



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2024 – 09:43 PM EDT

PDB ID : 2AJA
Title : X-Ray structure of an ankyrin repeat family protein Q5ZSV0 from Legionella pneumophila. Northeast Structural Genomics Consortium target LgR21.
Authors : Kuzin, A.P.; Chen, Y.; Acton, T.; Xiao, R.; Conover, K.; Ma, C.; Kellie, R.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2005-08-01
Resolution : 2.80 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

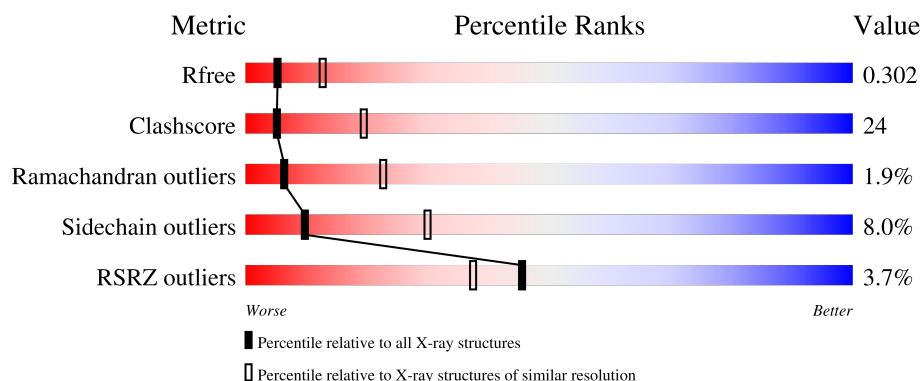
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3657 (2.80-2.80)
Clashscore	180529	4123 (2.80-2.80)
Ramachandran outliers	177936	4071 (2.80-2.80)
Sidechain outliers	177891	4073 (2.80-2.80)
RSRZ outliers	164620	3659 (2.80-2.80)

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	376	
1	B	376	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5644 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 ankyrin repeat family protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	Se	0	0	0
			2742	1757	477	491	9	8			
1	B	345	Total	C	N	O	S	Se	0	0	0
			2763	1769	482	494	10	8			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q5ZSV0
A	42	MSE	MET	modified residue	UNP Q5ZSV0
A	60	MSE	MET	modified residue	UNP Q5ZSV0
A	156	MSE	MET	modified residue	UNP Q5ZSV0
A	158	MSE	MET	modified residue	UNP Q5ZSV0
A	193	MSE	MET	modified residue	UNP Q5ZSV0
A	224	MSE	MET	modified residue	UNP Q5ZSV0
A	254	MSE	MET	modified residue	UNP Q5ZSV0
A	281	MSE	MET	modified residue	UNP Q5ZSV0
A	369	LEU	-	cloning artifact	UNP Q5ZSV0
A	370	GLU	-	cloning artifact	UNP Q5ZSV0
A	371	HIS	-	expression tag	UNP Q5ZSV0
A	372	HIS	-	expression tag	UNP Q5ZSV0
A	373	HIS	-	expression tag	UNP Q5ZSV0
A	374	HIS	-	expression tag	UNP Q5ZSV0
A	375	HIS	-	expression tag	UNP Q5ZSV0
A	376	HIS	-	expression tag	UNP Q5ZSV0
B	1	MSE	MET	modified residue	UNP Q5ZSV0
B	42	MSE	MET	modified residue	UNP Q5ZSV0
B	60	MSE	MET	modified residue	UNP Q5ZSV0
B	156	MSE	MET	modified residue	UNP Q5ZSV0
B	158	MSE	MET	modified residue	UNP Q5ZSV0
B	193	MSE	MET	modified residue	UNP Q5ZSV0
B	224	MSE	MET	modified residue	UNP Q5ZSV0
B	254	MSE	MET	modified residue	UNP Q5ZSV0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	281	MSE	MET	modified residue	UNP Q5ZSV0
B	369	LEU	-	cloning artifact	UNP Q5ZSV0
B	370	GLU	-	cloning artifact	UNP Q5ZSV0
B	371	HIS	-	expression tag	UNP Q5ZSV0
B	372	HIS	-	expression tag	UNP Q5ZSV0
B	373	HIS	-	expression tag	UNP Q5ZSV0
B	374	HIS	-	expression tag	UNP Q5ZSV0
B	375	HIS	-	expression tag	UNP Q5ZSV0
B	376	HIS	-	expression tag	UNP Q5ZSV0

