



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2017 – 09:48 AM EDT

PDB ID : 5NIE
Title : Crystal structure of human LTA4H mutant R563A in open conformation
Authors : Stsiapanava, A.
Deposited on : unknown
Resolution : 2.60 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

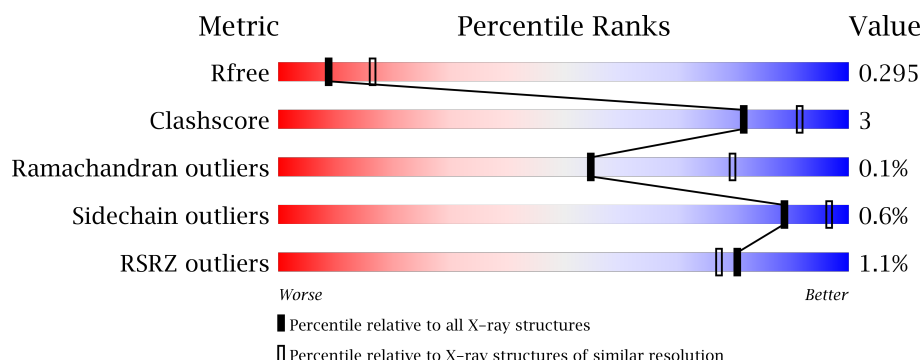
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


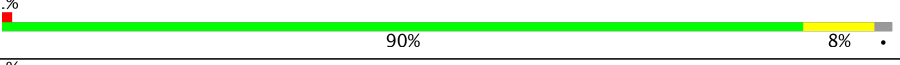

The reported resolution of this entry is 2.60 Å.

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}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	617	 90% 8% •
1	B	617	 90% 8% •
1	C	617	 89% 9% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 29107 atoms, of which 14417 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 Leukotriene A-4 hydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	606	Total	C	H	N	O	S	0	2	0
			9660	3115	4811	807	906	21			
1	B	607	Total	C	H	N	O	S	0	0	0
			9654	3113	4808	805	907	21			
1	C	606	Total	C	H	N	O	S	0	0	0
			9636	3107	4798	804	906	21			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P09960
A	-5	HIS	-	expression tag	UNP P09960
A	-4	HIS	-	expression tag	UNP P09960
A	-3	HIS	-	expression tag	UNP P09960
A	-2	HIS	-	expression tag	UNP P09960
A	-1	HIS	-	expression tag	UNP P09960
A	0	HIS	-	expression tag	UNP P09960
A	563	ALA	ARG	engineered mutation	UNP P09960
B	-6	MET	-	initiating methionine	UNP P09960
B	-5	HIS	-	expression tag	UNP P09960
B	-4	HIS	-	expression tag	UNP P09960
B	-3	HIS	-	expression tag	UNP P09960
B	-2	HIS	-	expression tag	UNP P09960
B	-1	HIS	-	expression tag	UNP P09960
B	0	HIS	-	expression tag	UNP P09960
B	563	ALA	ARG	engineered mutation	UNP P09960
C	-6	MET	-	initiating methionine	UNP P09960
C	-5	HIS	-	expression tag	UNP P09960
C	-4	HIS	-	expression tag	UNP P09960
C	-3	HIS	-	expression tag	UNP P09960
C	-2	HIS	-	expression tag	UNP P09960
C	-1	HIS	-	expression tag	UNP P09960
C	0	HIS	-	expression tag	UNP P09960

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Chain	Residue	Modelled	Actual	Comment	Reference
C	563	ALA	ARG	engineered mutation	UNP P09960

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	60	Total	O	0	0
			60	60		
3	B	46	Total	O	0	0
			46	46		
3	C	48	Total	O	0	0
			48	48		

- Molecule 1: Leukotriene A-4 hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.97Å 132.15Å 320.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.47 – 2.60 49.47 – 2.60	Depositor EDS
% Data completeness (in resolution range)	92.8 (49.47-2.60) 80.2 (49.47-2.60)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155)	Depositor
R, R_{free}	0.235 , 0.291 0.232 , 0.295	Depositor DCC
R_{free} test set	2679 reflections (4.84%)	DCC
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.825	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	29107	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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: ZN

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	0.26	0/4980	0.47	1/6770 (0.0%)
1	B	0.26	0/4970	0.44	0/6757
1	C	0.27	0/4962	0.45	0/6746
All	All	0.26	0/14912	0.45	1/20273 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	573	ASP	CB-CG-OD1	5.14	122.92	118.30

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	4849	4811	4811	29	0
1	B	4846	4808	4809	26	0
1	C	4838	4798	4798	34	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	60	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	46	0	0	1	0
3	C	48	0	0	2	0
All	All	14690	14417	14418	86	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 3.

