



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5RG4 / pdb_00005rg4
Title : Crystal Structure of Kemp Eliminase HG3 in unbound state, 277K
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Deposited on : 2020-03-19
Resolution : 1.99 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

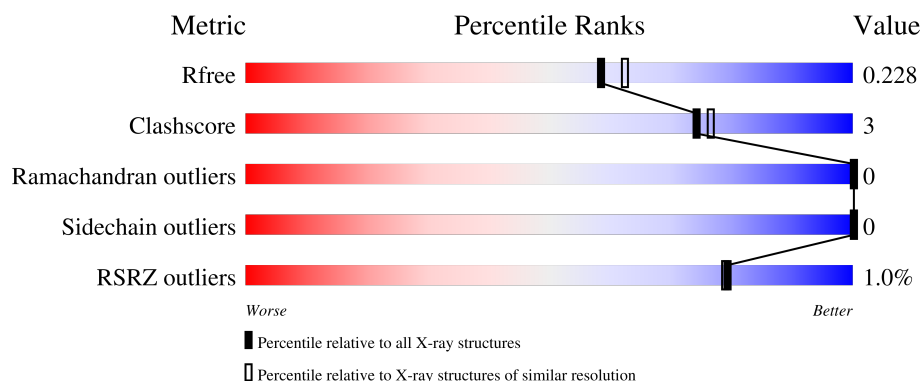
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	318	% 91% 6%
1	B	318	% 86% 8% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	A	401	-	-	X	-
2	ACT	B	401	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9868 atoms, of which 4672 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 Kemp Eliminase HG3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	300	Total	C	H	N	O	S	1	21	0
			4708	1502	2332	409	452	13			
1	B	300	Total	C	H	N	O	S	0	20	0
			4712	1503	2334	410	454	11			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP P23360
A	0	ALA	-	expression tag	UNP P23360
A	1	GLU	-	expression tag	UNP P23360
A	42	MET	GLN	engineered mutation	UNP P23360
A	44	TRP	THR	engineered mutation	UNP P23360
A	81	GLY	ARG	engineered mutation	UNP P23360
A	83	GLY	HIS	engineered mutation	UNP P23360
A	84	MET	THR	engineered mutation	UNP P23360
A	130	GLY	ASN	engineered mutation	UNP P23360
A	172	MET	ASN	engineered mutation	UNP P23360
A	234	SER	ALA	engineered mutation	UNP P23360
A	236	LEU	THR	engineered mutation	UNP P23360
A	237	MET	GLU	engineered mutation	UNP P23360
A	267	PHE	TRP	engineered mutation	UNP P23360
A	304	GLY	-	expression tag	UNP P23360
A	305	SER	-	expression tag	UNP P23360
A	306	ILE	-	expression tag	UNP P23360
A	307	GLU	-	expression tag	UNP P23360
A	308	GLY	-	expression tag	UNP P23360
A	309	ARG	-	expression tag	UNP P23360
A	310	GLY	-	expression tag	UNP P23360
A	311	HIS	-	expression tag	UNP P23360
A	312	HIS	-	expression tag	UNP P23360
A	313	HIS	-	expression tag	UNP P23360
A	314	HIS	-	expression tag	UNP P23360

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Chain	Residue	Modelled	Actual	Comment	Reference
A	315	HIS	-	expression tag	UNP P23360
A	316	HIS	-	expression tag	UNP P23360
B	-1	MET	-	initiating methionine	UNP P23360
B	0	ALA	-	expression tag	UNP P23360
B	1	GLU	-	expression tag	UNP P23360
B	42	MET	GLN	engineered mutation	UNP P23360
B	44	TRP	THR	engineered mutation	UNP P23360
B	81	GLY	ARG	engineered mutation	UNP P23360
B	83	GLY	HIS	engineered mutation	UNP P23360
B	84	MET	THR	engineered mutation	UNP P23360
B	130	GLY	ASN	engineered mutation	UNP P23360
B	172	MET	ASN	engineered mutation	UNP P23360
B	234	SER	ALA	engineered mutation	UNP P23360
B	236	LEU	THR	engineered mutation	UNP P23360
B	237	MET	GLU	engineered mutation	UNP P23360
B	267	PHE	TRP	engineered mutation	UNP P23360
B	304	GLY	-	expression tag	UNP P23360
B	305	SER	-	expression tag	UNP P23360
B	306	ILE	-	expression tag	UNP P23360
B	307	GLU	-	expression tag	UNP P23360
B	308	GLY	-	expression tag	UNP P23360
B	309	ARG	-	expression tag	UNP P23360
B	310	GLY	-	expression tag	UNP P23360
B	311	HIS	-	expression tag	UNP P23360
B	312	HIS	-	expression tag	UNP P23360
B	313	HIS	-	expression tag	UNP P23360
B	314	HIS	-	expression tag	UNP P23360
B	315	HIS	-	expression tag	UNP P23360
B	316	HIS	-	expression tag	UNP P23360