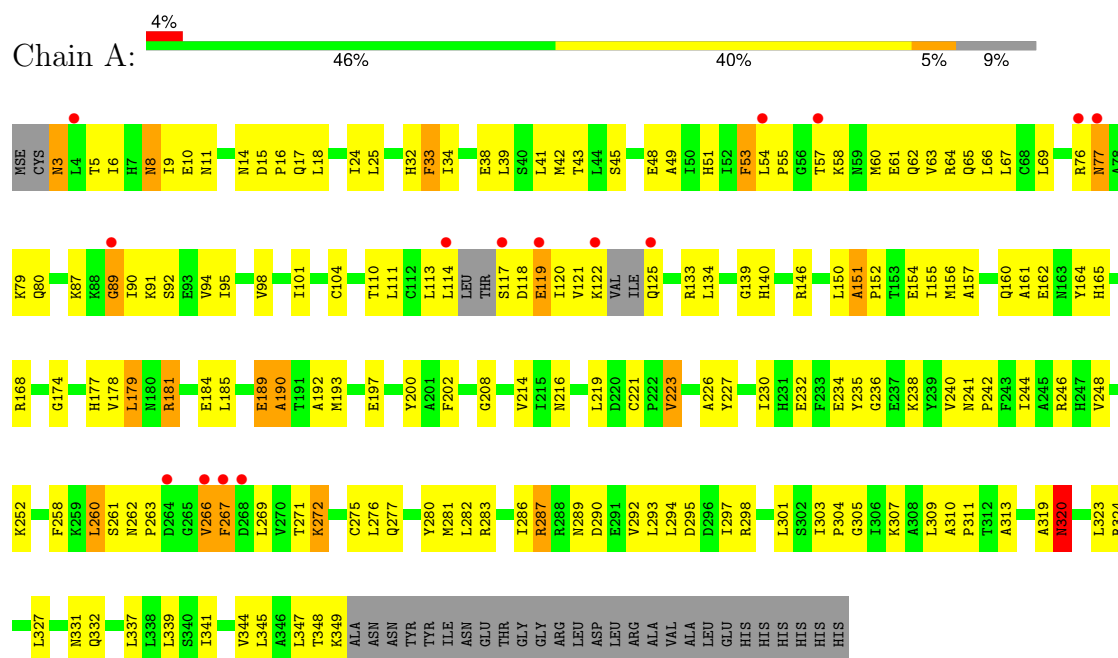
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	47	Total O 47 47	0	0
2	B	92	Total O 92 92	0	0

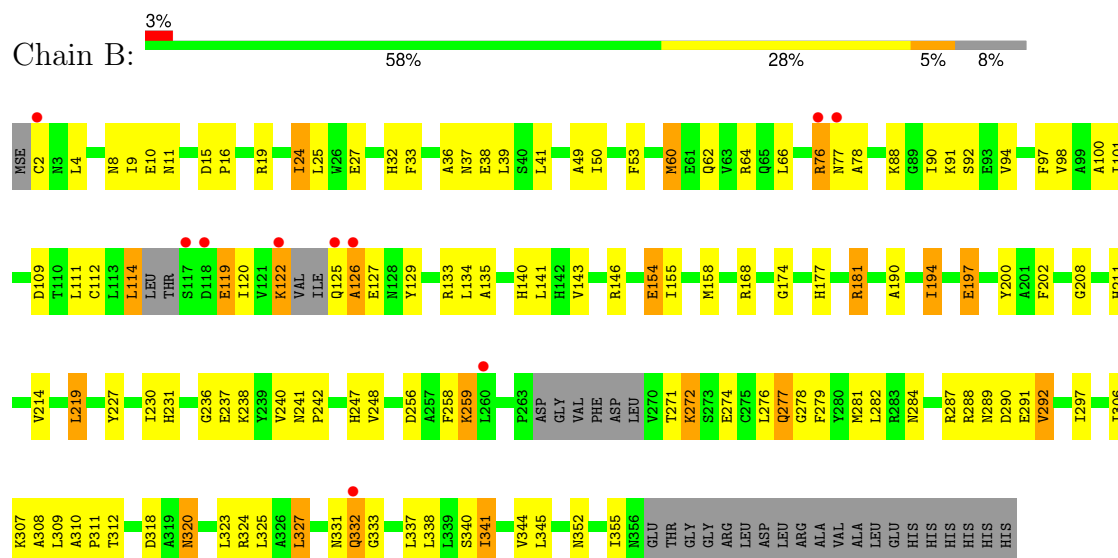
3 Residue-property plots

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: ankyrin repeat family protein



• Molecule 1: ankyrin repeat family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.61Å 90.46Å 118.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.92 – 2.80 19.92 – 2.81	Depositor EDS
% Data completeness (in resolution range)	92.2 (19.92-2.80) 97.1 (19.92-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.65 (at 2.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.221 , 0.286 0.240 , 0.302	Depositor DCC
R_{free} test set	1069 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 33.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5644	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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 [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	0.38	0/2793	0.61	0/3775
1	B	0.43	0/2814	0.61	1/3803 (0.0%)
All	All	0.40	0/5607	0.61	1/7578 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	126	ALA	N-CA-C	-5.70	95.61	111.00

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	2742	0	2737	166	0
1	B	2763	0	2753	106	0
2	A	47	0	0	3	0
2	B	92	0	0	8	0
All	All	5644	0	5490	265	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 24.

