06	0.55
1:A:293:ASN:ND2	1:A:307:SER:H	1.83	0.55
1:A:135:ILE:O	1:A:139:ILE:HG23	2.06	0.55
1:A:232:ILE:HG13	1:A:233:ARG:N	2.22	0.55
1:A:54:ASP:C	1:A:56:PRO:HD3	2.32	0.54
1:A:682:ASN:OD1	1:A:767:ARG:NH2	2.37	0.54
1:A:754:ASP:C	1:A:756:PRO:HD3	2.33	0.54
1:A:847:GLY:O	1:A:848:LEU:HB3	2.06	0.54
1:A:217:LEU:HB3	1:A:221:LEU:CD1	2.38	0.54
1:A:105:GLU:OE2	1:A:112:ALA:HB1	2.07	0.54
1:A:772:LEU:HD22	1:A:806:LEU:CD1	2.37	0.54
1:A:485:ASP:HB2	1:A:495:ILE:HD12	1.88	0.54
1:A:398:GLY:HA2	1:A:401:LEU:HD21	1.90	0.54
1:A:22:LEU:HD23	1:A:23:LEU:N	2.23	0.54
1:A:241:ARG:HD2	3:A:997:HOH:O	2.08	0.53
1:A:565:VAL:HG13	1:A:572:VAL:CG1	2.37	0.53
1:A:780:VAL:CG1	1:A:837:ARG:HB2	2.38	0.53
1:A:683:ASP:HA	1:A:686:PHE:CE2	2.43	0.53
1:A:790:LYS:O	1:A:792:PRO:HD3	2.08	0.53
1:A:0:SER:OG	1:A:86:THR:HG21	2.08	0.53
1:A:780:VAL:HG13	1:A:837:ARG:HB2	1.89	0.53
1:A:217:LEU:HB3	1:A:221:LEU:HD12	1.90	0.53
1:A:506:VAL:HG22	1:A:627:LYS:NZ	2.24	0.53
1:A:850:SER:HB3	1:A:854:ILE:HG13	1.91	0.53
1:A:916:LEU:HA	1:A:919:ASP:O	2.09	0.52
1:A:642:TYR:CE2	1:A:646:ILE:HD11	2.45	0.52
1:A:40:ASP:HA	1:A:93:LEU:HD13	1.91	0.52
1:A:773:ASN:ND2	1:A:810:TYR:OH	2.42	0.51
1:A:207:LYS:CB	1:A:209:GLN:HE22	2.17	0.51
1:A:43:LEU:HD23	1:A:97:TYR:HD2	1.75	0.51
1:A:99:VAL:CG2	1:A:134:ILE:HG23	2.38	0.51
1:A:12:THR:HG22	1:A:23:LEU:HD21	1.93	0.51
1:A:74:THR:HG22	1:A:80:ALA:HA	1.93	0.50
1:A:95:ILE:HD11	1:A:137:ARG:HH12	1.75	0.50
1:A:896:ASP:OD1	1:A:909:ARG:HD2	2.11	0.50
1:A:511:ASN:O	1:A:512:ALA:C	2.53	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:ALA:HA	3:A:1070:HOH:O	2.12	0.50
1:A:567:ARG:O	1:A:567:ARG:HD3	2.12	0.50
1:A:169:ASN:O	1:A:171:SER:N	2.44	0.50
1:A:173:ILE:O	1:A:177:VAL:HG23	2.12	0.50
1:A:137:ARG:HH11	1:A:137:ARG:HG2	1.77	0.49
1:A:611:ASN:HA	1:A:658:TYR:OH	2.12	0.49
1:A:884:GLU:HG3	1:A:885:PHE:CD2	2.47	0.49
1:A:175:ASN:HD22	1:A:263:ARG:NH1	2.10	0.49
1:A:297:ARG:CG	1:A:297:ARG:HH11	2.24	0.49
1:A:565:VAL:HG13	1:A:572:VAL:HG12	1.94	0.49
1:A:729:SER:HA	1:A:732:ARG:NH2	2.27	0.49
1:A:576:HIS:HB2	1:A:633:GLN:HE21	1.71	0.49
1:A:373:LYS:HA	1:A:373:LYS:NZ	2.25	0.49
1:A:592:LEU:HD13	1:A:596:SER:O	2.12	0.49
1:A:687:LEU:HD11	1:A:740:LEU:HD13	1.94	0.49
1:A:724:GLN:C	1:A:726:ARG:N	2.67	0.49
1:A:26:GLU:O	1:A:27:GLU:CB	2.59	0.49
1:A:316:THR:OG1	1:A:392:TYR:HB3	2.13	0.49
1:A:702:GLN:HE21	1:A:727:LEU:HD11	1.77	0.49
1:A:175:ASN:HD22	1:A:263:ARG:HH12	1.61	0.48
1:A:506:VAL:HG22	1:A:627:LYS:HZ1	1.76	0.48
