



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:48 PM UTC

PDB ID : 7K2F / pdb_00007k2f
Title : Kelch domain of human KEAP1 bound to Nrf2 cyclic peptide, c[GAEETGE]
Authors : Muellers, S.N.; Allen, K.N.
Deposited on : 2020-09-08
Resolution : 2.37 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

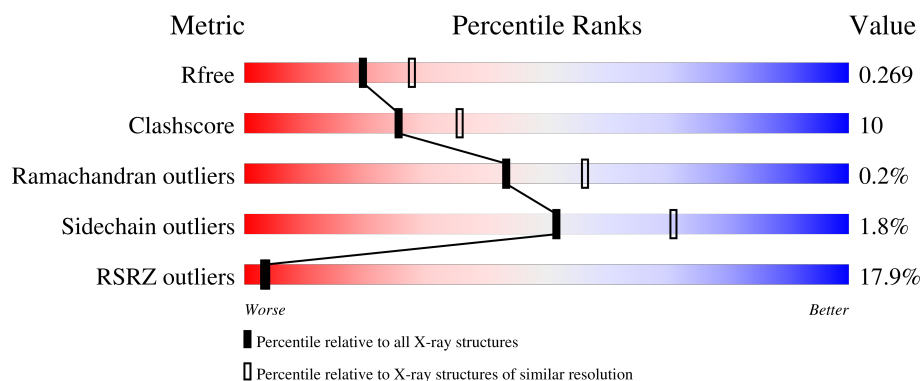
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	336	
1	X	336	
2	C	7	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4567 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 Kelch-like ECH-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	285	Total	C	N	O	S	0	17	0
			2260	1416	406	419	19			
1	A	285	Total	C	N	O	S	0	17	0
			2260	1416	406	419	19			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	289	MET	-	initiating methionine	UNP Q14145
X	290	GLY	-	expression tag	UNP Q14145
X	291	SER	-	expression tag	UNP Q14145
X	292	SER	-	expression tag	UNP Q14145
X	293	HIS	-	expression tag	UNP Q14145
X	294	HIS	-	expression tag	UNP Q14145
X	295	HIS	-	expression tag	UNP Q14145
X	296	HIS	-	expression tag	UNP Q14145
X	297	HIS	-	expression tag	UNP Q14145
X	298	HIS	-	expression tag	UNP Q14145
X	299	SER	-	expression tag	UNP Q14145
X	300	SER	-	expression tag	UNP Q14145
X	301	GLY	-	expression tag	UNP Q14145
X	302	GLY	-	expression tag	UNP Q14145
X	303	GLU	-	expression tag	UNP Q14145
X	304	ASN	-	expression tag	UNP Q14145
X	305	LEU	-	expression tag	UNP Q14145
X	306	TYR	-	expression tag	UNP Q14145
X	307	PHE	-	expression tag	UNP Q14145
X	308	GLN	-	expression tag	UNP Q14145
X	309	GLY	-	expression tag	UNP Q14145
X	310	HIS	-	expression tag	UNP Q14145
X	311	MET	-	expression tag	UNP Q14145
X	319	SER	CYS	conflict	UNP Q14145
X	613	SER	CYS	conflict	UNP Q14145