All (265) 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:272:LYS:H	1:A:272:LYS:HD3	1.16	1.08
1:B:146:ARG:NH1	2:B:466:HOH:O	1.90	1.02
1:A:287:ARG:HG2	1:A:287:ARG:HH11	1.29	0.97
1:A:208:GLY:HA2	1:B:24:ILE:HG12	1.46	0.97
1:A:62:GLN:NE2	1:A:91:LYS:H	1.68	0.91
1:A:62:GLN:HE22	1:A:91:LYS:N	1.68	0.90
1:B:97:PHE:HE1	1:B:126:ALA:HB1	1.36	0.90
1:B:92:SER:HB2	1:B:122:LYS:HD2	1.54	0.87
1:A:272:LYS:HD3	1:A:272:LYS:N	1.90	0.86
1:A:24:ILE:HG12	1:B:208:GLY:HA2	1.59	0.84
1:A:244:ILE:HD12	1:A:281:MSE:HG3	1.59	0.83
1:B:97:PHE:CE1	1:B:126:ALA:HB1	2.15	0.80
1:B:332:GLN:HA	1:B:332:GLN:HE21	1.46	0.80
1:A:269:LEU:HD23	1:A:303:ILE:HG21	1.62	0.79
1:A:113:LEU:O	1:A:114:LEU:HD12	1.82	0.79
1:A:121:VAL:HA	1:A:125:GLN:HE21	1.47	0.78
1:B:284:ASN:HD21	1:B:288:ARG:HE	1.32	0.77
1:A:121:VAL:HA	1:A:125:GLN:NE2	2.01	0.76
1:A:238:LYS:HG3	1:B:140:HIS:HE1	1.54	0.72
1:B:271:THR:OG1	1:B:274:GLU:HG3	1.89	0.72
1:B:307:LYS:HG3	2:B:458:HOH:O	1.88	0.71
1:A:62:GLN:HE22	1:A:91:LYS:H	0.84	0.71
1:A:10:GLU:CD	1:A:10:GLU:H	1.93	0.71
1:A:227:TYR:O	1:A:230:ILE:HG22	1.90	0.71
1:A:287:ARG:HH11	1:A:287:ARG:CG	2.02	0.70
1:B:338:LEU:O	1:B:341:ILE:HG23	1.91	0.70
1:A:113:LEU:HD12	1:A:114:LEU:HD12	1.74	0.70
1:B:309:LEU:HD12	1:B:312:THR:HG21	1.74	0.69
1:A:24:ILE:HD12	1:A:25:LEU:H	1.58	0.69
1:B:284:ASN:ND2	1:B:288:ARG:HE	1.91	0.69
1:B:50:ILE:O	1:B:88:LYS:HE3	1.93	0.68
1:A:104:CYS:HA	1:B:237:GLU:HG2	1.75	0.68
1:A:15:ASP:OD1	1:A:18:LEU:HB2	1.93	0.68
1:A:216:ASN:ND2	1:A:246:ARG:HH21	1.91	0.68
1:A:287:ARG:HG2	1:A:287:ARG:NH1	2.08	0.68
1:B:272:LYS:NZ	1:B:272:LYS:H	1.91	0.67
1:A:216:ASN:HD22	1:A:246:ARG:HH21	1.42	0.67
1:A:113:LEU:O	1:A:113:LEU:HD12	1.94	0.67
1:A:271:THR:HB	1:A:272:LYS:NZ	2.10	0.67
1:A:311:PRO:HA	1:A:320:ASN:ND2	2.09	0.67
1:A:241:ASN:HB2	1:A:242:PRO:HD3	1.75	0.66
1:A:119:GLU:HA	1:A:122:LYS:HG2	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:LEU:HD11	1:B:297:ILE:HG23	1.79	0.65
1:A:119:GLU:HG2	1:A:120:ILE:N	2.11	0.65
1:A:110:THR:O	1:A:113:LEU:HG	1.97	0.65
1:A:104:CYS:HA	1:B:237:GLU:CG	2.27	0.64
1:B:2:CYS:HB3	2:B:400:HOH:O	1.96	0.64
1:B:241:ASN:HB2	1:B:242:PRO:HD3	1.81	0.63
1:A:323:LEU:O	1:A:327:LEU:HG	1.98	0.63
1:B:119:GLU:O	1:B:122:LYS:HB2	1.98	0.62
1:B:129:TYR:CD2	1:B:158:MSE:HG2	2.34	0.62
1:A:236:GLY:HA2	1:A:240:VAL:HB	1.83	0.61
