



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:59 AM UTC

PDB ID : 7K2H / pdb_00007k2h
Title : Kelch domain of human KEAP1 bound to Nrf2 cyclic peptide, c[GDPETGE]
Authors : Muellers, S.N.; Allen, K.N.
Deposited on : 2020-09-08
Resolution : 2.09 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

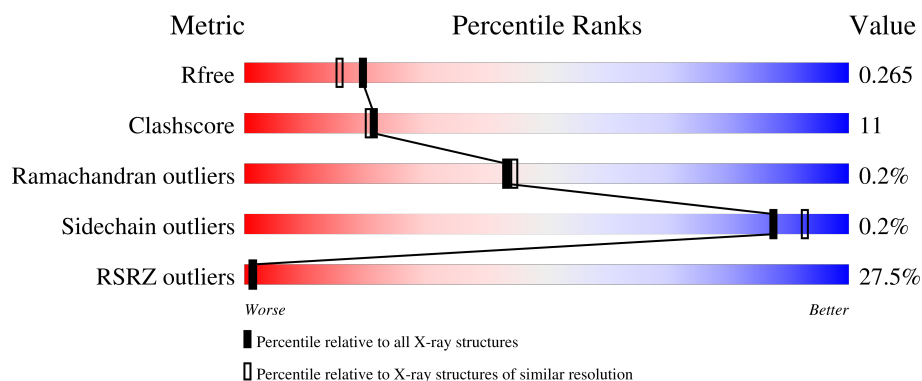
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	301	6% 83% 12% .
1	B	301	47% 68% 26% 6%
2	P	7	71% 29%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4652 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	A	288	Total	C	N	O	S	0	0	0
			2211	1375	400	420	16			
1	B	283	Total	C	N	O	S	0	0	0
			2158	1343	392	408	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	613	SER	CYS	conflict	UNP Q14145
B	613	SER	CYS	conflict	UNP Q14145

- Molecule 2 is a protein called GLY-ASP-PRO-GLU-THR-GLY-GLU.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	0	0	0
			48	27	7	14			

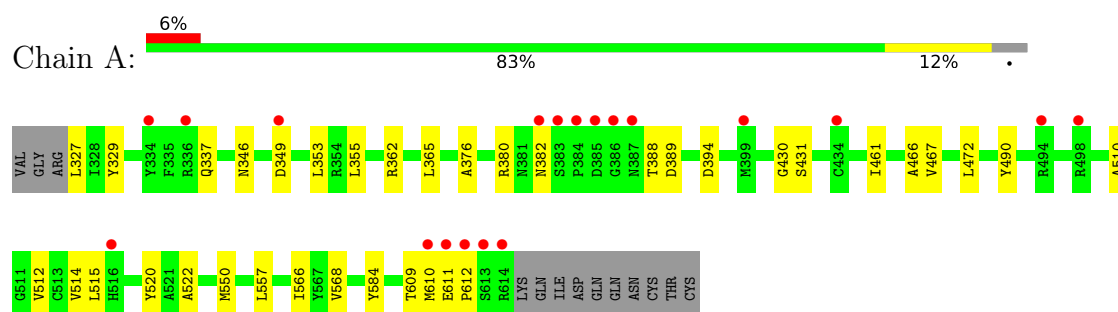
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	168	Total	O	0	0
			168	168		
3	B	64	Total	O	0	0
			64	64		
3	P	3	Total	O	0	0
			3	3		