1:A:242:SER:OG	1:A:245:GLN:HG3	2.12	0.48
1:A:832:ARG:HH11	1:A:832:ARG:HG2	1.77	0.48
1:A:412:LYS:O	1:A:416:GLU:HG3	2.13	0.48
1:A:68:GLN:NE2	1:A:71:LYS:HZ2	2.07	0.48
1:A:448:THR:O	1:A:452:LEU:HB2	2.13	0.48
1:A:4:ILE:O	1:A:8:LEU:HB2	2.14	0.48
1:A:209:GLN:CG	1:A:305:GLU:HA	2.43	0.48
1:A:137:ARG:HH11	1:A:137:ARG:CG	2.26	0.48
1:A:724:GLN:C	1:A:726:ARG:H	2.21	0.47
1:A:894:MET:HE2	1:A:897:PRO:HB3	1.95	0.47
1:A:78:PRO:C	1:A:80:ALA:H	2.22	0.47
1:A:574:ASN:OD1	1:A:576:HIS:HB3	2.14	0.47
1:A:215:THR:CG2	1:A:285:TYR:OH	2.61	0.47
1:A:594:ASP:O	1:A:595:ASN:HB2	2.14	0.47
1:A:510:ASP:C	1:A:512:ALA:N	2.72	0.47
1:A:780:VAL:HG13	1:A:837:ARG:CB	2.43	0.47
1:A:128:THR:HG23	1:A:129:ASP:N	2.29	0.47
1:A:162:HIS:HE1	3:A:1062:HOH:O	1.97	0.47
1:A:538:SER:HA	1:A:541:ILE:HD11	1.97	0.47
1:A:567:ARG:CG	1:A:613:ASN:HB3	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:GLY:C	1:A:507:GLU:N	2.70	0.47
1:A:92:ARG:HH12	1:A:93:LEU:HD21	1.80	0.46
1:A:831:ASN:ND2	1:A:833:ASN:HB3	2.30	0.46
1:A:228:ALA:HA	1:A:452:LEU:HD13	1.97	0.46
1:A:624:ILE:C	1:A:626:GLU:H	2.23	0.46
1:A:-1:ARG:C	1:A:2:THR:HG22	2.39	0.46
1:A:621:PHE:HD2	1:A:644:ILE:HD11	1.79	0.46
1:A:316:THR:O	1:A:320:VAL:HG23	2.15	0.46
1:A:390:LEU:HD13	1:A:530:VAL:HG22	1.96	0.46
1:A:588:GLY:O	1:A:600:MET:HB2	2.16	0.46
1:A:178:LEU:O	1:A:182:GLU:HG3	2.16	0.46
1:A:665:GLN:NE2	1:A:669:ASN:HD22	2.13	0.46
1:A:820:ILE:HD11	1:A:867:GLN:HB2	1.98	0.46
1:A:367:PHE:O	1:A:371:ASN:ND2	2.49	0.46
1:A:470:PHE:CZ	1:A:549:ILE:HG12	2.50	0.46
1:A:615:LEU:HD22	1:A:619:LEU:HG	1.98	0.46
1:A:636:ASP:HA	1:A:639:ASN:HD22	1.81	0.46
1:A:732:ARG:HB2	1:A:732:ARG:HH11	1.80	0.46
1:A:506:VAL:HG11	1:A:675:ARG:NH2	2.31	0.45
1:A:592:LEU:N	1:A:592:LEU:CD1	2.80	0.45
1:A:324:GLN:HB3	1:A:325:PRO:HD3	1.98	0.45
1:A:137:ARG:NH1	1:A:137:ARG:CG	2.80	0.45
1:A:363:GLU:OE2	1:A:516:ARG:HD3	2.17	0.45
1:A:506:VAL:C	1:A:508:ASN:H	2.24	0.45
1:A:43:LEU:HD23	1:A:97:TYR:CD2	2.52	0.45
1:A:953:GLU:C	1:A:954:GLU:HG3	2.41	0.45
1:A:78:PRO:O	1:A:80:ALA:N	2.49	0.45
1:A:95:ILE:HA	1:A:130:PHE:HE1	1.82	0.45
1:A:494:GLN:NE2	1:A:494:GLN:HA	2.32	0.45
1:A:563:THR:O	1:A:567:ARG:HB2	2.17	0.45
1:A:671:ASP:O	1:A:674:VAL:HG12	2.17	0.45
1:A:331:TYR:HD1	1:A:334:ILE:HD13	1.82	0.45
1:A:665:GLN:HE21	1:A:669:ASN:HB3	1.81	0.45
1:A:684:LEU:CD2	1:A:745:MET:HE2	2.44	0.45
1:A:832:ARG:HG2	1:A:832:ARG:NH1	2.32	0.45
1:A:330:SER:OG	1:A:332:LYS:HG3	2.17	0.45
1:A:529:PHE:C	1:A:529:PHE:CD2	2.95	0.45
1:A:-2:PHE:O	1:A:2:THR:HG22	2.16	0.45