1:B:111:LEU:O	1:B:114:LEU:HB2	2.00	0.61
1:A:133:ARG:HH11	1:A:165:HIS:HD2	1.48	0.61
1:A:38:GLU:HG2	1:A:65:GLN:HG2	1.83	0.60
1:A:156:MSE:O	1:A:160:GLN:HG2	2.00	0.60
1:A:258:PHE:C	1:A:260:LEU:H	2.04	0.60
1:A:133:ARG:HD2	1:A:165:HIS:HD2	1.66	0.60
1:A:140:HIS:HE1	1:B:238:LYS:HG3	1.67	0.60
1:A:277:GLN:HG2	1:A:281:MSE:HE3	1.82	0.60
1:A:258:PHE:CZ	1:A:266:VAL:HG12	2.37	0.59
1:A:92:SER:HB3	1:A:122:LYS:NZ	2.17	0.59
1:B:227:TYR:O	1:B:231:HIS:HD2	1.85	0.59
1:A:24:ILE:HD12	1:A:25:LEU:N	2.17	0.59
1:A:290:ASP:OD1	1:A:292:VAL:HG22	2.03	0.59
1:B:292:VAL:HG22	1:B:292:VAL:O	2.03	0.58
1:A:113:LEU:C	1:A:114:LEU:HD12	2.23	0.58
1:B:62:GLN:HB3	1:B:94:VAL:HG11	1.85	0.58
1:A:238:LYS:HG3	1:B:140:HIS:CE1	2.36	0.58
1:B:97:PHE:O	1:B:101:ILE:HG13	2.04	0.58
1:A:313:ALA:HB2	1:A:319:ALA:O	2.03	0.58
1:B:202:PHE:HE2	1:B:219:LEU:HD13	1.69	0.58
1:A:181:ARG:NE	1:A:185:LEU:HD21	2.19	0.57
1:A:216:ASN:HD22	1:A:246:ARG:NH2	2.02	0.57
1:B:332:GLN:HE21	1:B:332:GLN:CA	2.12	0.57
1:A:51:HIS:HA	2:A:399:HOH:O	2.03	0.57
1:A:118:ASP:O	1:A:122:LYS:HE3	2.05	0.57
1:A:168:ARG:HB3	1:A:200:TYR:CD2	2.40	0.57
1:A:292:VAL:HG23	1:A:293:LEU:HD12	1.87	0.57
1:B:100:ALA:O	1:B:140:HIS:HD2	1.87	0.57
1:A:55:PRO:HG3	1:A:89:GLY:HA3	1.86	0.57
1:A:298:ARG:HG2	1:A:337:LEU:HD11	1.87	0.57
1:A:91:LYS:HB2	1:A:94:VAL:HG23	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ARG:CG	1:A:287:ARG:NH1	2.64	0.56
1:A:39:LEU:O	1:A:39:LEU:HD23	2.06	0.56
1:B:277:GLN:O	1:B:281:MSE:HG3	2.06	0.56
1:A:101:ILE:HD11	1:A:134:LEU:HD13	1.87	0.56
1:B:190:ALA:O	1:B:194:ILE:HG23	2.06	0.56
1:A:190:ALA:HA	1:A:193:MSE:HE3	1.88	0.56
1:B:202:PHE:HE2	1:B:219:LEU:CD1	2.19	0.56
1:A:286:ILE:HG23	1:A:331:ASN:OD1	2.07	0.55
1:B:37:ASN:ND2	2:B:409:HOH:O	2.38	0.55
1:A:5:THR:HG22	1:A:33:PHE:HB2	1.89	0.55
1:A:133:ARG:HD2	1:A:165:HIS:CD2	2.42	0.55
1:A:66:LEU:HD23	1:A:98:VAL:HG21	1.88	0.54
1:B:66:LEU:HD23	1:B:98:VAL:HG21	1.89	0.54
1:B:122:LYS:O	1:B:126:ALA:HB2	2.08	0.54
1:A:345:LEU:O	1:A:348:THR:HG22	2.07	0.54
1:A:146:ARG:O	1:A:150:LEU:HG	2.08	0.54
1:B:271:THR:HA	1:B:272:LYS:HZ2	1.73	0.53
1:A:58:LYS:O	1:A:61:GLU:HB2	2.08	0.53
1:B:125:GLN:O	1:B:127:GLU:N	2.41	0.53
1:A:269:LEU:CD2	1:A:303:ILE:HG21	2.37	0.53
1:A:24:ILE:HD12	1:A:25:LEU:HG	1.90	0.52
1:B:15:ASP:O	1:B:19:ARG:HG2	2.08	0.52