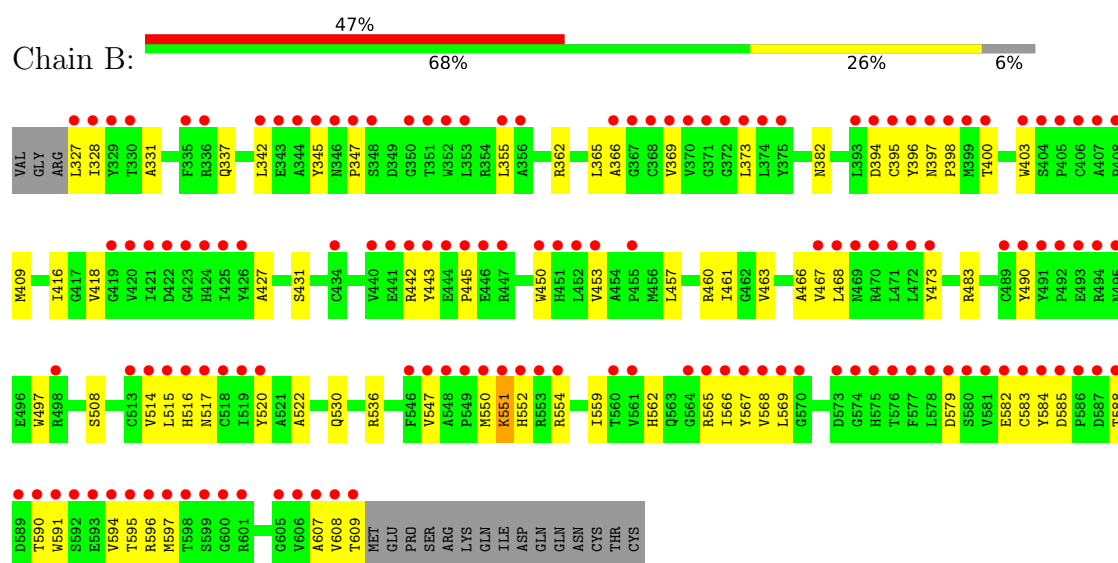
3 Residue-property plots [i](#)

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.

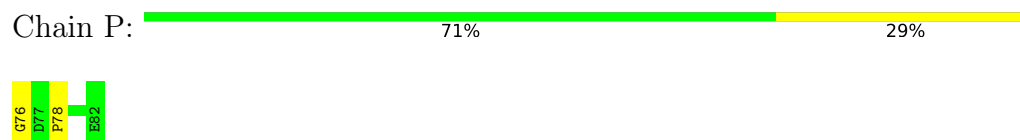
• Molecule 1: Kelch-like ECH-associated protein 1



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



• Molecule 2: GLY-ASP-PRO-GLU-THR-GLY-GLU



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.24Å 68.60Å 77.27Å 90.00° 117.74° 90.00°	Depositor
Resolution (Å)	27.67 – 2.09 27.67 – 2.09	Depositor EDS
% Data completeness (in resolution range)	97.8 (27.67-2.09) 97.7 (27.67-2.09)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.05 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.225 , 0.265 0.226 , 0.265	Depositor DCC
R_{free} test set	1992 reflections (4.47%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4652	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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

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	0.43	1/2265 (0.0%)	0.62	1/3085 (0.0%)
1	B	0.37	0/2210	0.58	0/3012
2	P	0.30	0/48	1.15	1/64 (1.6%)
All	All	0.40	1/4523 (0.0%)	0.61	2/6161 (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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	510	ALA	C-N	8.35	1.39	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	76	GLY	O-C-N	-7.75	110.60	123.00
1	A	337	GLN	N-CA-C	-6.84	98.25	108.99

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	551	LYS	Peptide

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	2211	0	2100	32	0
1	B	2158	0	2046	62	0
2	P	48	0	35	1	0
3	A	168	0	0	0	0
3	B	64	0	0	0	0
3	P	3	0	0	0	0
All	All	4652	0	4181	94	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 11.