1:A:83:LEU:O	1:A:84:HIS:C	2.60	0.44
1:A:494:GLN:NE2	1:A:494:GLN:CA	2.80	0.44
1:A:626:GLU:HA	1:A:626:GLU:OE1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:898:VAL:HG22	1:A:907:ILE:O	2.17	0.44
1:A:40:ASP:CA	1:A:93:LEU:HD13	2.48	0.44
1:A:745:MET:HG3	1:A:802:LEU:HD12	2.00	0.44
1:A:755:ILE:N	1:A:756:PRO:HD3	2.33	0.44
1:A:782:PRO:O	1:A:786:GLU:HB2	2.18	0.44
1:A:679:ARG:HH12	1:A:682:ASN:HD22	1.64	0.44
1:A:75:LYS:C	1:A:77:LYS:H	2.26	0.44
1:A:220:ILE:HA	1:A:223:LEU:HD22	2.00	0.44
1:A:11:THR:O	1:A:23:LEU:HD23	2.18	0.44
1:A:570:GLU:H	1:A:570:GLU:HG3	1.28	0.44
1:A:847:GLY:C	1:A:848:LEU:CD2	2.91	0.44
1:A:677:VAL:O	1:A:681:LEU:HB2	2.18	0.44
1:A:700:ASN:O	1:A:703:ASN:HB3	2.18	0.44
1:A:725:THR:O	1:A:729:SER:HB2	2.17	0.44
1:A:90:ILE:O	1:A:94:VAL:HG23	2.18	0.44
1:A:117:ILE:HG12	1:A:154:THR:CG2	2.47	0.44
1:A:210:ASP:CG	1:A:214:LYS:HE2	2.43	0.44
1:A:420:LYS:HE3	1:A:420:LYS:HB2	1.87	0.44
1:A:590:MET:HA	1:A:591:PRO:HD3	1.88	0.44
1:A:655:ILE:HA	1:A:656:PRO:HD2	1.91	0.44
1:A:394:HIS:O	1:A:398:GLY:HA3	2.18	0.43
1:A:521:VAL:CB	1:A:522:PRO:CD	2.95	0.43
1:A:693:SER:O	1:A:696:ALA:HB3	2.18	0.43
1:A:900:LEU:HD21	1:A:912:ILE:HG21	2.00	0.43
1:A:89:GLU:OE1	1:A:89:GLU:HA	2.18	0.43
1:A:357:LEU:HD13	1:A:528:GLU:HA	2.00	0.43
1:A:537:TYR:O	1:A:541:ILE:HG13	2.18	0.43
1:A:893:ILE:HD11	1:A:944:ILE:HG23	1.99	0.43
1:A:208:PRO:HA	1:A:211:PHE:CE1	2.53	0.43
1:A:357:LEU:HD23	1:A:523:PHE:CE1	2.53	0.43
1:A:631:SER:O	1:A:632:SER:CB	2.66	0.43
1:A:555:LEU:HD22	1:A:559:VAL:HG23	2.01	0.43
1:A:681:LEU:C	1:A:681:LEU:HD23	2.43	0.43
1:A:511:ASN:HB3	1:A:515:LEU:HG	2.01	0.43
1:A:906:ASN:HD21	1:A:937:ASN:ND2	2.16	0.43
1:A:893:ILE:HG23	1:A:893:ILE:O	2.18	0.43
1:A:209:GLN:HG2	1:A:304:LYS:C	2.44	0.43
1:A:850:SER:CB	1:A:851:PRO:HA	2.29	0.43
1:A:572:VAL:HG23	3:A:1004:HOH:O	2.19	0.43
1:A:624:ILE:C	1:A:626:GLU:N	2.76	0.43
1:A:13:ASP:HA	1:A:14:PRO:HD3	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:ARG:O	1:A:464:SER:C	2.62	0.42
1:A:466:GLN:HB3	1:A:548:PRO:CG	2.48	0.42
1:A:520:PRO:HG3	1:A:571:LEU:HD22	2.00	0.42
1:A:562:THR:HG23	1:A:581:LEU:HB3	2.01	0.42
1:A:438:GLN:HG2	1:A:442:MET:HE2	2.01	0.42
1:A:404:GLU:CB	1:A:456:LEU:HD13	2.48	0.42
1:A:907:ILE:HD13	1:A:912:ILE:HG23	2.00	0.42
1:A:14:PRO:HA	1:A:22:LEU:CD1	2.47	0.42
1:A:567:ARG:O	1:A:569:PRO:HD3	2.18	0.42
1:A:765:VAL:HG13	1:A:766:TYR:N	2.35	0.42
1:A:78:PRO:C	1:A:80:ALA:N	2.77	0.42
1:A:837:ARG:HB3	1:A:837:ARG:CZ	2.49	0.42