1:A:258:PHE:CE2	1:A:266:VAL:O	2.63	0.52
1:A:310:ALA:N	1:A:311:PRO:HD2	2.24	0.52
1:B:352:ASN:HB3	1:B:355:ILE:HG22	1.92	0.52
1:A:48:GLU:O	1:A:51:HIS:HB3	2.09	0.52
1:B:154:GLU:O	1:B:158:MSE:HG3	2.09	0.52
1:A:320:ASN:OD1	1:A:344:VAL:HG13	2.10	0.52
1:A:98:VAL:HG12	1:A:98:VAL:O	2.10	0.51
1:B:355:ILE:HG23	1:B:355:ILE:O	2.10	0.51
1:B:278:GLY:HA3	1:B:306:ILE:HD11	1.91	0.51
1:A:63:VAL:HG22	1:A:94:VAL:HG13	1.92	0.51
1:B:19:ARG:NH1	2:B:446:HOH:O	2.43	0.51
1:A:258:PHE:HE2	1:A:266:VAL:H	1.58	0.51
1:B:100:ALA:HA	1:B:143:VAL:HG11	1.93	0.51
1:A:275:CYS:HB3	1:A:305:GLY:O	2.10	0.50
1:A:307:LYS:HD2	1:A:341:ILE:HD12	1.92	0.50
1:A:262:ASN:N	1:A:263:PRO:HD3	2.27	0.50
1:B:333:GLY:O	1:B:337:LEU:HG	2.11	0.50
1:B:141:LEU:HD11	1:B:181:ARG:HG2	1.92	0.50
1:A:174:GLY:HA2	1:A:214:VAL:HG21	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:THR:HA	1:A:32:HIS:O	2.12	0.50
1:A:276:LEU:HD23	1:A:309:LEU:HD21	1.93	0.50
1:A:282:LEU:CD1	1:A:297:ILE:HG23	2.42	0.49
1:B:177:HIS:CD2	1:B:177:HIS:H	2.29	0.49
1:B:282:LEU:CD1	1:B:297:ILE:HG23	2.42	0.49
1:A:8:ASN:OD1	1:A:11:ASN:HB2	2.12	0.49
1:A:53:PHE:HZ	1:A:90:ILE:HD11	1.78	0.49
1:A:164:TYR:CE1	1:A:189:GLU:HG3	2.48	0.49
1:B:284:ASN:ND2	1:B:288:ARG:HH21	2.11	0.49
1:A:113:LEU:HD12	1:A:114:LEU:CD1	2.43	0.49
1:A:181:ARG:HA	1:A:184:GLU:OE2	2.13	0.48
1:A:277:GLN:O	1:A:281:MSE:HB2	2.13	0.48
1:B:168:ARG:HB3	1:B:200:TYR:CD2	2.47	0.48
1:A:323:LEU:HD12	1:A:344:VAL:CG1	2.44	0.48
1:B:92:SER:HB2	1:B:122:LYS:CD	2.37	0.48
1:B:241:ASN:N	1:B:241:ASN:HD22	2.11	0.48
1:B:119:GLU:HG3	1:B:120:ILE:N	2.27	0.48
1:B:49:ALA:O	1:B:53:PHE:HB2	2.13	0.48
1:A:6:ILE:O	1:A:32:HIS:HB3	2.13	0.48
1:A:67:LEU:HD23	1:A:98:VAL:HG13	1.94	0.48
1:A:267:PHE:O	1:A:304:PRO:HD2	2.13	0.48
1:B:141:LEU:HD11	1:B:181:ARG:CG	2.42	0.48
1:B:8:ASN:HB2	1:B:11:ASN:HD22	1.78	0.47
1:B:60:MSE:HE2	1:B:60:MSE:HA	1.96	0.47
1:A:303:ILE:HG22	1:A:305:GLY:H	1.78	0.47
1:A:267:PHE:O	1:A:303:ILE:HG23	2.15	0.47
1:B:290:ASP:OD2	1:B:292:VAL:HG12	2.14	0.47
1:B:91:LYS:HB2	1:B:94:VAL:HG23	1.97	0.47
1:B:310:ALA:N	1:B:311:PRO:HD2	2.30	0.47
1:A:244:ILE:O	1:A:248:VAL:HG23	2.15	0.47
1:B:101:ILE:HG12	1:B:134:LEU:HD22	1.97	0.47
1:B:320:ASN:HD21	1:B:344:VAL:HG13	1.79	0.47
1:A:242:PRO:O	1:A:246:ARG:HB2	2.14	0.47
1:A:139:GLY:HA2	1:A:178:VAL:HG21	1.97	0.46