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Chain	Residue	Modelled	Actual	Comment	Reference
X	622	SER	CYS	conflict	UNP Q14145
X	624	SER	-	expression tag	UNP Q14145
A	289	MET	-	initiating methionine	UNP Q14145
A	290	GLY	-	expression tag	UNP Q14145
A	291	SER	-	expression tag	UNP Q14145
A	292	SER	-	expression tag	UNP Q14145
A	293	HIS	-	expression tag	UNP Q14145
A	294	HIS	-	expression tag	UNP Q14145
A	295	HIS	-	expression tag	UNP Q14145
A	296	HIS	-	expression tag	UNP Q14145
A	297	HIS	-	expression tag	UNP Q14145
A	298	HIS	-	expression tag	UNP Q14145
A	299	SER	-	expression tag	UNP Q14145
A	300	SER	-	expression tag	UNP Q14145
A	301	GLY	-	expression tag	UNP Q14145
A	302	GLY	-	expression tag	UNP Q14145
A	303	GLU	-	expression tag	UNP Q14145
A	304	ASN	-	expression tag	UNP Q14145
A	305	LEU	-	expression tag	UNP Q14145
A	306	TYR	-	expression tag	UNP Q14145
A	307	PHE	-	expression tag	UNP Q14145
A	308	GLN	-	expression tag	UNP Q14145
A	309	GLY	-	expression tag	UNP Q14145
A	310	HIS	-	expression tag	UNP Q14145
A	311	MET	-	expression tag	UNP Q14145
A	319	SER	CYS	conflict	UNP Q14145
A	613	SER	CYS	conflict	UNP Q14145
A	622	SER	CYS	conflict	UNP Q14145
A	624	SER	-	expression tag	UNP Q14145

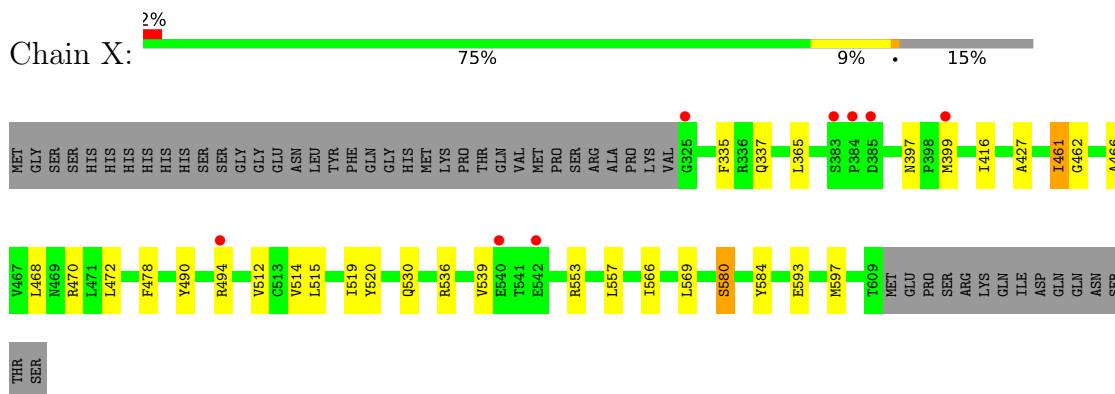
- Molecule 2 is a protein called Nrf2 cyclic peptide,c[GAEETGE].

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			47	26	7	14			

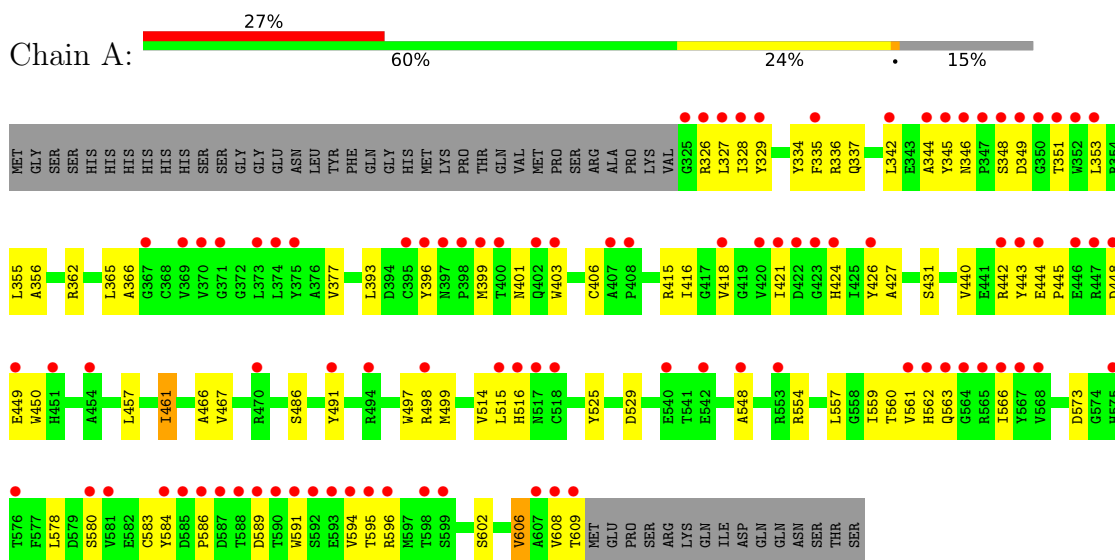
3 Residue-property plots [i](#)