1:A:894:MET:HE2	1:A:897:PRO:HA	2.01	0.42
1:A:927:MET:O	1:A:928:PRO:C	2.63	0.42
1:A:315:ILE:HG22	1:A:319:LEU:HD22	2.01	0.42
1:A:721:LYS:CG	1:A:722:GLU:H	2.31	0.42
1:A:847:GLY:C	1:A:848:LEU:HD23	2.45	0.42
1:A:234:ASN:HB3	1:A:249:ILE:HD11	2.02	0.42
1:A:466:GLN:HB3	1:A:548:PRO:HG3	2.01	0.42
1:A:117:ILE:HD11	1:A:158:TYR:HB2	2.01	0.41
1:A:791:ASP:HB2	1:A:794:SER:OG	2.19	0.41
1:A:683:ASP:O	1:A:687:LEU:HG	2.19	0.41
1:A:92:ARG:NH1	1:A:93:LEU:HD21	2.36	0.41
1:A:299:ASP:C	1:A:301:PRO:HD3	2.46	0.41
1:A:46:GLN:O	1:A:53:LEU:HD12	2.20	0.41
1:A:74:THR:CG2	1:A:80:ALA:HA	2.50	0.41
1:A:357:LEU:HD12	1:A:357:LEU:HA	1.73	0.41
1:A:47:LEU:HD11	1:A:60:LEU:HD21	2.03	0.41
1:A:365:ASP:O	1:A:368:TYR:HB2	2.20	0.41
1:A:388:LEU:HD23	1:A:388:LEU:HA	1.85	0.41
1:A:462:HIS:CD2	1:A:465:LEU:HG	2.55	0.41
1:A:640:SER:O	1:A:644:ILE:HG13	2.20	0.41
1:A:795:TYR:O	1:A:796:SER:HB2	2.20	0.41
1:A:850:SER:CB	1:A:851:PRO:CA	2.93	0.41
1:A:487:GLU:O	1:A:488:HIS:C	2.64	0.41
1:A:641:ARG:NH1	1:A:683:ASP:OD2	2.53	0.41
1:A:74:THR:O	1:A:75:LYS:C	2.64	0.41
1:A:209:GLN:HG3	1:A:305:GLU:C	2.45	0.41
1:A:467:LEU:HD23	1:A:467:LEU:HA	1.91	0.41
1:A:498:PRO:HG3	1:A:567:ARG:CZ	2.50	0.41
1:A:541:ILE:HD12	1:A:542:SER:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:791:ASP:CB	1:A:794:SER:OG	2.69	0.41
1:A:238:ASN:ND2	1:A:240:LEU:H	2.19	0.41
1:A:732:ARG:CZ	1:A:732:ARG:CB	3.00	0.41
1:A:576:HIS:ND1	1:A:633:GLN:HG3	2.36	0.40
1:A:76:ASN:C	1:A:77:LYS:HG3	2.46	0.40
1:A:167:ASP:OD2	1:A:169:ASN:HB2	2.22	0.40
1:A:706:ASP:O	1:A:707:ASN:CG	2.64	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	937/982 (95%)	848 (90%)	72 (8%)	17 (2%)	6 8

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	849	ALA
1	A	510	ASP
1	A	720	ASP
1	A	848	LEU
1	A	877	GLU
1	A	79	ASN
1	A	170	GLU
1	A	105	GLU
1	A	223	LEU
1	A	521	VAL
1	A	-4	SER
1	A	78	PRO
1	A	84	HIS
1	A	19	GLY

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Mol	Chain	Res	Type
1	A	569	PRO
1	A	504	ILE
1	A	847	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	854/882 (97%)	778 (91%)	76 (9%)	9 13

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-3	GLU
1	A	-2	PHE
1	A	13	ASP
1	A	25	SER
1	A	27	GLU
1	A	41	THR
1	A	44	LEU
1	A	51	GLU
1	A	54	ASP
1	A	81	GLU
1	A	114	ILE
1	A	137	ARG
1	A	139	ILE
1	A	141	GLU
1	A	147	LEU
1	A	151	VAL
1	A	168	LEU
1	A	180	ILE
1	A	190	ILE
1	A	193	ILE
1	A	209	GLN
1	A	215	THR
1	A	216	ILE

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Mol	Chain	Res	Type