1:B:307:LYS:HD3	1:B:341:ILE:HD12	1.96	0.46
1:B:320:ASN:ND2	1:B:344:VAL:HG13	2.30	0.46
1:A:232:GLU:O	1:A:235:TYR:O	2.32	0.46
1:B:287:ARG:HB2	1:B:325:LEU:HD21	1.98	0.46
1:A:17:GLN:HB3	1:A:42:MSE:HE2	1.97	0.46
1:A:17:GLN:NE2	1:A:43:THR:HG22	2.30	0.46
1:B:62:GLN:OE1	1:B:90:ILE:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:LYS:O	1:A:276:LEU:HG	2.16	0.46
1:B:174:GLY:HA2	1:B:214:VAL:HG21	1.98	0.46
1:B:272:LYS:H	1:B:272:LYS:HZ2	1.62	0.46
1:B:272:LYS:H	1:B:272:LYS:HZ3	1.61	0.46
1:A:151:ALA:N	1:A:152:PRO:HD3	2.31	0.46
1:A:282:LEU:HD11	1:A:297:ILE:HG23	1.97	0.46
2:A:379:HOH:O	1:B:211:HIS:HD2	1.97	0.46
1:B:38:GLU:HA	1:B:41:LEU:HD23	1.97	0.46
1:A:24:ILE:H	1:A:24:ILE:HG13	1.56	0.46
1:A:177:HIS:H	1:A:177:HIS:CD2	2.34	0.45
1:A:292:VAL:HG23	1:A:293:LEU:CD1	2.46	0.45
1:A:280:TYR:HD1	1:A:283:ARG:CZ	2.30	0.45
1:B:320:ASN:HD22	1:B:320:ASN:HA	1.60	0.45
1:A:92:SER:HB3	1:A:122:LYS:HE2	1.99	0.45
1:A:310:ALA:N	1:A:311:PRO:CD	2.79	0.45
1:A:160:GLN:HA	1:A:164:TYR:CD1	2.52	0.45
1:A:234:GLU:HB3	1:A:235:TYR:CE1	2.51	0.45
1:A:271:THR:HB	1:A:272:LYS:HZ2	1.79	0.45
1:B:9:ILE:HG23	1:B:10:GLU:N	2.32	0.45
1:A:49:ALA:O	1:A:53:PHE:HB2	2.17	0.45
1:A:248:VAL:HG12	1:A:252:LYS:HE3	1.98	0.45
1:A:282:LEU:O	1:A:286:ILE:HG13	2.17	0.45
1:B:66:LEU:HD23	1:B:98:VAL:CG2	2.47	0.45
1:B:109:ASP:O	1:B:112:CYS:HB2	2.17	0.45
1:B:284:ASN:HD22	1:B:288:ARG:HH21	1.64	0.45
1:A:152:PRO:O	1:A:155:ILE:HG13	2.17	0.44
1:B:100:ALA:HB1	1:B:135:ALA:HB2	1.98	0.44
1:B:241:ASN:N	1:B:241:ASN:ND2	2.65	0.44
1:A:272:LYS:H	1:A:272:LYS:CD	2.02	0.44
1:B:27:GLU:HG2	1:B:32:HIS:CE1	2.53	0.44
1:B:37:ASN:O	1:B:41:LEU:HD22	2.17	0.44
1:B:197:GLU:HB3	1:B:200:TYR:HB2	1.98	0.44
1:B:308:ALA:HB2	2:B:394:HOH:O	2.16	0.44
1:A:64:ARG:HB3	1:A:64:ARG:NH1	2.32	0.44
1:A:277:GLN:HG2	1:A:281:MSE:CE	2.46	0.44
1:B:318:ASP:CG	1:B:324:ARG:HH22	2.21	0.44
1:A:223:VAL:O	1:A:226:ALA:HB3	2.18	0.44
1:B:279:PHE:HB2	1:B:309:LEU:HD23	2.00	0.44
1:A:95:ILE:HB	1:A:111:LEU:HD11	1.99	0.43
1:A:181:ARG:HD3	1:A:185:LEU:HG	2.01	0.43
1:A:6:ILE:HG23	1:A:8:ASN:OD1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:GLU:HG2	2:A:383:HOH:O	2.18	0.43
1:A:92:SER:HB3	1:A:122:LYS:CE	2.48	0.43
1:B:4:LEU:O	1:B:33:PHE:HA	2.18	0.43
1:B:66:LEU:HB3	1:B:98:VAL:HG21	2.00	0.43
1:A:15:ASP:CG	1:A:18:LEU:HB2	2.38	0.43