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.

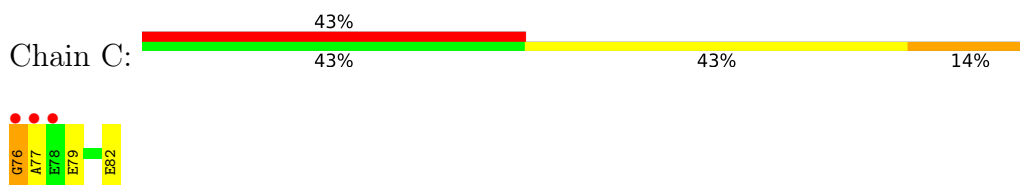
• Molecule 1: Kelch-like ECH-associated protein 1



• Molecule 1: Kelch-like ECH-associated protein 1



• Molecule 2: Nrf2 cyclic peptide,c[GAEETGE]



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	77.64Å 68.89Å 144.02Å 90.00° 90.95° 90.00°	Depositor
Resolution (Å)	27.15 – 2.37 27.15 – 2.37	Depositor EDS
% Data completeness (in resolution range)	98.8 (27.15-2.37) 98.7 (27.15-2.37)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 2.36Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.237 , 0.264 0.242 , 0.269	Depositor DCC
R_{free} test set	1982 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.404	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4567	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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, 0.333 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	0.19	0/2361	0.49	0/3215
1	X	0.18	0/2361	0.47	0/3215
2	C	2.75	2/46 (4.3%)	1.65	1/60 (1.7%)
All	All	0.33	2/4768 (0.0%)	0.50	1/6490 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	76	GLY	N-CA	14.80	1.69	1.45
2	C	82	GLU	CA-C	6.21	1.66	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	82	GLU	CA-C-O	-8.20	106.85	120.80

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	2260	0	2196	64	0
1	X	2260	0	2196	20	0
2	C	47	0	35	6	0
All	All	4567	0	4427	86	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 10.

