



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7LRZ / pdb_00007lrz
Title : Structure of the Human ALK GRD
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Deposited on : 2021-02-17
Resolution : 1.91 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

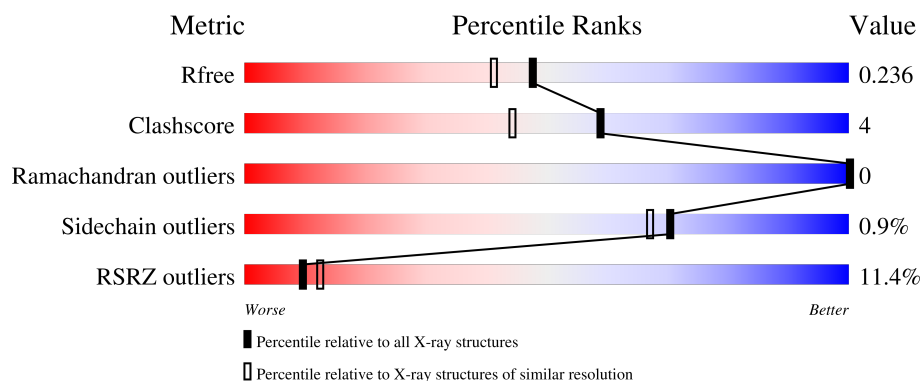
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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	311	11% 88% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2411 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 ALK tyrosine kinase receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	306	2198	1358	392	435	13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	676	SER	-	expression tag	UNP Q9UM73
A	677	LEU	-	expression tag	UNP Q9UM73

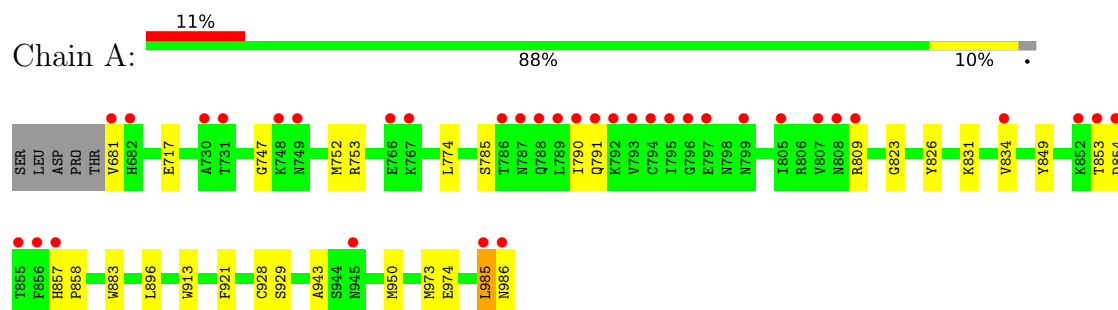
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	213	Total	O	0	0
			213	213		

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: ALK tyrosine kinase receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	76.14Å 76.14Å 230.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.43 – 1.91 43.43 – 1.91	Depositor EDS
% Data completeness (in resolution range)	97.5 (43.43-1.91) 97.6 (43.43-1.91)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 1.91Å)	Xtriage
Refinement program	PHENIX dev_3915	Depositor
R, R_{free}	0.188 , 0.214 0.219 , 0.236	Depositor DCC
R_{free} test set	1523 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.788	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2411	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 3.77% 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	0.58	0/2246	0.79	4/3035 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	929	SER	N-CA-C	-9.04	100.37	111.40
1	A	928	CYS	CA-C-O	-6.27	113.63	119.34
1	A	790	ILE	CA-C-O	-5.54	115.19	120.95
1	A	928	CYS	N-CA-C	-5.02	100.97	108.34

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	2198	0	2078	19	0
2	A	213	0	0	3	0
All	All	2411	0	2078	19	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 4.

All (19) 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:883:TRP:CZ3	1:A:896:LEU:HD22	2.17	0.80
1:A:853:THR:HG23	2:A:1007:HOH:O	1.94	0.68
1:A:752:MET:HE3	1:A:854:ASP:HB2	1.80	0.63
1:A:785:SER:O	1:A:791:GLN:HG2	2.05	0.57
1:A:717:GLU:N	1:A:717:GLU:OE2	2.38	0.57
1:A:943:ALA:HB2	1:A:950:MET:HG2	1.88	0.56
1:A:831:LYS:O	1:A:834:VAL:HG12	2.08	0.53
1:A:774:LEU:HD23	1:A:774:LEU:C	2.34	0.52
1:A:826:TYR:CG	1:A:896:LEU:HD13	2.48	0.49
1:A:896:LEU:O	1:A:896:LEU:HG	2.08	0.48
1:A:985:LEU:O	1:A:986:ASN:CB	2.61	0.48
1:A:681:VAL:HG13	2:A:1005:HOH:O	2.14	0.47
1:A:823:GLY:HA3	1:A:921:PHE:O	2.16	0.46
1:A:973:MET:HE3	2:A:1084:HOH:O	2.16	0.44
1:A:747:GLY:HA3	1:A:849:TYR:CD1	2.55	0.42
1:A:809:ARG:HH11	1:A:809:ARG:HG2	1.85	0.42
1:A:857:HIS:HB3	1:A:858:PRO:CD	2.50	0.42
1:A:752:MET:CE	1:A:854:ASP:HB2	2.50	0.41
1:A:753:ARG:HD2	1:A:974:GLU:O	2.21	0.41

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	304/311 (98%)	293 (96%)	11 (4%)	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	220/225 (98%)	218 (99%)	2 (1%)	70	67

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	913	TRP
1	A	985	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	706	GLN
1	A	724	GLN
1	A	778	GLN
1	A	787	ASN

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 ⓘ

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	306/311 (98%)	0.70	35 (11%)	10 12	20, 32, 63, 80	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	789	LEU	7.2
1	A	788	GLN	5.9
1	A	748	LYS	5.7
1	A	985	LEU	5.4
1	A	795	ILE	5.1
1	A	787	ASN	5.0
1	A	681	VAL	4.9
1	A	790	ILE	4.9
1	A	856	PHE	4.3
1	A	796	GLY	4.2
1	A	855	THR	3.9
1	A	853	THR	3.6
1	A	786	THR	3.5
1	A	807	VAL	3.4
1	A	794	CYS	3.0
1	A	854	ASP	2.8
1	A	986	ASN	2.8
1	A	730	ALA	2.7
1	A	799	ASN	2.7
1	A	852	LYS	2.5
1	A	749	ASN	2.5
1	A	808	ASN	2.5
1	A	731	THR	2.5
1	A	834	VAL	2.4
1	A	857	HIS	2.4
1	A	792	LYS	2.4
1	A	791	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	682	HIS	2.3
1	A	793	VAL	2.2
1	A	766	GLU	2.1
1	A	945	ASN	2.1
1	A	797	GLU	2.1
1	A	809	ARG	2.1
1	A	805	ILE	2.0
1	A	767	LYS	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.