1:A:24:ILE:CD1	1:A:25:LEU:HG	2.48	0.43
1:A:156:MSE:HG3	1:A:160:GLN:HE21	1.83	0.43
1:A:189:GLU:O	1:A:192:ALA:HB3	2.18	0.43
1:A:8:ASN:CG	1:A:11:ASN:HD22	2.22	0.43
1:A:63:VAL:CG2	1:A:94:VAL:HG13	2.48	0.43
1:A:258:PHE:CE2	1:A:266:VAL:HG12	2.54	0.43
1:B:323:LEU:O	1:B:327:LEU:HD22	2.18	0.43
1:A:62:GLN:NE2	1:A:90:ILE:HA	2.34	0.43
1:B:324:ARG:HD2	2:B:379:HOH:O	2.19	0.43
1:B:240:VAL:HG21	2:B:413:HOH:O	2.19	0.43
1:A:202:PHE:HE2	1:A:219:LEU:HD21	1.83	0.42
1:A:271:THR:HB	1:A:272:LYS:HZ1	1.81	0.42
1:B:15:ASP:HA	1:B:16:PRO:HD3	1.93	0.42
1:B:341:ILE:HG12	1:B:344:VAL:HG23	2.01	0.42
1:A:14:ASN:O	1:A:16:PRO:HD3	2.19	0.42
1:A:261:SER:C	1:A:263:PRO:HD3	2.39	0.42
1:B:259:LYS:NZ	1:B:259:LYS:HB3	2.34	0.42
1:A:45:SER:OG	1:A:48:GLU:HG3	2.19	0.42
1:A:221:CYS:SG	1:A:223:VAL:HG23	2.60	0.42
1:A:118:ASP:C	1:A:121:VAL:HG12	2.39	0.42
1:A:119:GLU:HA	1:A:122:LYS:CG	2.46	0.42
1:A:157:ALA:O	1:A:161:ALA:HB2	2.19	0.42
1:B:60:MSE:O	1:B:64:ARG:HG3	2.19	0.42
1:B:318:ASP:OD2	1:B:324:ARG:NH2	2.52	0.42
1:A:307:LYS:CD	1:A:341:ILE:HD12	2.49	0.42
1:A:54:LEU:HD23	1:A:55:PRO:HD2	2.02	0.42
1:A:174:GLY:HA2	1:A:214:VAL:CG2	2.49	0.42
1:A:119:GLU:C	1:A:121:VAL:H	2.24	0.41
1:A:307:LYS:HG3	1:A:341:ILE:HD12	2.02	0.41
1:A:339:LEU:HD12	1:A:339:LEU:N	2.35	0.41
1:B:289:ASN:HA	1:B:331:ASN:ND2	2.35	0.41
1:A:77:ASN:C	1:A:79:LYS:H	2.23	0.41
1:A:301:LEU:O	1:A:307:LYS:HD3	2.20	0.41
1:B:155:ILE:HA	1:B:158:MSE:HE2	2.02	0.41
1:B:227:TYR:O	1:B:230:ILE:HG22	2.20	0.41
1:A:41:LEU:HB3	1:A:69:LEU:CD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:PHE:CE2	1:A:219:LEU:HD21	2.56	0.41
1:A:117:SER:HA	1:A:120:ILE:HG12	2.02	0.41
1:A:303:ILE:HA	1:A:304:PRO:HD3	1.93	0.41
1:A:298:ARG:HG2	1:A:337:LEU:CD1	2.51	0.41
1:A:349:LYS:HE3	1:A:349:LYS:HB2	1.94	0.41
1:B:256:ASP:C	1:B:258:PHE:N	2.73	0.41
1:A:3:ASN:HB2	1:A:34:ILE:O	2.19	0.41
1:A:168:ARG:HD2	1:A:200:TYR:HB3	2.03	0.41
1:A:179:LEU:CD2	1:A:214:VAL:HG13	2.51	0.41
1:A:301:LEU:O	1:A:307:LYS:HB2	2.21	0.41
1:B:76:ARG:O	1:B:78:ALA:N	2.54	0.41
1:B:219:LEU:HD12	1:B:219:LEU:HA	1.88	0.41
1:A:9:ILE:HG23	1:A:10:GLU:N	2.36	0.40
1:A:164:TYR:O	1:A:168:ARG:HG3	2.21	0.40
1:B:247:HIS:O	1:B:248:VAL:C	2.59	0.40
1:A:267:PHE:CD2	1:A:267:PHE:N	2.89	0.40
1:A:5:THR:HG22	1:A:33:PHE:CB	2.51	0.40
1:B:36:ALA:HA	1:B:39:LEU:HD12	2.03	0.40