All (86) 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)
2:C:76:GLY:N	2:C:76:GLY:CA	1.69	1.53
1:A:328:ILE:HG12	1:A:608:VAL:HG12	1.12	1.10
1:A:328:ILE:HG21	1:A:560:THR:HG21	1.60	0.84
1:A:328:ILE:CG1	1:A:608:VAL:HG12	2.04	0.83
1:A:328:ILE:HG12	1:A:608:VAL:CG1	2.06	0.82
1:A:491:TYR:HE2	1:A:498:ARG:HB2	1.44	0.81
1:A:486:SER:HB2	1:A:499[B]:MET:HE1	1.68	0.74
1:A:491:TYR:CE2	1:A:498:ARG:HB2	2.26	0.70
2:C:76:GLY:N	2:C:76:GLY:C	2.48	0.69
1:A:443:TYR:HA	1:A:449:GLU:O	1.93	0.69
1:A:466:ALA:HB1	1:A:514[B]:VAL:HG23	1.76	0.68
1:A:561:VAL:HG22	1:A:566:ILE:HG12	1.77	0.66
1:A:583:CYS:HB2	1:A:594:VAL:CG2	2.26	0.65
1:X:466:ALA:HB1	1:X:514[B]:VAL:HG23	1.79	0.65
1:A:393:LEU:HD23	1:A:406:CYS:HB2	1.79	0.63
1:A:329:TYR:CE1	1:A:609:THR:HG22	2.33	0.63
1:X:515:LEU:HD22	1:X:566:ILE:HG13	1.81	0.63
1:A:416:ILE:HD11	1:A:427:ALA:HB1	1.82	0.62
1:A:554:ARG:HG3	1:A:557:LEU:HD22	1.81	0.61
1:A:415:ARG:NH2	2:C:79:GLU:OE1	2.27	0.60
1:A:344:ALA:HB3	1:A:353:LEU:HB3	1.83	0.60
1:A:515:LEU:HD21	1:A:586:PRO:HG3	1.84	0.60
1:A:377:VAL:HG22	1:A:393:LEU:HD12	1.86	0.58
1:A:399:MET:HE3	1:A:399:MET:HA	1.87	0.57
2:C:76:GLY:N	2:C:77:ALA:N	2.53	0.56
1:A:584:TYR:OH	1:A:589:ASP:OD1	2.20	0.55
1:A:349:ASP:HB2	1:A:351:THR:OG1	2.09	0.53
1:A:595:THR:OG1	1:A:596:ARG:N	2.39	0.53
1:A:443:TYR:HB2	1:A:450:TRP:CD2	2.44	0.53
1:A:562:HIS:CD2	1:A:563[B]:GLN:HG2	2.44	0.53
1:A:326[B]:ARG:HB2	1:A:562:HIS:CE1	2.43	0.53
1:A:366:ALA:HB1	1:A:418:VAL:HG22	1.91	0.52
1:X:365:LEU:HD23	1:X:365:LEU:H	1.75	0.52
1:A:424:HIS:ND1	1:A:442:ARG:HD2	2.24	0.52
1:X:335:PHE:C	1:X:337:GLN:H	2.18	0.51
1:X:494:ARG:NH2	1:A:586:PRO:O	2.43	0.51
1:X:557:LEU:HD23	1:X:557:LEU:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:573:ASP:OD2	1:A:578:LEU:HD11	2.11	0.50
2:C:76:GLY:N	2:C:77:ALA:H	2.09	0.50
1:A:362:ARG:HG3	1:A:365:LEU:HD13	1.93	0.50
1:X:569:LEU:HD23	1:X:597[A]:MET:HE3	1.93	0.50
1:A:335:PHE:C	1:A:337:GLN:H	2.21	0.49
1:X:468:LEU:HD22	1:X:519:ILE:HG13	1.94	0.49
1:X:461[B]:ILE:HG23	1:X:478:PHE:O	2.13	0.49
1:A:444:GLU:O	1:A:448:ASP:N	2.46	0.48
1:X:580[B]:SER:OG	1:X:593:GLU:OE2	2.26	0.48
1:A:499[B]:MET:HE2	1:A:499[B]:MET:HB3	1.71	0.48
1:A:560:THR:HB	1:A:606[B]:VAL:HG22	1.95	0.48