All (86) 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:C:156:TYR:OH	1:C:171:SER:O	1.96	0.83
1:A:78:ARG:NH2	1:A:80:SER:O	2.26	0.69
1:B:335:GLU:OE2	1:B:338:ARG:NH1	2.26	0.67
1:A:148:ASP:O	1:A:149:THR:OG1	2.16	0.64
1:B:58:ASP:OD2	1:B:78:ARG:NH2	2.31	0.62
1:B:437:ASP:OD1	1:B:438:VAL:N	2.34	0.60
1:B:225:GLU:OE1	1:B:225:GLU:N	2.36	0.59
1:B:363:THR:O	1:B:385:LYS:NZ	2.31	0.58
1:B:175:ASP:HB3	1:B:190:LYS:HB2	1.87	0.57
1:B:285:GLY:O	1:C:518:LYS:NZ	2.39	0.56
1:C:335:GLU:OE2	1:C:338:ARG:NH1	2.38	0.54
1:A:128:HIS:ND1	3:A:1001:HOH:O	2.33	0.54
1:A:217:ARG:O	1:A:255:GLN:NE2	2.42	0.52
1:A:228:GLU:HB3	1:B:178:THR:HG21	1.90	0.52
1:C:116:GLN:OE1	1:C:596:HIS:NE2	2.40	0.52
1:C:279:THR:OG1	3:C:1001:HOH:O	2.19	0.51
1:A:509:ARG:O	1:A:510:ALA:HB3	2.10	0.51
1:C:153:LYS:NZ	1:C:305:LEU:O	2.44	0.51
1:A:67:ASN:ND2	3:A:1005:HOH:O	2.44	0.51
1:B:445:ASN:OD1	3:B:1001:HOH:O	2.19	0.50
1:A:353:VAL:O	1:A:357:GLY:N	2.44	0.50
1:A:149:THR:HG22	1:A:151:SER:H	1.77	0.49
1:C:551:ILE:N	1:C:552:PRO:HD2	2.28	0.49
1:A:510:ALA:HB1	1:A:511:PRO:CD	2.43	0.49
1:B:561:GLN:OE1	1:B:563:ALA:N	2.44	0.49
1:C:510:ALA:HB1	1:C:511:PRO:CD	2.43	0.48
1:A:237:THR:HG21	1:A:258:LEU:HD11	1.97	0.47
1:A:500:ASN:OD1	1:A:537:ARG:NH1	2.48	0.47
1:A:479:LYS:O	1:A:482:ASP:N	2.47	0.47
1:C:527:ASN:OD1	1:C:538:TRP:NE1	2.39	0.46
1:C:603:VAL:O	1:C:607:LEU:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:435:LYS:O	1:C:438:VAL:HG12	2.15	0.46
1:A:466:ASN:HA	1:A:469:ILE:HG22	1.97	0.46
1:C:313:HIS:ND1	1:C:421:THR:HG23	2.31	0.46
1:B:118:LEU:HB2	1:B:130:TYR:HB3	1.97	0.46
1:B:233:GLU:OE2	1:B:287:LYS:N	2.45	0.45
1:C:48:ASN:OD1	1:C:50:ARG:NH1	2.49	0.45
1:C:52:LEU:HD12	1:C:53:VAL:H	1.81	0.45
1:A:232:TYR:O	1:A:287:LYS:NZ	2.49	0.45
1:B:303:GLY:HA2	1:B:306:VAL:O	2.16	0.45
1:A:261:LEU:O	1:A:280:PRO:HG3	2.17	0.44
1:C:582:ASP:OD1	1:C:583:GLN:N	2.47	0.44
1:A:234:PHE:O	1:A:237:THR:HG23	2.17	0.44
1:A:335:GLU:OE2	1:A:338:ARG:NH1	2.51	0.44
1:B:153:LYS:NZ	1:B:305:LEU:O	2.51	0.44
1:C:511:PRO:HB3	1:C:544:GLN:O	2.18	0.44
1:B:301:TRP:O	1:B:305:LEU:HB2	2.18	0.44
1:A:263:PRO:HA	1:A:280:PRO:HG2	1.99	0.44
1:A:514:LEU:HD13	1:C:354:LYS:HD3	2.00	0.44
1:B:360:HIS:O	1:B:363:THR:HG22	2.17	0.44
1:A:223:GLU:O	1:A:227:VAL:HG23	2.18	0.43
1:C:309:LYS:HA	1:C:418:SER:HB3	2.00	0.43
1:C:512:LEU:HD11	1:C:517:ILE:CD1	2.48	0.43
1:B:183:ASP:OD1	1:B:185:SER:OG	2.34	0.43
1:C:237:THR:HG21	1:C:258:LEU:HD11	2.01	0.43
1:C:266:PRO:HA	1:C:563:ALA:HA	2.00	0.43
1:C:31:ARG:NH1	1:C:33:THR:OG1	2.51	0.43
1:A:337:PHE:O	1:A:341:ASN:ND2	2.47	0.43
1:B:272:ASN:HB2	1:B:275:LEU:O	2.19	0.43
1:B:31:ARG:NH2	1:B:107:GLU:OE2	2.48	0.42
1:B:513:PRO:HG2	1:B:516:HIS:CG	2.54	0.42
1:C:586:ARG:NH1	1:C:590:GLU:OE1	2.46	0.42
1:A:303:GLY:HA2	1:A:306:VAL:O	2.18	0.42
1:B:86:MET:HE1	1:B:104:ILE:HD13	2.00	0.42
1:B:568:ARG:HB3	1:B:569:PRO:HD3	2.00	0.42
1:C:121:GLU:N	1:C:121:GLU:OE1	2.46	0.42
1:C:266:PRO:O	1:C:267:TYR:CD1	2.72	0.42
1:C:509:ARG:O	1:C:510:ALA:HB3	2.20	0.42
1:B:315:TRP:HZ3	1:B:421:THR:OG1	2.02	0.42
1:A:11:SER:O	1:A:147:GLN:NE2	2.53	0.41
1:B:483:LEU:HD21	1:B:516:HIS:CG	2.55	0.41
1:C:432:PHE:O	1:C:435:LYS:N	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:LYS:HB3	3:C:1018:HOH:O	2.20	0.41
1:C:510:ALA:HB1	1:C:511:PRO:HD2	2.02	0.41
1:A:510:ALA:HB1	1:A:511:PRO:HD2	2.01	0.41
1:A:536:PHE:CZ	1:A:540:ARG:HD2	2.56	0.41
1:C:360:HIS:O	1:C:363:THR:OG1	2.37	0.41
1:C:20:HIS:HA	1:C:155:THR:O	2.21	0.41
1:B:251:TYR:HE2	1:B:254:GLY:O	2.04	0.41
1:C:336:LYS:HD3	1:C:336:LYS:H	1.85	0.41
1:A:148:ASP:HA	1:A:199:CYS:SG	2.61	0.40
1:A:150:PRO:HB2	1:A:308:ASN:O	2.21	0.40
1:A:433:LYS:O	1:A:436:VAL:HG23	2.21	0.40
1:C:245:GLU:HA	1:C:249:GLY:O	2.22	0.40
1:B:138:ILE:O	1:B:138:ILE:HG13	2.21	0.40
1:C:118:LEU:HB2	1:C:130:TYR:HB3	2.02	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	606/617 (98%)	583 (96%)	23 (4%)	0	100	100
1	B	605/617 (98%)	585 (97%)	19 (3%)	1 (0%)	51	76
1	C	604/617 (98%)	579 (96%)	24 (4%)	1 (0%)	51	76
All	All	1815/1851 (98%)	1747 (96%)	66 (4%)	2 (0%)	55	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	172	ALA
1	C	510	ALA