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	337/376 (90%)	281 (83%)	47 (14%)	9 (3%)	4	15
1	B	337/376 (90%)	308 (91%)	25 (7%)	4 (1%)	11	34
All	All	674/752 (90%)	589 (87%)	72 (11%)	13 (2%)	6	23

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	GLU
1	B	77	ASN
1	A	320	ASN
1	B	236	GLY
1	A	53	PHE
1	A	77	ASN
1	A	89	GLY
1	A	190	ALA
1	A	87	LYS
1	A	289	ASN
1	B	291	GLU
1	B	292	VAL
1	A	151	ALA

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	292/311 (94%)	268 (92%)	24 (8%)	9	29
1	B	294/311 (94%)	271 (92%)	23 (8%)	10	31
All	All	586/622 (94%)	539 (92%)	47 (8%)	10	30

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	8	ASN
1	A	33	PHE
1	A	57	THR
1	A	60	MSE
1	A	76	ARG
1	A	80	GLN
1	A	119	GLU
1	A	162	GLU
1	A	179	LEU
1	A	181	ARG

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Mol	Chain	Res	Type
1	A	189	GLU
1	A	223	VAL
1	A	260	LEU
1	A	266	VAL
1	A	267	PHE
1	A	272	LYS
1	A	287	ARG
1	A	294	LEU
1	A	295	ASP
1	A	320	ASN
1	A	324	ARG
1	A	332	GLN
1	A	347	LEU
1	B	24	ILE
1	B	25	LEU
1	B	60	MSE
1	B	76	ARG
1	B	114	LEU
1	B	119	GLU
1	B	122	LYS
1	B	133	ARG
1	B	154	GLU
1	B	181	ARG
1	B	194	ILE
1	B	197	GLU
1	B	219	LEU
1	B	259	LYS
1	B	272	LYS
1	B	276	LEU
1	B	277	GLN
1	B	320	ASN
1	B	327	LEU
1	B	332	GLN
1	B	340	SER
1	B	341	ILE
1	B	345	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	11	ASN

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Mol	Chain	Res	Type
1	A	14	ASN
1	A	28	ASN
1	A	32	HIS
1	A	62	GLN
1	A	80	GLN
1	A	125	GLN
1	A	160	GLN
1	A	165	HIS
1	A	177	HIS
1	A	180	ASN
1	A	211	HIS
1	A	216	ASN
1	A	231	HIS
1	A	255	HIS
1	A	277	GLN
1	A	284	ASN
1	A	320	ASN
1	B	8	ASN
1	B	11	ASN
1	B	32	HIS
1	B	37	ASN
1	B	140	HIS
1	B	160	GLN
1	B	177	HIS
1	B	211	HIS
1	B	216	ASN
1	B	231	HIS
1	B	241	ASN
1	B	249	ASN
1	B	284	ASN
1	B	320	ASN
1	B	332	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 [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	335/376 (89%)	0.24	15 (4%) 39 31	11, 45, 61, 61	0
1	B	337/376 (89%)	-0.27	10 (2%) 52 44	11, 24, 57, 61	0
All	All	672/752 (89%)	-0.02	25 (3%) 45 37	11, 33, 60, 61	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	125	GLN	5.3
1	B	126	ALA	4.0
1	B	117	SER	3.9
1	B	260	LEU	3.7
1	A	268	ASP	3.6
1	B	118	ASP	3.3
1	B	122	LYS	3.1
1	A	267	PHE	2.9
1	A	77	ASN	2.8
1	A	114	LEU	2.6
1	A	122	LYS	2.4
1	B	77	ASN	2.4
1	A	4	LEU	2.3
1	B	332	GLN	2.3
1	A	54	LEU	2.3
1	B	2	CYS	2.3
1	A	119	GLU	2.3
1	A	125	GLN	2.2
1	B	76	ARG	2.2
1	A	89	GLY	2.1
1	A	57	THR	2.1
1	A	76	ARG	2.1
1	A	266	VAL	2.1
1	A	264	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	117	SER	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 monosaccharides 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.