All (94) 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:327:LEU:HD11	1:A:611:GLU:HG3	1.44	0.97
1:A:522:ALA:HB1	1:A:550:MET:HE3	1.55	0.86
1:B:328:ILE:HG12	1:B:608:VAL:HG12	1.60	0.82
1:B:466:ALA:HB1	1:B:514:VAL:HG23	1.61	0.81
1:B:515:LEU:HD22	1:B:566:ILE:HG13	1.63	0.80
1:A:327:LEU:CD1	1:A:611:GLU:HG3	2.15	0.76
1:A:329:TYR:CE1	1:A:609:THR:HG22	2.24	0.71
1:A:466:ALA:HB1	1:A:514:VAL:HG23	1.72	0.71
1:A:550:MET:CE	1:A:568:VAL:HG11	2.23	0.68
1:A:353:LEU:HD22	1:A:355:LEU:HD21	1.75	0.67
1:A:550:MET:HE1	1:A:568:VAL:HG11	1.77	0.66
1:B:466:ALA:HB1	1:B:514:VAL:CG2	2.26	0.66
1:B:559:ILE:HD12	1:B:568:VAL:HG12	1.78	0.64
1:A:557:LEU:HD23	1:A:557:LEU:H	1.64	0.62
1:A:329:TYR:CE1	1:A:609:THR:CG2	2.82	0.62
1:B:483:ARG:HG2	1:B:508:SER:HB2	1.82	0.62
1:B:468:LEU:HB3	1:B:473:TYR:HE1	1.65	0.61
1:A:329:TYR:OH	1:A:612:PRO:HD3	2.00	0.61
1:B:550:MET:HE2	1:B:568:VAL:HG21	1.82	0.60
1:B:551:LYS:HB2	1:B:582:GLU:OE1	2.02	0.60
1:B:457:LEU:HD22	1:B:497:TRP:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:VAL:HG21	1:B:608:VAL:O	2.04	0.56
1:B:565:ARG:HG2	1:B:584:TYR:O	2.06	0.55
1:A:515:LEU:HD22	1:A:566:ILE:HG13	1.89	0.55
1:A:346:ASN:CG	1:A:349:ASP:HB2	2.32	0.55
1:A:329:TYR:CD1	1:A:609:THR:HG22	2.42	0.54
1:A:430:GLY:C	1:A:461:ILE:HG22	2.32	0.54
1:B:467:VAL:O	1:B:514:VAL:HG21	2.08	0.54
1:B:551:LYS:HB2	1:B:582:GLU:CD	2.32	0.54
1:A:388:THR:HG22	1:A:389:ASP:O	2.08	0.53
1:A:430:GLY:O	1:A:461:ILE:HG22	2.08	0.53
1:B:355:LEU:HD23	1:B:396:TYR:OH	2.08	0.53
1:B:365:LEU:H	1:B:365:LEU:HD23	1.74	0.53
1:A:353:LEU:HD22	1:A:355:LEU:CD2	2.38	0.52
1:A:611:GLU:CG	1:A:612:PRO:HD2	2.38	0.52
1:B:416:ILE:HD11	1:B:427:ALA:HB1	1.91	0.52
1:B:562:HIS:HB3	1:B:567:TYR:CE2	2.45	0.52
1:B:362:ARG:NH1	1:B:394:ASP:OD2	2.43	0.52
1:B:562:HIS:HB3	1:B:567:TYR:HE2	1.74	0.52
1:B:584:TYR:HB2	1:B:591:TRP:CE2	2.46	0.51
1:B:584:TYR:HB2	1:B:591:TRP:CZ2	2.46	0.51
1:B:396:TYR:CE2	1:B:398:PRO:HA	2.46	0.50
1:B:369:VAL:HG23	1:B:607:ALA:HB1	1.92	0.50
1:B:457:LEU:CD2	1:B:497:TRP:HB3	2.41	0.49
1:B:397:ASN:HB2	1:B:400:THR:OG1	2.13	0.49
1:B:552:HIS:HB2	1:B:554:ARG:HH21	1.78	0.49
1:B:585:ASP:HB3	1:B:590:THR:OG1	2.13	0.48
1:B:442:ARG:HH11	1:B:453:VAL:HG12	1.79	0.48
1:B:443:TYR:HB2	1:B:450:TRP:CE2	2.49	0.48