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			7	2	3	2		
2	B	1	Total	C	H	O	0	0
			7	2	3	2		

- 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	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	220	Total 220	O 220	0	1
4	B	203	Total 204	O 204	0	2

- Molecule 1: Kemp Eliminase HG3



- | HIS | HIS | HIS | HIS | HIS | HIS |
|-----|-----|-----|-----|-----|------|
| MET | ALA | GLU | ALA | ALA | Q4 |
| | | | | | V20 |
| | | | | | D23 |
| | | | | | R26 |
| | | | | | T36 |
| | | | | | M42 |
| | | | | | V43 |
| | | | | | M44 |
| | | | | | P45 |
| | | | | | M49 |
| | | | | | T54 |
| | | | | | F61 |
| | | | | | G81 |
| | | | | | G82 |
| | | | | | G83 |
| | | | | | M84 |
| | | | | | Q90 |
| | | | | | N110 |
| | | | | | G130 |
| | | | | | M172 |
| | | | | | Q207 |
| | | | | | L236 |
| | | | | | M237 |
| | | | | | D271 |
| | | | | | P272 |
| | | | | | D273 |
| | | | | | T279 |
| | | | | | T280 |
| | | | | | Q303 |
| | | | | | GLY |
| | | | | | SER |
| | | | | | ILE |
| | | | | | GLU |
| | | | | | GLY |
| | | | | | ARG |
| | | | | | GLY |
| | | | | | GLY |

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.14Å 79.97Å 99.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.52 – 1.99 41.52 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.9 (41.52-1.99) 99.9 (41.52-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.177 , 0.216 (Not available) , 0.228	Depositor DCC
R_{free} test set	2003 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.002 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9868	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% 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: SO4, ACT

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	0.22	0/2509	0.49	0/3424
1	B	0.23	0/2516	0.47	0/3433
All	All	0.22	0/5025	0.48	0/6857

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	2376	2332	2240	12	0
1	B	2378	2334	2248	18	0
2	A	4	3	3	3	0
2	B	4	3	3	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	220	0	0	2	1
4	B	204	0	0	4	2
All	All	5196	4672	4494	29	2

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 3.

The worst 5 of 29 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:B:42:MET:SD	4:B:673[A]:HOH:O	2.27	0.90
1:B:23[B]:ASP:OD2	4:B:501:HOH:O	1.96	0.83
1:A:42:MET:SD	4:A:684[A]:HOH:O	2.50	0.68
1:B:207:GLN:HG3	1:B:237[A]:MET:HE3	1.79	0.63
1:A:207:GLN:HG3	1:A:237[A]:MET:HE3	1.80	0.62

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:502:HOH:O	4:B:515:HOH:O[2_455]	1.83	0.37
4:A:695:HOH:O	4:B:526:HOH:O[2_555]	2.10	0.10

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	319/318 (100%)	313 (98%)	6 (2%)	0	100	100
1	B	318/318 (100%)	312 (98%)	6 (2%)	0	100	100
All	All	637/636 (100%)	625 (98%)	12 (2%)	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	261/255 (102%)	261 (100%)	0	100	100
1	B	259/255 (102%)	259 (100%)	0	100	100
All	All	520/510 (102%)	520 (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 (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	185	GLN
1	B	74	GLN

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 ⓘ

4 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
2	ACT	B	401	-	3,3,3	1.17	0	3,3,3	1.52	0
3	SO4	A	402	-	4,4,4	0.20	0	6,6,6	0.21	0
3	SO4	B	402	-	4,4,4	0.24	0	6,6,6	0.13	0
2	ACT	A	401	-	3,3,3	0.86	0	3,3,3	1.68	1 (33%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	ACT	OXT-C-O	2.13	129.91	122.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	ACT	2	0
2	A	401	ACT	3	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	300/318 (94%)	-0.34	3 (1%) 79 79	9, 22, 35, 79	14 (4%)
1	B	300/318 (94%)	-0.16	3 (1%) 79 79	9, 24, 41, 92	13 (4%)
All	All	600/636 (94%)	-0.25	6 (1%) 79 79	9, 23, 38, 92	27 (4%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	303	GLN	3.9
1	B	303	GLN	2.7
1	B	90	GLN	2.4
1	A	275	TRP	2.3
1	A	44[A]	TRP	2.2

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](#)

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($\text{\AA}^2$)	Q<0.9
3	SO4	B	402	5/5	0.62	0.17	101,102,102,102	0
3	SO4	A	402	5/5	0.72	0.18	70,71,72,73	5
2	ACT	A	401	4/4	0.91	0.13	32,33,40,40	0
2	ACT	B	401	4/4	0.93	0.11	33,34,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.