1:X:397:ASN:OD1	1:X:399:MET:HE3	2.14	0.48
1:A:329:TYR:HB3	1:A:342:LEU:HD11	1.96	0.47
1:X:512:VAL:HA	1:X:520:TYR:O	2.15	0.47
1:X:519:ILE:O	1:X:536:ARG:HA	2.14	0.47
1:X:416:ILE:HD11	1:X:427:ALA:HB1	1.96	0.47
1:A:557:LEU:HD23	1:A:557:LEU:H	1.81	0.46
1:A:559:ILE:H	1:A:606[A]:VAL:HG21	1.81	0.46
1:A:457:LEU:CD2	1:A:497:TRP:CB	2.93	0.46
1:A:457:LEU:CD2	1:A:497:TRP:HB2	2.46	0.46
1:A:525:TYR:HB3	2:C:79:GLU:HG3	1.98	0.45
1:A:431:SER:HB3	1:A:461[B]:ILE:HG21	1.97	0.45
1:A:342:LEU:HD22	1:A:403:TRP:CZ2	2.52	0.45
1:A:355:LEU:HD13	1:A:396:TYR:OH	2.17	0.45
1:A:345:TYR:CE2	1:A:595:THR:HG21	2.52	0.44
1:A:421:ILE:HG22	1:A:467:VAL:HG11	1.99	0.44
1:X:461[B]:ILE:HG13	1:X:462:GLY:N	2.32	0.44
1:A:342:LEU:HB3	1:A:356:ALA:O	2.17	0.44
1:A:327:LEU:HD22	1:A:346:ASN:CB	2.47	0.44
1:A:329:TYR:HE1	1:A:609:THR:HG22	1.76	0.44
1:A:442:ARG:CZ	1:A:442:ARG:HB3	2.44	0.44
1:X:472:LEU:HB3	1:X:490:TYR:HB3	1.99	0.44
1:X:566:ILE:HB	1:X:584:TYR:HB3	2.00	0.43
1:A:548:ALA:O	1:A:591:TRP:NE1	2.51	0.43
1:A:328:ILE:CG2	1:A:560:THR:HG21	2.41	0.42
1:A:562:HIS:NE2	1:A:563[B]:GLN:HG2	2.34	0.42
1:A:348[B]:SER:OG	1:A:349:ASP:OD1	2.36	0.42
1:A:334:TYR:N	1:A:602:SER:O	2.53	0.42
1:X:515:LEU:HB3	1:X:520:TYR:CE1	2.55	0.42
1:A:443:TYR:HB2	1:A:450:TRP:CE2	2.55	0.41
1:A:457:LEU:CD2	1:A:497:TRP:HB3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:VAL:HG21	1:A:497:TRP:HZ2	1.85	0.41
1:A:421:ILE:HG12	1:A:426:TYR:HE2	1.86	0.41
1:X:470[A]:ARG:HH12	1:A:516:HIS:HD2	1.69	0.41
1:A:326[A]:ARG:HB2	1:A:562:HIS:CE1	2.56	0.41
1:A:396:TYR:CE1	1:A:401:ASN:HA	2.56	0.41
1:A:562:HIS:CD2	1:A:563[A]:GLN:H	2.38	0.40
1:A:418:VAL:HA	1:A:426:TYR:O	2.22	0.40
1:X:530:GLN:HB2	1:X:553[A]:ARG:HG3	2.02	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	300/336 (89%)	284 (95%)	15 (5%)	1 (0%)	36	48
1	X	300/336 (89%)	294 (98%)	6 (2%)	0	100	100
2	C	5/7 (71%)	5 (100%)	0	0	100	100
All	All	605/679 (89%)	583 (96%)	21 (4%)	1 (0%)	43	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	445	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	243/277 (88%)	233 (96%)	10 (4%)	27	43
1	X	243/277 (88%)	237 (98%)	6 (2%)	42	61
2	C	4/4 (100%)	4 (100%)	0	100	100
All	All	490/558 (88%)	474 (97%)	16 (3%)	51	52

