



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:18 AM UTC

PDB ID : 9TU0 / pdb_00009tu0
Title : Crystal structure of human ERK1 in complex with the KIM1 motif of the T. gondii protein GRA24
Authors : Juyoux, P.; von Velsen, J.; Bowler, M.W.
Deposited on : 2026-01-08
Resolution : 2.17 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

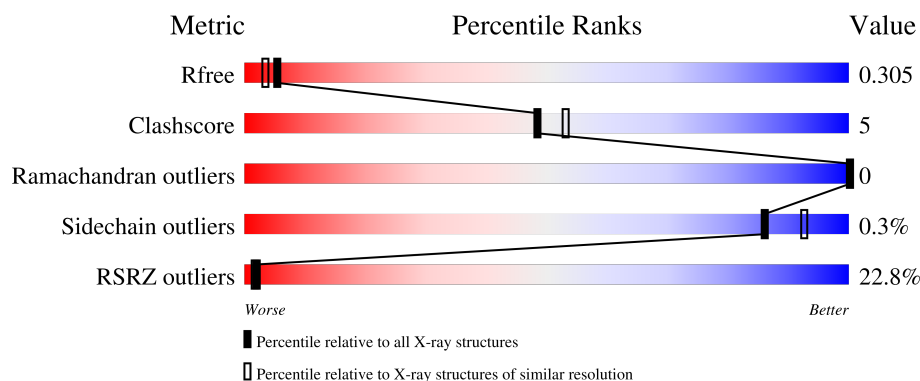
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	379	<div> <div>18%</div> <div>71%</div> <div>15%</div> <div>14%</div> </div>
2	D	542	<div> <div>%</div> <div>97%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2894 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 Mitogen-activated protein kinase 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	P	S	0	0	0
			2682	1718	460	488	1	15			

- Molecule 2 is a protein called Putative transmembrane protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	16	Total	C	N	O	0	0	0
			127	83	22	22			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	70	Total	O	0	0
			70	70		

GLN	SER	ARG	GLY	PRO	PRO	ARG	THR	ARG	PRO	PRO	PHE	ASN	PRO	TRP	SER	SER	THR	LYS	THR	G-2	V5	S6	E7	L8	P9	P10	L11	Y12	I13	PRO	ARG	PRO	PRO	LEU	ALA	SER	GLY	GLY	TYR	ARG	ASN	PRO	ALA	ASP	SER	ARG	LYS	HIS	SER	THR	VAL	THR	PRO	GLN	THR	THR	PRO	PRO	ALA	ARG	LYS
SER	SER	THR	SER	SER	SER	GLN	HIS	LEU	GLU	ALA	ARG	LEU	SER	GLN	SER	ARG	GLY	PRO	PRO	ARG	THR	THR	ARG	PRO	PRO	PHE	ASN	PRO	TRP	SER	THR	LYS	THR	GLY	LEU	GLY	ARG	ARG	GLY	VAL	SER	GLU	LEU	PRO	PRO	LEU	ARG	ILE	VAL	LYS	PRO	PRO	THR	THR	LYS	GLY	ASN				

4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	59.82Å 59.82Å 388.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.93 – 2.17 19.93 – 2.17	Depositor EDS
% Data completeness (in resolution range)	76.1 (19.93-2.17) 76.2 (19.93-2.17)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419+SVN	Depositor
R, R_{free}	0.237 , 0.292 0.246 , 0.305	Depositor DCC
R_{free} test set	891 reflections (3.82%)	wwPDB-VP
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2894	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% 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

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, SO4

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	0.12	0/2729	0.30	0/3689
2	D	0.08	0/129	0.22	0/174
All	All	0.12	0/2858	0.29	0/3863

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

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	2682	0	2703	31	0
2	D	127	0	138	0	0
3	A	15	0	0	0	0
4	A	70	0	0	0	0
All	All	2894	0	2841	31	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 (31) 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:269:LEU:HD21	1:A:282:GLN:HE22	1.55	0.72
1:A:216:MET:HE1	1:A:253:GLN:HG2	1.73	0.71
1:A:208:ARG:HE	1:A:211:ARG:HD2	1.56	0.71
1:A:70:ILE:HG12	1:A:121:VAL:HG22	1.76	0.66
1:A:258:LEU:HD11	1:A:264:PRO:HD3	1.82	0.62
1:A:306:LEU:HG	1:A:310:MET:HE2	1.81	0.61
1:A:351:GLU:HG2	1:A:353:ASP:OD2	2.09	0.53
1:A:158:HIS:CE1	1:A:224:LYS:HB3	2.44	0.52
1:A:152:ARG:HG3	1:A:339:GLU:HG2	1.92	0.52
1:A:270:ASN:ND2	1:A:278:ARG:HH21	2.07	0.51
1:A:302:LYS:HE3	1:A:328:PRO:HB2	1.92	0.51
1:A:95:PHE:HZ	1:A:162:VAL:HG11	1.74	0.51
1:A:86:LEU:HD23	1:A:352:LEU:HD22	1.93	0.50
1:A:148:TYR:HB2	1:A:330:LEU:HD22	1.94	0.50
1:A:108:ARG:HD3	1:A:115:MET:SD	2.51	0.49
1:A:172:LEU:HD11	1:A:234:ILE:HD13	1.95	0.48
1:A:50:GLU:HG3	1:A:51:GLY:H	1.77	0.48
1:A:165:ARG:HB2	1:A:187:LEU:O	2.15	0.47
1:A:172:LEU:HB3	1:A:180:LEU:HD21	1.97	0.47
1:A:284:LEU:HD23	1:A:285:PRO:HD2	1.98	0.46
1:A:48:ILE:HD11	1:A:58:SER:HB3	1.98	0.45
1:A:143:ILE:HD13	1:A:239:LEU:HD23	1.99	0.44
1:A:83:GLN:NE2	1:A:353:ASP:HA	2.33	0.43
1:A:125:MET:HG3	1:A:173:LEU:HB3	2.01	0.42
1:A:143:ILE:HG23	1:A:238:MET:HE3	2.01	0.42
1:A:223:THR:O	1:A:226:ILE:HG12	2.20	0.42
1:A:357:LYS:HE2	1:A:358:GLU:OE2	2.20	0.41
1:A:47:TYR:OH	1:A:50:GLU:HB2	2.20	0.41
1:A:82:CYS:HB3	1:A:360:LEU:HB3	2.01	0.41
1:A:174:ILE:HA	1:A:179:ASP:O	2.21	0.41
1:A:111:THR:HG22	1:A:113:GLU:H	1.85	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	320/379 (84%)	303 (95%)	17 (5%)	0	100	100
2	D	14/542 (3%)	14 (100%)	0	0	100	100
All	All	334/921 (36%)	317 (95%)	17 (5%)	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	295/328 (90%)	294 (100%)	1 (0%)	86	92
2	D	14/457 (3%)	14 (100%)	0	100	100
All	All	309/785 (39%)	308 (100%)	1 (0%)	86	92