1:B:551:LYS:HB3	1:B:552:HIS:CD2	2.49	0.48
1:B:516:HIS:CE1	1:B:520:TYR:CE1	3.02	0.47
1:A:353:LEU:CD2	1:A:355:LEU:HD21	2.41	0.47
1:A:550:MET:HE2	1:A:568:VAL:HG11	1.95	0.47
1:B:460:ARG:HB3	1:B:463:VAL:HB	1.97	0.47
1:B:520:TYR:OH	1:B:536:ARG:NH1	2.45	0.47
1:B:342:LEU:HG	1:B:403:TRP:HZ2	1.80	0.47
1:A:611:GLU:HG2	1:A:612:PRO:HD2	1.97	0.46
1:A:467:VAL:O	1:A:514:VAL:HG21	2.15	0.46
1:B:331:ALA:HB2	1:B:342:LEU:HD23	1.98	0.46
1:B:516:HIS:CE1	1:B:520:TYR:HE1	2.34	0.46
1:B:366:ALA:HB1	1:B:418:VAL:HG22	1.96	0.46
1:A:362:ARG:NH1	1:A:394:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:551:LYS:HB3	1:B:552:HIS:CG	2.51	0.46
1:A:522:ALA:HB1	1:A:550:MET:CE	2.37	0.45
1:B:345:TYR:CE2	1:B:595:THR:HG21	2.50	0.45
1:A:512:VAL:HA	1:A:520:TYR:O	2.17	0.45
1:A:566:ILE:HB	1:A:584:TYR:HB3	1.98	0.45
1:B:327:LEU:N	1:B:609:THR:O	2.50	0.45
1:B:530:GLN:NE2	2:P:78:PRO:O	2.49	0.45
1:B:409:MET:HE1	1:B:416:ILE:HD12	1.99	0.45
1:B:443:TYR:HB2	1:B:450:TRP:CD2	2.52	0.45
1:B:579:ASP:OD2	1:B:596:ARG:HB3	2.16	0.44
1:A:353:LEU:CD2	1:A:355:LEU:CD2	2.96	0.44
1:A:365:LEU:HD12	1:A:376:ALA:HB1	1.99	0.44
1:B:396:TYR:HB2	1:B:403:TRP:CE3	2.52	0.44
1:B:584:TYR:HA	1:B:590:THR:O	2.18	0.44
1:A:472:LEU:HB3	1:A:490:TYR:HB3	1.99	0.43
1:B:373:LEU:HB3	1:B:395:CYS:SG	2.58	0.43
1:B:516:HIS:HB2	1:B:517:ASN:H	1.54	0.43
1:A:431:SER:HB3	1:A:461:ILE:HG21	2.00	0.43
1:B:569:LEU:HD23	1:B:597:MET:HE3	1.99	0.43
1:B:347:PRO:HG2	1:B:562:HIS:CE1	2.54	0.43
1:B:443:TYR:CE2	1:B:445:PRO:HA	2.55	0.42
1:B:337:GLN:HA	1:B:382:ASN:O	2.20	0.41
1:B:516:HIS:HE1	1:B:520:TYR:CE1	2.38	0.41
1:B:522:ALA:HB1	1:B:550:MET:HE3	2.02	0.41
1:B:468:LEU:HD21	1:B:517:ASN:O	2.20	0.41
1:B:585:ASP:HB3	1:B:588:THR:OG1	2.21	0.41
1:B:457:LEU:HD22	1:B:497:TRP:CB	2.50	0.40
1:B:431:SER:HB3	1:B:461:ILE:HG21	2.03	0.40
1:B:490:TYR:HB2	1:B:497:TRP:CZ2	2.56	0.40
1:B:583:CYS:HB3	1:B:594:VAL:HG21	2.03	0.40
1:B:328:ILE:HD11	1:B:562:HIS:HB2	2.04	0.40
1:A:380:ARG:HD3	1:A:382:ASN:OD1	2.21	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	286/301 (95%)	277 (97%)	9 (3%)	0	100	100
1	B	281/301 (93%)	266 (95%)	14 (5%)	1 (0%)	30	28
2	P	5/7 (71%)	5 (100%)	0	0	100	100
All	All	572/609 (94%)	548 (96%)	23 (4%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	547	VAL

