



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:08 PM UTC

PDB ID : 7K2A / pdb_00007k2a
Title : Kelch domain of human KEAP1 bound to Nrf2 peptide, LDEETGEFA
Authors : Muellers, S.N.; Allen, K.N.
Deposited on : 2020-09-08
Resolution : 1.90 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
Mogul : 2022.3.0, CSD as543be (2022)
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

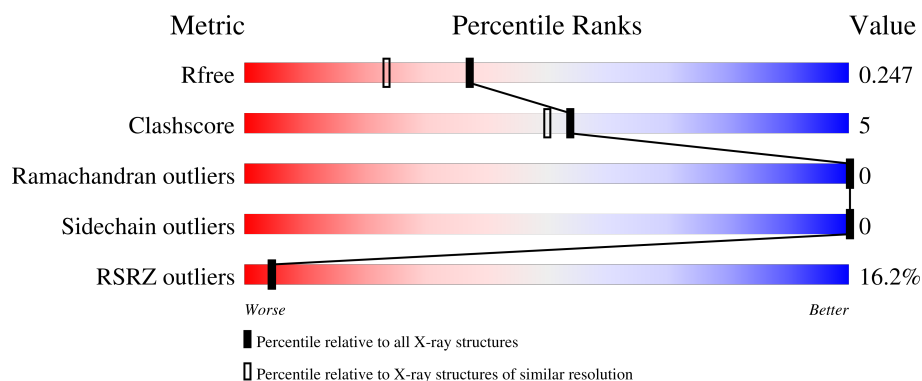
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	26% 81% 13% 6%
1	B	301	5% 88% 8% .
2	P	11	9% 82% 18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4662 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	283	Total	C	N	O	S	0	0	0
			2170	1351	392	412	15			
1	B	290	Total	C	N	O	S	0	1	0
			2229	1385	405	423	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	540	ALA	GLU	conflict	UNP Q14145
A	542	ALA	GLU	conflict	UNP Q14145
A	613	SER	CYS	conflict	UNP Q14145
B	540	ALA	GLU	conflict	UNP Q14145
B	542	ALA	GLU	conflict	UNP Q14145
B	613	SER	CYS	conflict	UNP Q14145

- Molecule 2 is a protein called ACE-LEU-ASP-GLU-GLU-THR-GLY-GLU-PHE-ALA-NH2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	11	Total	C	N	O	0	0	1
			74	45	10	19			

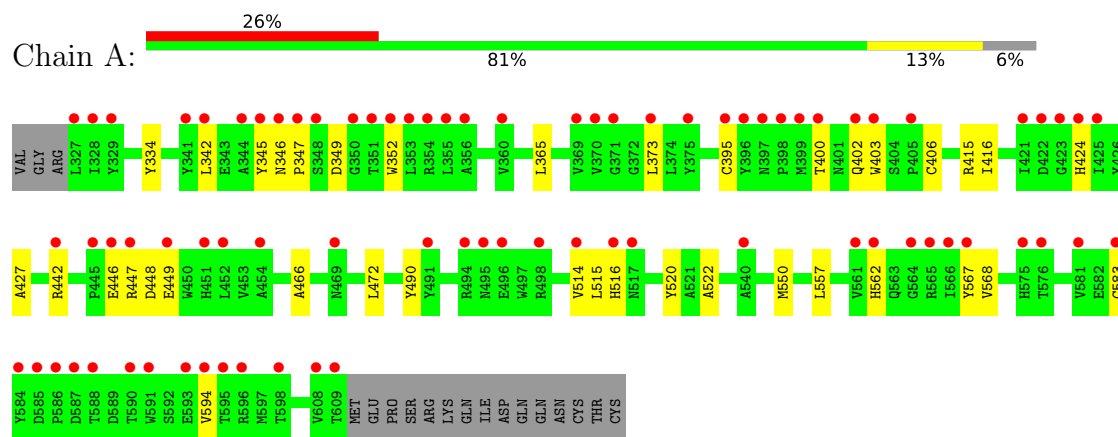
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	52	Total	O	0	0
			52	52		
3	B	134	Total	O	0	0
			134	134		
3	P	3	Total	O	0	0
			3	3		

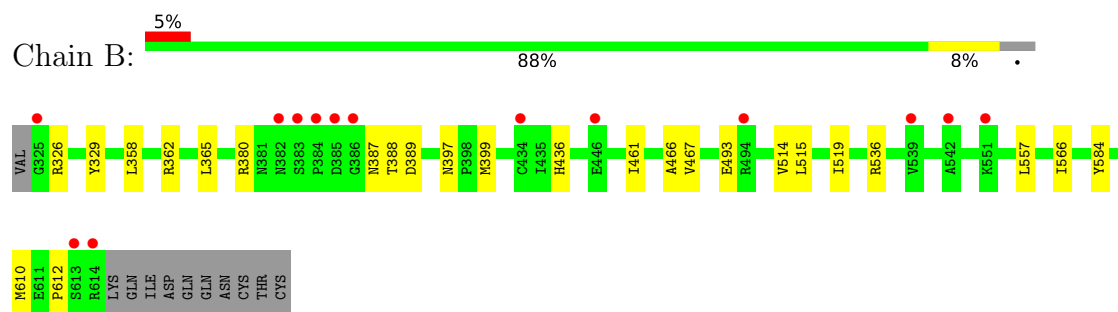
3 Residue-property plots

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.