1	A	217	LEU
1	A	223	LEU
1	A	249	ILE
1	A	253	LEU
1	A	258	LYS
1	A	264	LEU
1	A	277	ASN
1	A	297	ARG
1	A	317	LEU
1	A	318	LEU
1	A	319	LEU
1	A	327	LEU
1	A	357	LEU
1	A	373	LYS
1	A	378	LYS
1	A	393	LEU
1	A	404	GLU
1	A	418	ILE
1	A	444	LYS
1	A	452	LEU
1	A	494	GLN
1	A	496	LYS
1	A	497	LEU
1	A	541	ILE
1	A	551	ARG
1	A	555	LEU
1	A	566	LEU
1	A	570	GLU
1	A	582	VAL
1	A	585	LEU
1	A	594	ASP
1	A	614	LEU
1	A	615	LEU
1	A	625	VAL
1	A	633	GLN
1	A	636	ASP
1	A	648	LEU
1	A	677	VAL
1	A	719	GLU
1	A	733	GLN
1	A	740	LEU
1	A	742	ASP

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Mol	Chain	Res	Type
1	A	750	ILE
1	A	763	GLU
1	A	820	ILE
1	A	858	LEU
1	A	859	ASN
1	A	912	ILE
1	A	925	ASN
1	A	926	ARG
1	A	932	GLU
1	A	935	THR
1	A	954	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	61	ASN
1	A	68	GLN
1	A	76	ASN
1	A	103	GLN
1	A	106	ASN
1	A	136	GLN
1	A	162	HIS
1	A	175	ASN
1	A	209	GLN
1	A	238	ASN
1	A	250	HIS
1	A	293	ASN
1	A	314	ASN
1	A	344	ASN
1	A	394	HIS
1	A	462	HIS
1	A	494	GLN
1	A	508	ASN
1	A	518	HIS
1	A	639	ASN
1	A	660	ASN
1	A	661	GLN
1	A	665	GLN
1	A	667	GLN
1	A	668	ASN
1	A	702	GLN

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Mol	Chain	Res	Type
1	A	724	GLN
1	A	733	GLN
1	A	773	ASN
1	A	775	ASN
1	A	812	ASN
1	A	831	ASN
1	A	833	ASN
1	A	906	ASN
1	A	915	HIS
1	A	925	ASN
1	A	942	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

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	943/982 (96%)	0.19	43 (4%) 37 38	35, 56, 106, 136	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	849	ALA	5.2
1	A	506	VAL	4.6
1	A	521	VAL	4.5
1	A	635	TYR	4.4
1	A	38	PHE	4.1
1	A	634	PHE	4.1
1	A	509	VAL	3.7
1	A	78	PRO	3.6
1	A	848	LEU	3.4
1	A	880	ASP	3.2
1	A	846	THR	3.2
1	A	378	LYS	3.0
1	A	847	GLY	3.0
1	A	377	SER	3.0
1	A	379	PRO	2.9
1	A	510	ASP	2.8
1	A	-2	PHE	2.8
1	A	-5	GLY	2.7
1	A	504	ILE	2.7
1	A	507	GLU	2.7
1	A	10	ILE	2.6
1	A	1	MET	2.6
1	A	628	THR	2.6
1	A	954	GLU	2.6
1	A	703	ASN	2.6
1	A	632	SER	2.5
1	A	700	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	23	LEU	2.5
1	A	24	LYS	2.5
1	A	707	ASN	2.4
1	A	-4	SER	2.3
1	A	705	LEU	2.3
1	A	375	ALA	2.3
1	A	718	GLU	2.2
1	A	35	GLY	2.2
1	A	79	ASN	2.2
1	A	633	GLN	2.2
1	A	27	GLU	2.2
1	A	876	LEU	2.1
1	A	850	SER	2.1
1	A	631	SER	2.1
1	A	630	SER	2.1
1	A	11	THR	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](#)

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	K	A	962	1/1	0.96	0.05	56,56,56,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.