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

Mol	Chain	Res	Type
1	A	162	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	ASN
1	A	282	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	A	286	1	8,9,10	1.63	1 (12%)	7,12,14	1.35	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	286	1	-	6/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	286	SEP	P-O1P	3.55	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	286	SEP	OG-CB-CA	2.88	110.94	108.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	286	SEP	N-CA-CB-OG
1	A	286	SEP	C-CA-CB-OG
1	A	286	SEP	CB-OG-P-O1P
1	A	286	SEP	CB-OG-P-O2P
1	A	286	SEP	CB-OG-P-O3P
1	A	286	SEP	CA-CB-OG-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	402	-	4,4,4	0.67	0	6,6,6	0.09	0
3	SO4	A	403	-	4,4,4	0.67	0	6,6,6	0.07	0
3	SO4	A	401	-	4,4,4	0.68	0	6,6,6	0.14	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	326/379 (86%)	1.27	70 (21%) 2 2	28, 53, 92, 125	0
2	D	16/542 (2%)	2.48	8 (50%) 0 0	46, 71, 93, 111	0
All	All	342/921 (37%)	1.33	78 (22%) 2 2	28, 54, 92, 125	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	13	ILE	9.4
1	A	222	TYR	6.4
1	A	191	ALA	6.0
1	A	273	ILE	5.7
1	A	53	TYR	5.3
1	A	208	ARG	5.2
1	A	348	PHE	4.7
1	A	280	TYR	4.3
2	D	-2	GLY	4.0
1	A	250	TYR	3.7
2	D	12	TYR	3.7
1	A	52	ALA	3.5
1	A	271	CYS	3.5
1	A	55	MET	3.4
1	A	51	GLY	3.3
1	A	28	VAL	3.3
1	A	176	THR	3.3
1	A	352	LEU	3.3
1	A	216	MET	3.2
1	A	162	VAL	3.2
1	A	209	TRP	3.1
1	A	350	MET	3.1
1	A	355	LEU	3.1
2	D	10	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	349	ALA	3.0
1	A	295	LEU	3.0
1	A	217	LEU	3.0
1	A	80	THR	3.0
1	A	36	PHE	2.9
1	A	65	LYS	2.9
1	A	354	ASP	2.9
1	A	277	ALA	2.9
1	A	251	LEU	2.8
1	A	40	PRO	2.8
1	A	353	ASP	2.7
1	A	66	THR	2.7
1	A	30	MET	2.7
1	A	31	VAL	2.7
1	A	258	LEU	2.6
1	A	270	ASN	2.6
1	A	281	LEU	2.6
2	D	8	LEU	2.6
1	A	84	ARG	2.6
1	A	83	GLN	2.5
1	A	39	GLY	2.5
1	A	77	GLU	2.5
1	A	45	LEU	2.5
1	A	370	ARG	2.5
2	D	7	GLU	2.5
1	A	246	PRO	2.5
1	A	49	GLY	2.4
1	A	81	TYR	2.4
1	A	60	TYR	2.3
1	A	351	GLU	2.3
1	A	79	GLN	2.3
1	A	247	GLY	2.3
1	A	32	LYS	2.3
1	A	189	ARG	2.3
1	A	38	VAL	2.3
1	A	269	LEU	2.3
2	D	5	VAL	2.3
1	A	144	CYS	2.3
1	A	187	LEU	2.3
1	A	373	PRO	2.2
1	A	249	HIS	2.2
1	A	313	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	254	LEU	2.2
2	D	11	LEU	2.2
1	A	54	GLY	2.1
1	A	360	LEU	2.1
1	A	347	THR	2.1
1	A	356	PRO	2.1
1	A	253	GLN	2.1
1	A	371	PHE	2.1
1	A	135	SER	2.1
1	A	33	GLY	2.1
1	A	190	ILE	2.0
1	A	50	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	SEP	A	286	10/11	0.59	0.21	73,104,140,152	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	A	403	5/5	0.40	0.16	102,104,141,146	0
3	SO4	A	402	5/5	0.49	0.17	92,96,108,139	0
3	SO4	A	401	5/5	0.81	0.19	60,76,85,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.