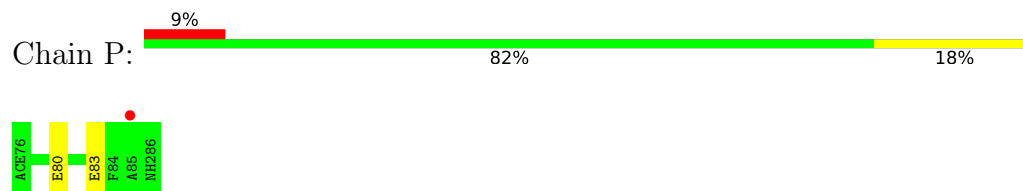
- Molecule 1: Kelch-like ECH-associated protein 1



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



- Molecule 2: ACE-LEU-ASP-GLU-GLU-THR-GLY-GLU-PHE-ALA-NH2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.08Å 68.97Å 78.26Å 90.00° 117.81° 90.00°	Depositor
Resolution (Å)	29.63 – 1.90 29.63 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (29.63-1.90) 97.4 (29.63-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.210 , 0.244 0.213 , 0.247	Depositor DCC
R_{free} test set	2000 reflections (3.33%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4662	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.17% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NH2, ACE

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	0.30	0/2223	0.53	0/3029
1	B	0.34	0/2286	0.58	0/3112
2	P	0.35	0/71	0.79	0/95
All	All	0.32	0/4580	0.56	0/6236

There are no bond length outliers.

There are no bond angle outliers.

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	2170	0	2066	28	0
1	B	2229	0	2127	17	0
2	P	74	0	60	2	0
3	A	52	0	0	0	0
3	B	134	0	0	0	0
3	P	3	0	0	0	0
All	All	4662	0	4253	43	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 5.

All (43) 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:466:ALA:HB1	1:A:514:VAL:HG23	1.68	0.74
1:B:326:ARG:HE	1:B:610:MET:HE2	1.51	0.73
1:B:466:ALA:HB1	1:B:514:VAL:HG23	1.70	0.73
1:A:522:ALA:HB1	1:A:550:MET:HE3	1.75	0.69
1:A:516:HIS:CD2	1:B:493:GLU:HG3	2.28	0.68
1:A:550:MET:HE2	1:A:568:VAL:HG21	1.80	0.62
1:A:424:HIS:HD2	1:A:442:ARG:HD2	1.68	0.59
1:B:436:HIS:ND1	1:B:461:ILE:HD11	2.18	0.59
1:A:416:ILE:HD11	1:A:427:ALA:HB1	1.88	0.55
1:A:347:PRO:HG2	1:A:562:HIS:CE1	2.43	0.54
1:A:447:ARG:HB3	1:A:449:GLU:OE1	2.08	0.53
1:A:550:MET:CE	1:A:568:VAL:HG11	2.39	0.53
1:B:397:ASN:OD1	1:B:399:MET:HE3	2.10	0.51
1:A:365:LEU:HD23	1:A:365:LEU:H	1.76	0.51
1:A:346:ASN:HB3	1:A:349:ASP:OD1	2.12	0.50
1:B:388:THR:HG22	1:B:389:ASP:O	2.12	0.49
1:A:415:ARG:NH2	2:P:80:GLU:OE1	2.37	0.49
1:A:345:TYR:HB2	1:A:352:TRP:CZ3	2.49	0.48
1:A:472:LEU:HB3	1:A:490:TYR:HB3	1.96	0.47
1:B:515:LEU:HD22	1:B:566:ILE:HG13	1.97	0.46
1:B:557:LEU:H	1:B:557:LEU:HD23	1.80	0.46
1:A:400:THR:O	1:A:402:GLN:HG3	2.15	0.46
1:A:557:LEU:HD23	1:A:557:LEU:H	1.79	0.46
1:B:467:VAL:O	1:B:514:VAL:HG21	2.15	0.46
1:A:516:HIS:CG	1:B:493:GLU:HG3	2.51	0.45
1:B:365:LEU:H	1:B:365:LEU:HD23	1.80	0.45
1:B:566:ILE:HB	1:B:584:TYR:HB3	1.98	0.45
1:A:345:TYR:HB2	1:A:352:TRP:CH2	2.52	0.45
1:A:406:CYS:HB3	1:A:448:ASP:OD1	2.17	0.45
1:A:562:HIS:HB3	1:A:567:TYR:CE1	2.52	0.45
1:A:373:LEU:HB3	1:A:395:CYS:SG	2.57	0.44
1:A:334:TYR:CE1	2:P:83:GLU:HA	2.52	0.44
1:A:447:ARG:O	1:A:449:GLU:HG3	2.17	0.44
1:A:342:LEU:HD22	1:A:403:TRP:CZ2	2.54	0.42
1:B:519:ILE:O	1:B:536:ARG:HA	2.20	0.42
1:B:380:ARG:NH2	1:B:387:ASN:HB3	2.34	0.42
1:A:446:GLU:HA	1:A:446:GLU:OE2	2.19	0.42
1:A:583:CYS:CB	1:A:594:VAL:HG21	2.50	0.41
1:B:436:HIS:HB3	1:B:461:ILE:HD11	2.03	0.41
1:A:515:LEU:HB3	1:A:520:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:TYR:OH	1:B:612:PRO:HD3	2.20	0.40
1:B:358:LEU:HD13	1:B:362:ARG:HG2	2.04	0.40
1:A:424:HIS:CD2	1:A:442:ARG:HD2	2.52	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	281/301 (93%)	269 (96%)	12 (4%)	0	100	100
1	B	289/301 (96%)	282 (98%)	7 (2%)	0	100	100
2	P	9/11 (82%)	9 (100%)	0	0	100	100
All	All	579/613 (94%)	560 (97%)	19 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	228/245 (93%)	228 (100%)	0	100	100
1	B	235/245 (96%)	235 (100%)	0	100	100
2	P	7/7 (100%)	7 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	470/497 (95%)	470 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	424	HIS
1	A	469	ASN
1	A	517	ASN
1	A	563	GLN
1	B	432	HIS
1	B	482	ASN