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	539/548 (98%)	538 (100%)	1 (0%)	94	99
1	B	538/548 (98%)	532 (99%)	6 (1%)	78	92
1	C	537/548 (98%)	535 (100%)	2 (0%)	93	98
All	All	1614/1644 (98%)	1605 (99%)	9 (1%)	89	96

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	LEU
1	B	126	LYS
1	B	175	ASP
1	B	315	TRP
1	B	356	PHE
1	B	514	LEU
1	B	577	PHE
1	C	336	LYS
1	C	512	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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	606/617 (98%)	0.28	7 (1%) 79 75	27, 51, 76, 98	0
1	B	607/617 (98%)	0.23	6 (0%) 82 79	31, 58, 82, 126	0
1	C	606/617 (98%)	0.26	7 (1%) 79 75	29, 57, 85, 137	0
All	All	1819/1851 (98%)	0.26	20 (1%) 80 77	27, 55, 82, 137	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ILE	5.8
1	A	584	ALA	4.2
1	A	510	ALA	3.6
1	C	483	LEU	3.3
1	B	112	SER	2.8
1	A	479	LYS	2.7
1	C	378	TYR	2.6
1	A	529	ILE	2.5
1	B	67	ASN	2.4
1	A	4	VAL	2.4
1	C	582	ASP	2.3
1	C	473	GLN	2.2
1	A	78	ARG	2.2
1	B	50	ARG	2.2
1	C	92	ILE	2.1
1	B	241	LEU	2.1
1	C	414	PHE	2.1
1	A	16	CYS	2.0
1	C	377	ALA	2.0
1	B	549	ASP	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	B	900	1/1	0.98	0.17	-1.11	46,46,46,46	0
2	ZN	A	900	1/1	0.97	0.19	-1.14	47,47,47,47	0
2	ZN	C	900	1/1	0.97	0.15	-1.25	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.