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	233/247 (94%)	232 (100%)	1 (0%)	84	89
1	B	225/247 (91%)	225 (100%)	0	100	100
2	P	5/5 (100%)	5 (100%)	0	100	100
All	All	463/499 (93%)	462 (100%)	1 (0%)	87	93

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

Mol	Chain	Res	Type
1	A	610	MET

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

Mol	Chain	Res	Type
1	A	387	ASN
1	A	516	HIS

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Mol	Chain	Res	Type
1	B	414	ASN
1	B	516	HIS
1	B	552	HIS

5.3.3 RNA [i](#)

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	288/301 (95%)	0.03	19 (6%) 24 26	15, 24, 48, 101	0
1	B	283/301 (94%)	2.15	140 (49%) 0 0	18, 51, 85, 104	0
2	P	7/7 (100%)	0.01	0 100 100	24, 33, 36, 38	0
All	All	578/609 (94%)	1.07	159 (27%) 1 1	15, 32, 79, 104	0

All (159) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	591	TRP	9.0
1	B	516	HIS	7.2
1	B	592	SER	7.2
1	B	515	LEU	6.8
1	B	352	TRP	6.7
1	A	610	MET	6.7
1	B	518	CYS	6.3
1	A	336	ARG	6.2
1	B	491	TYR	6.1
1	B	329	TYR	6.0
1	B	421	ILE	6.0
1	B	369	VAL	5.9
1	B	517	ASN	5.8
1	B	514	VAL	5.8
1	A	613	SER	5.7
1	B	373	LEU	5.6
1	B	595	THR	5.5
1	B	351	THR	5.5
1	B	586	PRO	5.4
1	B	395	CYS	5.4
1	B	353	LEU	5.4
1	B	344	ALA	5.4
1	B	328	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	345	TYR	5.2
1	A	387	ASN	5.0
1	B	608	VAL	5.0
1	B	397	ASN	5.0
1	B	399	MET	4.9
1	B	467	VAL	4.9
1	B	565	ARG	4.8
1	B	420	VAL	4.8
1	B	568	VAL	4.7
1	B	567	TYR	4.7
1	B	347	PRO	4.7
1	B	327	LEU	4.7
1	B	426	TYR	4.5
1	B	593	GLU	4.5
1	B	519	ILE	4.5
1	B	552	HIS	4.5
1	B	442	ARG	4.4
1	B	445	PRO	4.4
1	B	425	ILE	4.4
1	B	590	THR	4.4
1	B	561	VAL	4.4
1	B	606	VAL	4.4
1	B	550	MET	4.3
1	B	609	THR	4.3
1	B	471	LEU	4.3
1	B	566	ILE	4.3
1	B	580	SER	4.3
1	B	594	VAL	4.2
1	B	370	VAL	4.1
1	A	614	ARG	4.1
1	B	492	PRO	4.1
1	B	583	CYS	4.0
1	B	398	PRO	4.0
1	B	375	TYR	4.0
1	B	581	VAL	3.9
1	B	368	CYS	3.9
1	B	367	GLY	3.9
1	A	383	SER	3.9
1	B	336	ARG	3.9
1	B	578	LEU	3.9
1	A	384	PRO	3.9
1	B	371	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	513	CYS	3.8
1	B	589	ASP	3.8
1	B	596	ARG	3.8
1	B	443	TYR	3.8
1	B	422	ASP	3.7
1	B	423	GLY	3.7
1	B	350	GLY	3.6
1	B	579	ASP	3.6
1	B	576	THR	3.6
1	B	374	LEU	3.6
1	B	585	ASP	3.6
1	B	408	PRO	3.5
1	B	468	LEU	3.5
1	B	335	PHE	3.5
1	A	349	ASP	3.5
1	B	498	ARG	3.4
1	B	549	PRO	3.4
1	B	587	ASP	3.4
1	B	569	LEU	3.4
1	B	346	ASN	3.3
1	B	470	ARG	3.3
1	B	597	MET	3.3
1	B	575	HIS	3.2
1	B	396	TYR	3.2
1	B	394	ASP	3.2
1	B	348	SER	3.2
1	A	386	GLY	3.2
1	A	382	ASN	3.2
1	B	548	ALA	3.2
1	B	607	ALA	3.2
1	B	330	THR	3.2
1	B	440	VAL	3.1
1	B	424	HIS	3.1
1	B	546	PHE	3.1
1	B	419	GLY	3.1
1	B	493	GLU	3.1
1	B	355	LEU	3.1
1	B	372	GLY	3.0
1	B	343	GLU	3.0
1	B	588	THR	3.0
1	B	584	TYR	3.0
1	B	453	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	490	TYR	2.9
1	B	605	GLY	2.9
1	B	400	THR	2.9
1	B	553	ARG	2.9
1	B	406	CYS	2.9
1	B	446	GLU	2.9
1	B	600	GLY	2.9
1	B	407	ALA	2.8
1	B	452	LEU	2.8
1	A	494	ARG	2.7
1	B	551	LYS	2.7
1	B	582	GLU	2.7
1	A	385	ASP	2.7
1	B	403	TRP	2.7
1	B	444	GLU	2.7
1	B	554	ARG	2.7
1	B	564	GLY	2.7
1	B	356	ALA	2.6
1	B	599	SER	2.6
1	B	560	THR	2.6
1	B	434	CYS	2.5
1	B	473	TYR	2.5
1	B	366	ALA	2.5
1	B	520	TYR	2.5
1	B	404	SER	2.5
1	A	612	PRO	2.5
1	B	405	PRO	2.5
1	A	334	TYR	2.4
1	B	577	PHE	2.4
1	B	447	ARG	2.4
1	B	598	THR	2.4
1	B	342	LEU	2.4
1	B	450	TRP	2.4
1	B	469	ASN	2.3
1	B	495	ASN	2.3
1	B	574	GLY	2.3
1	A	399	MET	2.3
1	A	516	HIS	2.3
1	B	472	LEU	2.3
1	B	441	GLU	2.3
1	B	489	CYS	2.2
1	B	601	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	455	PRO	2.2
1	B	494	ARG	2.1
1	A	434	CYS	2.1
1	A	611	GLU	2.1
1	B	547	VAL	2.1
1	B	393	LEU	2.1
1	B	573	ASP	2.1
1	A	498	ARG	2.0
1	B	570	GLY	2.0
1	B	451	HIS	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.