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	283/301 (94%)	1.20	79 (27%) 1 1	22, 41, 69, 79	0
1	B	290/301 (96%)	0.07	14 (4%) 35 38	16, 27, 50, 87	1 (0%)
2	P	9/11 (81%)	0.78	1 (11%) 10 11	28, 35, 50, 51	0
All	All	582/613 (94%)	0.63	94 (16%) 4 4	16, 32, 66, 87	1 (0%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	353	LEU	4.7
1	A	327	LEU	4.5
1	A	516	HIS	4.0
1	A	329	TYR	4.0
1	A	352	TRP	3.8
1	A	344	ALA	3.7
1	A	446	GLU	3.6
1	B	384	PRO	3.6
1	A	608	VAL	3.5
1	A	452	LEU	3.4
1	A	445	PRO	3.4
1	B	613	SER	3.3
1	B	614	ARG	3.2
1	A	403	TRP	3.2
1	A	575	HIS	3.2
1	A	469	ASN	3.1
1	A	423	GLY	3.1
1	A	397	ASN	3.1
1	A	399	MET	3.1
1	A	328	ILE	3.1
1	B	386	GLY	3.1
1	A	370	VAL	3.1
1	A	405	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	348	SER	3.1
1	A	347	PRO	3.1
1	A	350	GLY	3.1
1	A	567	TYR	3.0
1	B	382	ASN	3.0
1	A	562	HIS	3.0
1	A	595	THR	3.0
1	A	491	TYR	2.9
1	A	421	ILE	2.9
1	A	355	LEU	2.9
1	A	351	THR	2.9
1	A	598	THR	2.8
1	A	395	CYS	2.8
1	A	581	VAL	2.8
1	B	539	VAL	2.8
1	B	434	CYS	2.8
1	A	369	VAL	2.8
1	A	345	TYR	2.7
1	A	424	HIS	2.7
1	A	400	THR	2.7
1	A	422	ASP	2.7
1	A	396	TYR	2.7
1	A	540	ALA	2.7
1	A	561	VAL	2.7
1	A	451	HIS	2.7
1	A	588	THR	2.6
1	A	402	GLN	2.6
1	A	373	LEU	2.6
1	A	576	THR	2.6
1	A	354	ARG	2.6
1	B	325	GLY	2.5
1	A	342	LEU	2.5
1	A	593	GLU	2.5
1	B	551	LYS	2.5
1	A	498	ARG	2.4
1	A	586	PRO	2.4
1	A	517	ASN	2.4
1	A	609	THR	2.4
1	A	442	ARG	2.4
1	A	596	ARG	2.4
1	A	375	TYR	2.4
1	A	587	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	446	GLU	2.4
1	A	594	VAL	2.4
1	A	591	TRP	2.4
1	B	494	ARG	2.3
1	A	454	ALA	2.3
1	A	584	TYR	2.3
1	A	346	ASN	2.3
1	A	566	ILE	2.3
1	B	383	SER	2.3
1	A	496	GLU	2.3
1	A	583	CYS	2.3
2	P	85	ALA	2.3
1	A	356	ALA	2.2
1	A	449	GLU	2.2
1	A	514	VAL	2.2
1	A	398	PRO	2.2
1	B	385	ASP	2.2
1	A	447	ARG	2.2
1	A	495	ASN	2.2
1	A	425	ILE	2.1
1	A	360	VAL	2.1
1	A	494	ARG	2.1
1	A	565	ARG	2.1
1	A	590	THR	2.1
1	A	371	GLY	2.1
1	A	341	TYR	2.1
1	A	585	ASP	2.1
1	B	542	ALA	2.0
1	A	564	GLY	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.