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	461[A]	ILE
1	X	461[B]	ILE
1	X	539[A]	VAL
1	X	539[B]	VAL
1	X	580[A]	SER
1	X	580[B]	SER
1	A	336[A]	ARG
1	A	336[B]	ARG
1	A	461[A]	ILE
1	A	461[B]	ILE
1	A	529[A]	ASP
1	A	529[B]	ASP
1	A	580[A]	SER
1	A	580[B]	SER
1	A	606[A]	VAL
1	A	606[B]	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	424	HIS
1	X	575	HIS
1	A	359	GLN
1	A	516	HIS
1	A	517	ASN

5.3.3 RNA ⓘ

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	285/336 (84%)	1.47	92 (32%) 1 1	13, 48, 89, 112	17 (5%)
1	X	285/336 (84%)	0.05	8 (2%) 55 54	10, 21, 39, 72	17 (5%)
2	C	7/7 (100%)	1.42	3 (42%) 0 0	29, 31, 56, 59	0
All	All	577/679 (84%)	0.77	103 (17%) 3 3	10, 28, 82, 112	34 (5%)

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	347	PRO	6.1
1	A	595	THR	6.0
1	A	329	TYR	5.8
1	A	325	GLY	5.2
1	A	423	GLY	5.2
1	A	344	ALA	5.0
1	A	346	ASN	4.8
1	A	353	LEU	4.8
1	A	350	GLY	4.7
1	A	373	LEU	4.7
1	A	447	ARG	4.6
1	A	326[A]	ARG	4.5
1	A	352	TRP	4.4
1	A	371	GLY	4.4
1	A	553[A]	ARG	4.3
1	A	446	GLU	4.3
1	A	575	HIS	4.2
1	A	399	MET	4.2
1	A	422	ASP	4.2
1	A	421	ILE	4.1
1	A	498	ARG	4.0
1	A	587	ASP	4.0
1	A	609	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	X	542	GLU	3.8
1	A	345	TYR	3.7
1	A	517	ASN	3.6
1	A	563[A]	GLN	3.6
1	A	591	TRP	3.6
1	A	590	THR	3.6
1	A	608	VAL	3.6
1	A	348[A]	SER	3.4
1	A	594	VAL	3.4
1	A	351	THR	3.3
1	A	561	VAL	3.3
1	A	397	ASN	3.2
1	A	369	VAL	3.2
2	C	76	GLY	3.2
1	A	327	LEU	3.2
1	A	424	HIS	3.2
1	A	420	VAL	3.1
1	A	426	TYR	3.1
1	A	562	HIS	3.1
2	C	77	ALA	3.1
1	A	494	ARG	3.0
1	A	407	ALA	3.0
1	X	540	GLU	3.0
1	A	516	HIS	3.0
1	A	589	ASP	3.0
1	A	540	GLU	3.0
1	A	400	THR	3.0
1	A	518	CYS	3.0
1	A	349	ASP	3.0
1	A	515	LEU	2.9
1	A	576	THR	2.9
1	A	585	ASP	2.9
1	A	581	VAL	2.9
1	A	328	ILE	2.9
1	A	592	SER	2.9
1	A	565	ARG	2.9
1	A	588	THR	2.9
1	A	599	SER	2.9
1	A	491	TYR	2.9
1	A	596	ARG	2.8
1	A	398	PRO	2.8
1	A	593	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	470[A]	ARG	2.8
1	A	567	TYR	2.8
1	X	399	MET	2.7
1	A	342	LEU	2.7
1	A	448	ASP	2.7
1	A	444	GLU	2.7
1	A	584	TYR	2.7
1	A	370	VAL	2.7
1	A	367	GLY	2.7
1	A	408	PRO	2.6
1	A	374	LEU	2.6
1	A	542	GLU	2.6
1	A	607	ALA	2.6
1	A	454	ALA	2.5
1	X	384	PRO	2.5
1	X	383	SER	2.5
1	A	449	GLU	2.5
1	A	580[A]	SER	2.4
1	A	564	GLY	2.4
1	A	375	TYR	2.4
1	A	548	ALA	2.4
1	A	451	HIS	2.3
1	X	325	GLY	2.3
1	A	566	ILE	2.3
1	A	442	ARG	2.2
1	X	385	ASP	2.2
1	A	402	GLN	2.2
1	A	395	CYS	2.2
1	A	598	THR	2.1
1	A	396	TYR	2.1
1	A	443	TYR	2.1
2	C	78	GLU	2.1
1	A	418	VAL	2.1
1	A	586	PRO	2.1
1	X	494	ARG	2.1
1	A	403	TRP	2.1
1	A	568	VAL	2.0
1	A	335	PHE	2.0

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

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.